

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 28, 2005, 00:52:17 ; Search time 12680 Seconds

(Without alignments)
11662.880 Million cell updates/sec

Title: US-10-790-562-33

Perfect score: 3052

Sequence: 1 cgtgagtgatcttacc.....cgtggaagatcacagattgag 3052

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmb1:*

1: gb_da:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_seg:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3052	100.0	11570	14	AD5001 X02996 Adenovirus
2	3052	100.0	32802	6	CQ854906 Sequence
3	3052	100.0	33699	6	AX084506 Sequence
4	3052	100.0	34448	6	AX084507 Sequence
5	3052	100.0	35934	14	AY339865 Human ade
6	3052	100.0	35935	6	AR091513 Sequence
7	3052	100.0	35935	6	AR102226 Sequence
8	3052	100.0	35935	6	AR116313 Sequence
9	3052	100.0	35935	6	CQ854907 Sequence
10	3052	100.0	35935	6	AR230724 Sequence
11	3052	100.0	35935	6	AX451988 Sequence
12	3052	100.0	35935	6	AX683770 Sequence
13	3052	100.0	35935	14	ADRCOMGEN M73360 Mastadenov
14	3052	100.0	35978	6	AR403723 Sequence
15	3006.8	98.5	7090	6	AR310582 Sequence
16	3006.8	98.5	7090	6	AX150263 Sequence
17	2994	98.1	3408	6	AX770195 Sequence
18	2959.4	97.0	11152	6	BD268208 Adenoviru
19	2959.4	97.0	11152	6	AX356041 Sequence

20	2959.4	97.0	11152	6	BD021940 Packaging
21	2959.4	97.0	14455	6	BD268211 Adenoviru
22	2959.4	97.0	14455	6	AX356044 Sequence
23	2959.4	97.0	14455	6	BD021943 Packaging
24	2959	97.0	7607	6	BD268237 Adenoviru
25	2948	96.6	35937	6	AX770200 Sequence
26	2948	96.6	35937	14	ADRCG J01917 Adenovirus
27	2903.6	95.1	36001	14	AF534906 Human ade
28	2822	92.5	33592	6	AX084504 Sequence
29	2822	92.5	33988	6	AX084517 Sequence
30	2822	92.5	34341	6	AX084505 Sequence
31	2822	92.5	34737	6	AX084518 Sequence
32	2822	92.5	35724	6	AX084516 Sequence
33	2822	92.5	35871	6	AR403724 Sequence
34	2822	92.5	36114	6	AX084519 Sequence
35	2161	70.8	34303	6	AR091536 Sequence
36	2161	70.8	34303	6	AR102229 Sequence
37	2161	70.8	34303	6	AR230727 Sequence
38	2043	66.9	31976	6	CQ854905 Sequence
39	2041.4	66.9	31976	6	CQ854904 Sequence
40	1432.4	46.9	6575	6	AX449148 Sequence
41	1229	40.3	1802	6	AX817767 Sequence
42	1229	40.3	1802	6	AX838364 Sequence
43	1066.8	35.0	1356	6	I32051 Sequence 1
44	1066.8	35.0	1356	6	I38383 Sequence 1
45	1066.8	35.0	1356	6	I43358 Sequence 1

ALIGNMENTS

RESULT 1	AD5001	11570 bp	DNA	linear	VRL 09-SEP-2004
LOCUS	AD5001				
DEFINITION	Adenovirus type 5 left 32% of the genome (coordinates 0% to 32.39% as measured by <ad2>).				
ACCESSION	X02996 J01967 J01968 J01970 J01971 J01972 J01974 J01976 J01977				
VERSION	J01978 J01979 K00515 V00025 V00026 V00027 V00029				
KEYWORDS	X02996.1 GI:58484				
	alternate splicing; DNA polymerase; overlapping genes; polymerase; RNA polymerase III; terminal protein; terminal repeat; transfer RNA.				
SOURCE	Human adenovirus type 5				
ORGANISM	Human adenovirus type 5				
REFERENCE	1 (bases 1 to 194)				
AUTHORS	Steenbergh, P.H., Maat, J., van Ormondt, H. and Sussenbach, J.S.				
TITLE	The nucleotide sequence at the termini of adenovirus type 5 DNA				
JOURNAL	Nucleic Acids Res. 4 (12), 4371-4389 (1977)				
MEDLINE	78093872				
PUBMED	600799				
REFERENCE	2 (bases 1 to 1574)				
AUTHORS	Van Ormondt, H., Maat, J., De Waard, A. and Van der Eb, A.J.				
TITLE	The nucleotide sequence of the transforming HpaI-E fragment of adenovirus type 5 DNA				
JOURNAL	Gene 4 (4), 309-328 (1978)				
MEDLINE	79128735				
PUBMED	744489				
REFERENCE	3 (bases 1575 to 2809)				
AUTHORS	Maat, J. and Van Ormondt, H.				
TITLE	The nucleotide sequence of the transforming HindIII-G fragment of adenovirus type 5 DNA. The region between map positions 4.5 (HpaI site) and 8.0 (HindIII site)				
JOURNAL	Gene 6 (1), 75-90 (1979)				
MEDLINE	80004833				
PUBMED	478299				
REFERENCE	4				
AUTHORS	Perricaudet, M., Akusjärvi, G., Vartanen, A. and Pettersson, U.				
TITLE	Structure of two spliced mRNAs from the transforming region of human subgroup C adenoviruses				
JOURNAL	Nature 281 (5733), 694-696 (1979)				
MEDLINE	81012104				
PUBMED	551290				

REFERENCE 5 (bases 10524 to 10696)
 AUTHORS Thimmapaya,B., Jones,N. and Shenk,T.
 TITLE A mutation which alters initiation of transcription by RNA
 JOURNAL polymerase III on the Ad5 chromosome
 MEDLINE Cell 18 (4), 947-954 (1979)
 PUBMED 80090080

REFERENCE 6 (bases 1 to 6246)
 AUTHORS Broker,T.R.
 TITLE Appendix d: nucleotide sequences, transcription and translation
 analyses, and restriction endonuclease cleavage maps of group-c
 human adenoviruses
 JOURNAL (in) Toozee,J. (Ed.) ;
 MEDLINE DNA Tumor Viruses: 937-1002;
 PUBMED Cold Spring Harbor Laboratory (1980)
 7 (bases 2804 to 4125)
 REFERENCE Maat,J., van Beveren,C.P. and van Ormondt,H.
 AUTHORS The nucleotide sequence of adenovirus type 5 early region E1: the
 TITLE region between map positions 8.0 (HindIII site) and 11.8 (SmaI
 site)
 JOURNAL Gene 10 (1), 27-38 (1980)
 MEDLINE 81005097
 PUBMED 6250944

REFERENCE 8
 AUTHORS Pericaudet,M., Le Moulec,J.M. and Pettersson,U.
 TITLE Predicted structure of two adenovirus tumor antigens
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3778-3782 (1980)
 MEDLINE 81054654
 PUBMED 6253988

REFERENCE 9 (bases 1 to 4125)
 AUTHORS van Ormondt,H., Maat,J. and van Beveren,C.P.
 TITLE The nucleotide sequence of the transforming early region E1 of
 adenovirus type 5 DNA
 JOURNAL Gene 11 (3-4), 299-309 (1980)
 MEDLINE 81165537
 PUBMED 6260576

REFERENCE 10 (bases 10555 to 10733)
 AUTHORS Fowlkes,D.M. and Shenk,T.
 TITLE Transcriptional control regions of the adenovirus VAI RNA gene
 JOURNAL Cell 22 (2 Pt 2), 405-413 (1980)
 MEDLINE 81088343
 PUBMED 7448868

REFERENCE 11 (bases 1653 to 4043)
 AUTHORS Bos,J.L., Polder,L.J., Bernards,R., Schrier,P.I., van den
 Elsen,P.J., van der Eb,A.J. and van Ormondt,H.
 TITLE The 2.2 kb E1b mRNA of human Ad12 and Ad5 codes for two tumor
 antigens starting at different AUG triplets
 JOURNAL Cell 27 (1 Pt 2), 121-131 (1981)
 MEDLINE 82115327
 PUBMED 7326748

REFERENCE 12 (bases 4001 to 6246)
 AUTHORS van Beveren,C.P., Maat,J., Dekker,B.M. and van Ormondt,H.
 TITLE The nucleotide sequence of the gene for protein IVa2 and of the 5'
 leader segment of the major late mRNAs of adenovirus type 5
 JOURNAL Gene 16 (1-3), 179-189 (1981)
 MEDLINE 82211779
 PUBMED 7343420

REFERENCE 13 (bases 325 to 604)
 AUTHORS Hearing,P. and Shenk,T.
 TITLE Functional analysis of the nucleotide sequence surrounding the cap
 site for adenovirus type 5 region E1a messenger RNAs
 JOURNAL J. Mol. Biol. 167 (4), 809-823 (1983)
 MEDLINE 83268691
 PUBMED 6876165

REFERENCE 14 (bases 1 to 66)
 AUTHORS Negata,K., Guggenheim,R.A. and Hurwitz,J.
 TITLE Specific binding of a cellular DNA replication protein to the
 origin of replication of adenovirus DNA
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (20), 6177-6181 (1983)
 MEDLINE 84016017
 PUBMED 6336326

REFERENCE 15 (bases 6242 to 11570)

AUTHORS Dekker,B.M. and van Ormondt,H.
 TITLE The nucleotide sequence of fragment HindIII-C of human adenovirus
 JOURNAL type 5 DNA (map positions 17.1-31.7)
 MEDLINE Gene 27 (1), 115-120 (1984)
 PUBMED 84183604
 6325298

REFERENCE 16
 AUTHORS Downey,J.F., Ewelesgh,C.M., Branton,P.E. and Bayley,S.T.
 TITLE Peptide maps and N-terminal sequences of polypeptides from early
 JOURNAL region 1A of human adenovirus 5
 MEDLINE J. Virol. 50 (1), 30-37 (1984)
 PUBMED 84138826
 6699947

REMARK sites; cds start for E1a proteins
 COMMENT sites; splice sites in E1a 13S mRNA
 sites; splice sites and termini for E1b mRNAs
 Notes on the presentation of ADENO in the EMBL data library: The
 genetic map of Adeno is customarily presented from left to right,
 the 0% position being left and the 100% position being right. The
 two strands of Adeno are normally represented like this: r-strand:
 3'-----5'
 1-strand: 5'-----3'

0% 100%
 This often causes confusion because the generally accepted way to
 represent DNA molecules is:
 5'-----3'
 3'-----5'

Here Adeno virus sequences are always given in 5' to 3' direction
 and the sequence of the 1-strand is displayed irrespective of the
 direction the viral transcription takes.
 This sequence corresponds to bases 1 to 11560 of <ad3>, which serve
 as some basis for the annotation of sites. the differences between
 <ad2> and <ad5> are too many to report herein, however a printout
 of those is available upon request from genbank. the map
 coordinates in the sites presume 360 bases per map unit. although
 there are approximately 115 sequence differences between the two
 strains over this region, no site difference exceeds 0.02% by this
 calculation.
 the sequence represents the early mrna transcripts e1a and e1b and
 the intermediate mrna transcript ix, all of which are transcribed
 rightwardly off the r-strand; the 1va2 and e2b mnas which are
 transcribed leftwardly off the 1-strand (indicated by '(c)' and
 'comp strand' below); and the 5' end of the 28 kb major late mrna.
 the cap sites and possible promoter sequences for these are
 summarized in the following table:
 mrna cap site possible promoter region -----
 ----- e1a 499
 taccataa at bases 468-475 [6] e1b 3582
 taccataa at bases 1672-1678[6] ix 5838 +/- 2 (c)
 taccataa at bases 3551-3557 [6] 1va2
 taccataa at bases 5979-5974 on the comp strand (10)
 major 6049 taccataa at bases 6018-6024 [10] as
 with ad2, not all the transcripts from this region have been
 characterized at the sequence level. the nine proteins given in
 features table below are not the only possible gene products (see
 the main adenovirus 2 entry).
 large amounts of small mnas are produced from the vai and vaii
 genes late in development for unknown reasons. [5] and [6]
 demonstrate that vai gene activity influences vaii expression; that
 the 5' flank affects the start site of the rna but that an
 intragenic promoter (bases 10626 to 10690 below) determines whether
 the rna is actually produced; and that there is striking similarity
 between this rna and rta.

FEATURES
 source
 Location/Qualifiers
 1. 11570
 /organism="Human adenovirus type 5"
 /mol_type="genomic DNA"
 /db_xref="taxon:28285"
 precursor_RNA 499..1632
 mRNA /note="primary transcript of E1a region"
 join(499..1112,1229..1632)
 /note="mrna 1 (part 1)"

```
mRNA
CD8
Join(499..974,1229..1632)
/nc="mRNA 2 (part 1)"
Join(560..1112,1229..1545)
/nc="unnamed protein product; B1a protein from 13s mrna
(32k,regulation and transformation)"
/codon_start=1
/protein_id="CABA0663.1"
/db_xref="GI:4584382"
/db_xref="GO:PO3255"
/translation="MRHICGVITEEMASLSDQLEBIYADNLPPSPHPEPTLH
EYLDVTPADPEBAVSQIPDSVLMVAOEGDILTFPPASPPSPHLSRQEPD
EQALGVSMPNVYPRVIDLCHGASPPSDDBEBSEBRYLDVYRHHGCRSCYH
RRTGDDPIMCSLCYMRTCGMFVTSVSEPEPEPEPEPARPRKMAPIILRPT
Query Match 100.0%; Score 3052; DB 14; Length 11570;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGTAGTATATTTTATACCCGCTGAGTTCTCAAGAGGCCACTTGAGTCCAGCGAGT 60
D 459 CGGTAGTATATTTTATACCCGCTGAGTTCTCAAGAGGCCACTTGAGTCCAGCGAGT 518
QY 61 AGAGTTTCTCCTCGAGCCGCTCGACACCGGGAGTGAATGACATATTTATCTGCC 120
D 519 AGAGTTTCTCCTCGAGCCGCTCGACACCGGGAGTGAATGACATATTTATCTGCC 578
QY 121 ACGAGAGTGTATATACCGAAGAAATGGCCGCTGTTTGAACAGCTGATCGAAGAG 180
D 579 ACGAGAGTGTATATACCGAAGAAATGGCCGCTGTTTGAACAGCTGATCGAAGAG 638
QY 181 TACTGGCTGATATCTTCCACTCTTACCCATTTTGAACACCTTACCTTACGACACT 240
D 639 TACTGGCTGATATCTTCCACTCTTACCCATTTTGAACACCTTACCTTACGACACT 698
QY 241 ATGATTTAGACGTACGGCCCGGAGATGCCAAGAGAGCGGTTTCGACATTTTTC 300
D 699 ATGATTTAGACGTACGGCCCGGAGATGCCAAGAGAGCGGTTTCGACATTTTTC 758
QY 301 CCGACTCTGATATGTTGGCGGTGACGAGAGGATTTGACTTACTCTTCCGCGGCGC 360
D 759 CCGACTCTGATATGTTGGCGGTGACGAGAGGATTTGACTTACTCTTCCGCGGCGC 818
QY 361 CCGGTTCTCGGAGCCGCTTACCTTTCGCGGACCCGAGACGCGGAGAGAGCTT 420
D 819 CCGGTTCTCGGAGCCGCTTACCTTTCGCGGACCCGAGACGCGGAGAGAGCTT 878
QY 421 TGGGTCGGGTTTCTATGCAAACTGTACCGGAGGTGATGATCTTACCTGCGACGAG 480
D 879 TGGGTCGGGTTTCTATGCAAACTGTACCGGAGGTGATGATCTTACCTGCGACGAG 938
QY 481 CTGGCTTTCCACCCAGTACGACGAGATGAAAGAGGTGAGAGTGTGTAGATTATG 540
D 939 CTGGCTTTCCACCCAGTACGACGAGATGAAAGAGGTGAGAGTGTGTAGATTATG 998
QY 541 TGGAGCACCCCGGACAGGTTGCAAGTCTTGTCAATTACCGAGAGAAATCGGGGAGC 600
D 999 TGGAGCACCCCGGACAGGTTGCAAGTCTTGTCAATTACCGAGAGAAATCGGGGAGC 1058
QY 601 CAGATTTATGTGTGCTTGTGATATAGAGACCTGAGCATGTTGTCTACAGTAAGT 660
D 1059 CAGATTTATGTGTGCTTGTGATATAGAGACCTGAGCATGTTGTCTACAGTAAGT 1118
QY 661 GAAATTTATGGGAGTGGGTGATAGAGTGTGGTGTGGTAAATTTTTTTTTTAAT 720
D 1119 GAAATTTATGGGAGTGGGTGATAGAGTGTGGTGTGGTAAATTTTTTTTTTAAT 1178
QY 721 TTTTACAGTTTGTGCTTTAAAGAAATTTGTATTGTGATTTTTTTAAAGGTCTGTGTC 780
D 1179 TTTTACAGTTTGTGCTTTAAAGAAATTTGTATTGTGATTTTTTTAAAGGTCTGTGTC 1238
QY 781 TGAACCTGAGCTGAGCCGAGCAAGACCGAGCTGCAAGACTCCGCGGTCTAA 840
```

```
D 1239 TGAACCTGAGCTGAGCCGAGCAAGACCGAGCTGCAAGACTCCGCGGTCTAA 1298
QY 841 AATGGCCCTGCTATTCCTGAGACGCCGACATCACTGTGTCTAGAGAAATGCAATAGTAG 900
D 1299 AATGGCCCTGCTATTCCTGAGACGCCGACATCACTGTGTCTAGAGAAATGCAATAGTAG 1358
QY 901 TACGGAATGCTGATCTCCGCTCTTTTAAACACCTCCCTGAGATACACCCGCTGCTCC 960
D 1359 TACGGAATGCTGATCTCCGCTCTTTTAAACACCTCCCTGAGATACACCCGCTGCTCC 1418
QY 961 GCTGTGCCCATTTAAACAGTGGCCGAGAGTGTGGGCGTGGCAGGCTGTGGAATG 1020
D 1419 GCTGTGCCCATTTAAACAGTGGCCGAGAGTGTGGGCGTGGCAGGCTGTGGAATG 1478
QY 1021 TATGAGAGCTTGTCTTAAAGAGCTGGGCAACTTTGGAATTGAGCTGTAACGCCCCAG 1080
D 1479 TATGAGAGCTTGTCTTAAAGAGCTGGGCAACTTTGGAATTGAGCTGTAACGCCCCAG 1538
QY 1081 GCCATAAGTGTAAACCTGTGATTTGCTGTGTGTAAAGCTTGTGTTTGTGTAATAGT 1140
D 1539 GCCATAAGTGTAAACCTGTGATTTGCTGTGTGTAAAGCTTGTGTTTGTGTAATAGT 1598
QY 1141 TGATGTAAATTTAAAGGTGATATGTTTAACTTGCAATGCGGTGTTAAATGAGGCG 1200
D 1599 TGATGTAAATTTAAAGGTGATATGTTTAACTTGCAATGCGGTGTTAAATGAGGCG 1658
QY 1201 GGGGCTTAAAGGTATATATGCGCGGTGATCTTGTGTTAATCTGACCTCATGGA 1260
D 1659 GGGGCTTAAAGGTATATATGCGCGGTGATCTTGTGTTAATCTGACCTCATGGA 1718
QY 1261 GGCCTGGAGATGTTTGAAGATTTTCTGCTGTGCTGTAATCTTGTAAGACAGACTCTAA 1320
D 1719 GGCCTGGAGATGTTTGAAGATTTTCTGCTGTGCTGTAATCTTGTAAGACAGACTCTAA 1778
QY 1321 CAGTACCTCTTGTGTTGAGAGTTTCTGTGGGCGTCAATCCAGCAAGATTAGCTGAG 1380
D 1779 CAGTACCTCTTGTGTTGAGAGTTTCTGTGGGCGTCAATCCAGCAAGATTAGCTGAG 1838
QY 1381 AATTAAGAGATTTACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1440
D 1839 AATTAAGAGATTTACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1898
QY 1441 TGATTTCTTTGAATCTGTGTGACACGAGCGCTTTTCCAGAGAGAGTCAATCAAGACTTTCGA 1500
D 1899 TGATTTCTTTGAATCTGTGTGACACGAGCGCTTTTCCAGAGAGAGTCAATCAAGACTTTCGA 1958
QY 1501 TTTTTCACACCGGGGCGCGCTGCGCTGTGTGTTTGTAGTTTAAAGATTA 1560
D 1959 TTTTTCACACCGGGGCGCGCTGCGCTGTGTGTTTGTAGTTTAAAGATTA 2018
QY 1561 ATGAGCGGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTCTGCGCATGACTT 1620
D 2019 ATGAGCGGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTCTGCGCATGACTT 2078
QY 1621 GTGAGAGCGGTTGTGAGACACAAAGATTCGCTGTCTACTGTGTCTTCCGTCGCCCGGCGC 1680
D 2079 GTGAGAGCGGTTGTGAGACACAAAGATTCGCTGTCTACTGTGTCTTCCGTCGCCCGGCGC 2138
QY 1681 GATTAATCCGACGAGAGAGACGACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
D 2139 GATTAATCCGACGAGAGAGAGACGACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2198
QY 1741 GCAGAGCCATGGAACCCGAGAGCGGAGCTGTGACCTTGGGATGAAATGTTTGAACAGTGTG 1800
D 2199 GCAGAGCCATGGAACCCGAGAGCGGAGCTGTGACCTTGGGATGAAATGTTTGAACAGTGTG 2258
QY 1801 GCTGAATCTGTATCCAGAACTGAGACGATTTTGAATTAAGAGATGCGCAGAGGCGCTA 1860
D 2259 GCTGAATCTGTATCCAGAACTGAGACGATTTTGAATTAAGAGATGCGCAGAGGCGCTA 2318
QY 1861 AAGGGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
D 2319 AAGGGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2378
```

QY 1921 TTTAGCTTAATGACACGACACCGTCTGAGTATTAATCTTTCAACAGATGAGATAT 1980
DB 2379 TTTAGCTTAATGACACGACACCGTCTGAGTATTAATCTTTCAACAGATGAGATAT 2438
QY 1981 TGCCTAATGACTTGATCTGCTGGCGAGAGATATTCATAGAGACAGCTGACCTTAC 2040
DB 2439 TGCCTAATGACTTGATCTGCTGGCGAGAGATATTCATAGAGACAGCTGACCTTAC 2498
QY 2041 TGGCTGCAGCCAGGGGATGATTTTGGAGAGGCTATTAGGGTATATGCAAGGTGGCACTT 2100
DB 2499 TGGCTGCAGCCAGGGGATGATTTTGGAGAGGCTATTAGGGTATATGCAAGGTGGCACTT 2558
QY 2101 AGGCGAGATTGCAATGACAGATGACGAACTTGTAATATCAGGAATGTGTGCTACAT 2160
DB 2559 AGGCGAGATTGCAATGACAGATGACGAACTTGTAATATCAGGAATGTGTGCTACAT 2618
QY 2161 TCTGGGAAACGGGGCCGAGGTGAGATAGATACGAGATAGGGTGGCTTTAGATGTAGC 2220
DB 2619 TCTGGGAAACGGGGCCGAGGTGAGATAGATACGAGATAGGGTGGCTTTAGATGTAGC 2678
QY 2221 ATGATTAATATGTGGCCCGGGGCTGCTTGGCATGACGCGGGTGTATTATGATGTAAAG 2280
DB 2679 ATGATTAATATGTGGCCCGGGGCTGCTTGGCATGACGCGGGTGTATTATGATGTAAAG 2738
QY 2281 TTTACTGGCCCAATTTTAGCGGTACGGTTTCTGGCCCAATPCCAACTTATCCTACAC 2340
DB 2739 TTTACTGGCCCAATTTTAGCGGTACGGTTTCTGGCCCAATPCCAACTTATCCTACAC 2798
QY 2341 GGTGTAAAGCTTCTATGGGTTTAAACATACCTGTGTGAAGCCTGGAACGATGTAAAGGTT 2400
DB 2799 GGTGTAAAGCTTCTATGGGTTTAAACATACCTGTGTGAAGCCTGGAACGATGTAAAGGTT 2858
QY 2401 CGGGGCTGTGGCTTTTACTGCTGCTGGAAGGGGGTGTGTGCGCCCAAAAGAGGGCT 2460
DB 2859 CGGGGCTGTGGCTTTTACTGCTGCTGGAAGGGGGTGTGTGCGCCCAAAAGAGGGCT 2918
QY 2461 TCAATTTAAGAAATGCTCTTTGAAAGGTGACTTTGGGTATCTGTCTGAGGGTAACTCC 2520
DB 2919 TCAATTTAAGAAATGCTCTTTGAAAGGTGACTTTGGGTATCTGTCTGAGGGTAACTCC 2978
QY 2521 AGGGTGCAGCAATGTGGCTCTCGACTGTGGTCTTCACTGATGTAAGAAAGCTGGCT 2580
DB 2979 AGGGTGCAGCAATGTGGCTCTCGACTGTGGTCTTCACTGATGTAAGAAAGCTGGCT 3038
QY 2581 GTGATTAAGCAATACTGATGTGTGCAACTGCGAGACAGGGGCTCTCAATGTCTGACC 2640
DB 3039 GTGATTAAGCAATACTGATGTGTGCAACTGCGAGACAGGGGCTCTCAATGTCTGACC 3098
QY 2641 TGTCTCGACGGCACTGCTCACTGCTGAGACCAATTCACGTAGCCAGCCCTCTCGCAG 2700
DB 3099 TGTCTCGACGGCACTGCTCACTGCTGAGACCAATTCACGTAGCCAGCCCTCTCGCAG 3158
QY 2701 GCCTGGCCAGTGTGTTGAGCATTAACATACCTGCTGCTGCTTGGGTTGAGCAGG 2760
DB 3159 GCCTGGCCAGTGTGTTGAGCATTAACATACCTGCTGCTGCTTGGGTTGAGCAGG 3218
QY 2761 AGGGGGGGTGTCCCACTTAACATGCAATTGAGTCACTAAGATTTGCTTGAAGCC 2820
DB 3219 AGGGGGGGTGTCCCACTTAACATGCAATTGAGTCACTAAGATTTGCTTGAAGCC 3278
QY 2821 GAGAGCATGTCCTCAAGGTGAACTGAAACGGGGTGTGTCATGACATGAAATCTGAAAG 2880
DB 3279 GAGAGCATGTCCTCAAGGTGAACTGAAACGGGGTGTGTCATGACATGAAATCTGAAAG 3338
QY 2881 GTGCTGAGTACGATGAGACCCGCAACAGGTGCAAGCCCTGCGAGTGTGCGGGTAAACAT 2940
DB 3339 GTGCTGAGTACGATGAGACCCGCAACAGGTGCAAGCCCTGCGAGTGTGCGGGTAAACAT 3398
QY 2941 ATTGAGAAACGAGCTGTGATGCTGTGATGATGACCGAGAGGCTGAGAGCCGATCTGCTG 3000
DB 3399 ATTGAGAAACGAGCTGTGATGCTGTGATGATGACCGAGAGGCTGAGAGCCGATCTGCTG 3458

QY 3001 CTGGCTGACCCCGCGGTGAGTTTGCTTACGATGAGATGACAGATTGAG 3052
DB 3459 CTGGCTGACCCCGCGGTGAGTTTGCTTACGATGAGATGACAGATTGAG 3510

RESULT 2
COB54906 32802 bp DNA linear PAT 23-AUG-2004
LOCUS Sequence 3 from Patent WO2004066947.
DEFINITION
VERSION COB54906 GI:51510466
KEYWORDS
SOURCE
ORGANISM
unidentified adenovirus
unidentified adenovirus
viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

REFERENCE
1 Hu, F. and Wu, B.
Therapy for primary and metastatic cancers
Patent: WO 2004066947-A 3 12-AUG-2004;
JOURNAL Shanghai Sunway Biotech Co Ltd (CN)

FEATURES
source
1..32802
/organism="unidentified adenovirus"
/mol_type="unassigned DNA"
/db_xref="taxon:10535"

ORIGIN

Query Match 100.0%; Score 3052; DB 6; Length 32802;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTGTAGTATTAATACCGGTGAGTTTCTCAAGAGGCACTCTTGAAGTCCAGCAGT 60
DB 459 CGTGTAGTATTAATACCGGTGAGTTTCTCAAGAGGCACTCTTGAAGTCCAGCAGT 518
QY 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAATGAGACATATTATCTGCC 120
DB 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAATGAGACATATTATCTGCC 578
QY 121 ACGGAGGTGTTATACCGAAGAAATGGCCGCGCACTCTTTGGACCACTGATCGAAGAG 180
DB 579 ACGGAGGTGTTATACCGAAGAAATGGCCGCGCACTCTTTGGACCACTGATCGAAGAG 638
QY 181 TACTGGCTGATTAATCTTCCACTCTCTAGCCATTGTAACCACTTACCTTACGAACTGT 240
DB 639 TACTGGCTGATTAATCTTCCACTCTCTAGCCATTGTAACCACTTACCTTACGAACTGT 698
QY 181 TACTGGCTGATTAATCTTCCACTCTCTAGCCATTGTAACCACTTACCTTACGAACTGT 240
DB 639 TACTGGCTGATTAATCTTCCACTCTCTAGCCATTGTAACCACTTACCTTACGAACTGT 698
QY 241 ATGATTTAAGCTGACGGCCCGCAAGATCCCAAGAGGCGGTTTCGCAATTTTTC 300
DB 699 ATGATTTAAGCTGACGGCCCGCAAGATCCCAAGAGGCGGTTTCGCAATTTTTC 758
QY 301 CCGACTCTGTAATTTGGCGGTGAGAGAGGATTAATCACTTATCCGCGGCGC 360
DB 759 CCGACTCTGTAATTTGGCGGTGAGAGAGGATTAATCACTTATCCGCGGCGC 818
QY 361 CCGGTTTCTCGAGAGCCGCTCACTTCCCGGAGCCCGAGACCCGAGAGAGAGGCT 420
DB 819 CCGGTTTCTCGAGAGCCGCTCACTTCCCGGAGCCCGAGACCCGAGAGAGAGGCT 878
QY 421 TGGGTCCGGTTTCTAGCCAAACCTTGTACCGAGGTGATGATCTTACCTGCCAGAG 480
DB 879 TGGGTCCGGTTTCTAGCCAAACCTTGTACCGAGGTGATGATCTTACCTGCCAGAG 938
QY 481 CTGGCTTTCAACCGAGTGAAGAGATGAAGAGGTGAGGATTTGTCTAATATTATG 540
DB 939 CTGGCTTTCAACCGAGTGAAGAGATGAAGAGGTGAGGATTTGTCTAATATTATG 998
QY 541 TGGAGACACCCGGGACGAGTTGACAGTCTTGTCTTATCAACCGAGGAAATACGGGGAGCC 600
DB 999 TGGAGACACCCGGGACGAGTTGACAGTCTTGTCTTATCAACCGAGGAAATACGGGGAGCC 1058
QY 601 CAGATTAATGTGTGCTTGTCTTATGAGAGCCTGTGATGTTGTCTTACAGTAAGT 660

Dh 1059 CAGATATTATGCTTCGCTTTCCTATATGAGACCTGTGSCATGTTTGTCTACAGTAAGT 1118
Qy 661 GAAATTTATGGGCAAGTGGGTGATAGAGTGTGGGTTTGTGTGTAATTTTTTTTTTAT 720
Db 1119 GAAATTTATGGGCAAGTGGGTGATAGAGTGTGGGTTTGTGTGTAATTTTTTTTTTAT 1178
Qy 721 TTTTACAGTTTGTGCTTAAAGAAATTTTGTATGTAATTTTTTTTAAAGGTCCTGTGTC 780
Db 1179 TTTTACAGTTTGTGCTTAAAGAAATTTTGTATGTAATTTTTTTTAAAGGTCCTGTGTC 1238
Qy 781 TGAACCTGAGCCTGAGCCGAGCCGAGAACCGGAGCCTCAAGACCTACCCGCGCTCA 840
Db 1239 TGAACCTGAGCCTGAGCCGAGCCGAGAACCGGAGCCTCAAGACCTACCCGCGCTCA 1298
Qy 841 AATGGCGCTGCTATCTCTGAGACGCGCCGACATCACCTGTGTCTAGAGAAATCAATAGTAG 900
Db 1299 AATGGCGCTGCTATCTCTGAGACGCGCCGACATCACCTGTGTCTAGAGAAATCAATAGTAG 1358
Qy 901 TAGCGATGAGCTGTGATCTCGGTCCTTCTTACACACCTCTGAGATACACCGGTCCTCC 960
Db 1359 TAGCGATGAGCTGTGATCTCGGTCCTTCTTACACACCTCTGAGATACACCGGTCCTCC 1418
Qy 961 GCTGTGCCCATTTAAACCAAGTTCGCTGAGAGTGTGGGCGTGCSCAGGCTGTGAAATG 1020
Db 1419 GCTGTGCCCATTTAAACCAAGTTCGCTGAGAGTGTGGGCGTGCSCAGGCTGTGAAATG 1478
Qy 1021 TATGAGAGACTTGTCTTAAACGAGCCTGGGCAACCTTTGAGCTTGAAGCTGTAACCGCCAG 1080
Db 1479 TATGAGAGACTTGTCTTAAACGAGCCTGGGCAACCTTTGAGCTTGAAGCTGTAACCGCCAG 1538
Qy 1081 GCCATTAAGCTTAAACCTGTGATTCGCTGTGTGTGTAACGCTTGTGTGTGTAATGAGT 1140
Db 1539 GCCATTAAGCTTAAACCTGTGATTCGCTGTGTGTGTAACGCTTGTGTGTGTAATGAGT 1598
Qy 1141 TGATGTAAGTTTAAAGAGGTGAGATATATGTTTAACTTGCATGGCGGTGTAATGGGCG 1200
Db 1599 TGATGTAAGTTTAAAGAGGTGAGATATATGTTTAACTTGCATGGCGGTGTAATGGGCG 1658
Qy 1201 GGGGCTTAAAGGTAATATATGCGCGCGTGGCTAATCTTGGTAACTGTGACCTCATGGA 1260
Db 1659 GGGGCTTAAAGGTAATATATGCGCGCGTGGCTAATCTTGGTAACTGTGACCTCATGGA 1718
Qy 1261 GGGCTTGGAGAGTGTGGAAGATTTTTCGCTGTGTGTGTAACCTGCTGGAACAGAGCTCAA 1320
Db 1719 GGGCTTGGAGAGTGTGGAAGATTTTTCGCTGTGTGTGTAACCTGCTGGAACAGAGCTCAA 1778
Qy 1321 CAGTACCTCTTGTGTTTGAAGAGTTCCTGTGGGCTCATCCAGGCAAGTAACTGTGAG 1380
Db 1779 CAGTACCTCTTGTGTTTGAAGAGTTCCTGTGGGCTCATCCAGGCAAGTAACTGTGAG 1838
Qy 1381 AATTAAAGAGATTAACAAGTGGGAATTTGAAGAGCTTTGAAATCTCTGTGTGAGACTGTT 1440
Db 1839 AATTAAAGAGATTAACAAGTGGGAATTTGAAGAGCTTTGAAATCTCTGTGTGAGACTGTT 1898
Qy 1441 TGATTTCTTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCAATCAAGACTTTGGA 1500
Db 1899 TGATTTCTTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCAATCAAGACTTTGGA 1958
Qy 1501 TTTTTCACACCGGGGCGCGCTGCGGCTGTGTTTGTGTTTGAAGTTTAAAGGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGGCTGTGTTTGTGTTTGAAGTTTAAAGGATTA 2018
Qy 1561 ATGAGAGCAAGAAACCATCTGAGCGGGGGTACCTGCTGGAATTTTCTGGCCATGATCT 1620
Db 2019 ATGAGAGCAAGAAACCATCTGAGCGGGGGTACCTGCTGGAATTTTCTGGCCATGATCT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACACAAGAAATCCGCTGTACTATGTGTCTTCCGCGCCGCGG 1680
Db 2079 GTGAGAGCGGTTGTGAGACACAAGAAATCCGCTGTACTATGTGTCTTCCGCGCGCGG 2138
Qy 1681 GATATATACCGAGAGAGAGACAGACAGACAGAGAGAAACCAAGGCGCGCGGCGAGGA 1740
Db 2139 GATATATACCGAGAGAGAGAGACAGACAGAGAGAAACCAAGGCGCGCGGCGAGGA 2198

Qy 1741 GCAGAGCCCATGGAACCCGAGAGCCGCGCTGTGACCTCTCGGAAATGATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCCGCGCTGTGACCTCTCGGAAATGATGTTGTACAGGTG 2258
Qy 1801 GCTAACCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGGATGGGCGAGGCGCTA 1860
Db 2259 GCTAACCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGGATGGGCGAGGCGCTA 2318
Qy 1861 AAGGGGGTAAAGAGAGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT 1920
Db 2319 AAGGGGGTAAAGAGAGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT 2378
Qy 1921 TTTAGCTTAATGACCAACACCGTCTGAGTATTAATCTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACCAACACCGTCTGAGTATTAATCTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGGGCTAATGAGCTTGAATCTGTGGCGAGAAATTCATAGAGCAAGCTGACCACTTAC 2040
Db 2439 TGGGCTAATGAGCTTGAATCTGTGGCGAGAAATTCATAGAGCAAGCTGACCACTTAC 2498
Qy 2041 TGGCTGAGCCGAGGAGATGATTTTGAAGAGGCTATTAGGTAATGCAAAAGTGGCACTT 2100
Db 2499 TGGCTGAGCCGAGGAGATGATTTTGAAGAGGCTATTAGGTAATGCAAAAGTGGCACTT 2558
Qy 2101 AGCCCAAGTTGCAAGTACAGATCAGCAACTTGTAAATATCAGAAATTTGTCTACATT 2160
Db 2559 AGCCCAAGTTGCAAGTACAGATCAGCAACTTGTAAATATCAGAAATTTGTCTACATT 2618
Qy 2161 TCTGGGAAACGGGGCGAGAGTGAATGATACGAGATAGGGGCTTATGATGATAGC 2220
Db 2619 TCTGGGAAACGGGGCGAGAGTGAATGATACGAGATAGGGGCTTATGATGATAGC 2678
Qy 2221 ATGATTAATATGTCGCGGGGGTCTTGGCATGGAACGGGGTGTATTAATGATGATAGG 2280
Db 2679 ATGATTAATATGTCGCGGGGGTCTTGGCATGGAACGGGGTGTATTAATGATGATAGG 2738
Qy 2281 TTTACTGGCCCAATTTTACGGGTGACGGTTTTCTGTGCAATACCAACCTTATCTTACAC 2340
Db 2739 TTTACTGGCCCAATTTTACGGGTGACGGTTTTCTGTGCAATACCAACCTTATCTTACAC 2798
Qy 2341 GGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGTGGAAGCTGGAACGATTAAGGTT 2400
Db 2799 GGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGTGGAAGCTGGAACGATTAAGGTT 2858
Qy 2401 CGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT 2460
Db 2859 CGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTTTGAAGGTTTACTTGGGTAATCTGTCTGAGGGTAACTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTTTGAAGGTTTACTTGGGTAATCTGTCTGAGGGTAACTCC 2978
Qy 2521 AAGGTGGGCAACAATGTGGGCTCCGACTGTGGTGTCTCAATGCTAGGAAAGGGTGGCT 2580
Db 2979 AAGGTGGGCAACAATGTGGGCTCCGACTGTGGTGTCTCAATGCTAGGAAAGGGTGGCT 3038
Qy 2581 GTGATTAAGCATTAACATGTATGTGCAACTGCGAGAGACAGGGGCTCTCAGATCTGACC 2640
Db 3039 GTGATTAAGCATTAACATGTATGTGCAACTGCGAGAGACAGGGGCTCTCAGATCTGACC 3098
Qy 2641 TGTCTGGAACGGCAACTGTCACTGTCTGTAAGCACTTACGTAAGCAAGCACTCTGCAAG 2700
Db 3099 TGTCTGGAACGGCAACTGTCACTGTCTGTAAGCACTTACGTAAGCAAGCACTCTGCAAG 3158
Qy 2701 GCTTGGCAAGTGTGTGAGCATTAACATCTGACCGGCTGTTCTTGCATTTGGGTTAACGG 2760
Db 3159 GCTTGGCAAGTGTGTGAGCATTAACATCTGACCGGCTGTTCTTGCATTTGGGTTAACGG 3218
Qy 2761 AGGGGGGTGTTCCTTACCTTACCAATGCAATTTGAGTCACTAAGATATTTGCTGAGCCC 2820
Db 3219 AGGGGGGTGTTCCTTACCTTACCAATGCAATTTGAGTCACTAAGATATTTGCTGAGCCC 3278

QY 1561 ATGAGCGAGAGAAACCCATCTGAGCGGGGTACTGCTGATTTTCTGCGCATGACATCT 1620
 DB 2019 ATGAGCGAGAGAAACCCATCTGAGCGGGGTACTGCTGATTTTCTGCGCATGACATCT 2078
 QY 1521 GTGAGAGCGGTTGTGAGACAAGAAATGCGCTGCTACTGTGTCTTCCGTCGCGCCGCGC 1680
 DB 2079 GTGAGAGCGGTTGTGAGACAAGAAATGCGCTGCTACTGTGTCTTCCGTCGCGCCGCGC 2138
 QY 1681 GATTAATACCGAGCGAGGAGCAGCAGCAGCAGAGAGAGAACCCAGCGCGCGCGCAGAGA 1740
 DB 2139 GATTAATACCGAGCGAGGAGCAGCAGCAGCAGAGAGAGAACCCAGCGCGCGCGCAGAGA 2198
 QY 1741 GCAGAGCCCATGGAACCCGAGAGCCGCGCTTGACCTCTCGGAAATGATGTTGTAACAGGTG 1800
 DB 2199 GCAGAGCCCATGGAACCCGAGAGCCGCGCTTGACCTCTCGGAAATGATGTTGTAACAGGTG 2258
 QY 1801 GCTGAACGTATCCAGAACCTGAGACCGATTTTGAACAATTACAGAGAGTGGCGAGGCGCTA 1860
 DB 2259 GCTGAACGTATCCAGAACCTGAGACCGATTTTGAACAATTACAGAGAGTGGCGAGGCGCTA 2318
 QY 1861 AAGCGGGTAAAGAGGAGCGCGGGGCTTGTAGGCTACAGAGAGGCTTAGAGATCTAGCT 1920
 DB 2319 AAGCGGGTAAAGAGGAGCGCGGGGCTTGTAGGCTACAGAGAGGCTTAGAGATCTAGCT 2378
 QY 1921 TTTAGCTTAATGACCAAGACACCGTCTGAGTGTATTAATCTTTTCAACAGATCAAGATTAAT 1980
 DB 2379 TTTAGCTTAATGACCAAGACACCGTCTGAGTGTATTAATCTTTTCAACAGATCAAGATTAAT 2438
 QY 1981 TGGGCTAATGAGCTTGAATCTGCTGGCGAGAAATTCCTCATAGAGCGCTAGACCACTTAC 2040
 DB 2439 TGGGCTAATGAGCTTGAATCTGCTGGCGAGAAATTCCTCATAGAGCGCTAGACCACTTAC 2498
 QY 2041 TGGCTGACGCGGAGGATGATTTTGTAGAGGCTATTAGGATATATGCAAGATGAGCACTT 2100
 DB 2499 TGGCTGACGCGGAGGATGATTTTGTAGAGGCTATTAGGATATATGCAAGATGAGCACTT 2558
 QY 2101 AGGCGAAGTTGCAAGTACAGATCAGCAACTTGTAAATATCAGAAATTTGTTGCTACAT 2160
 DB 2559 AGGCGAAGTTGCAAGTACAGATCAGCAACTTGTAAATATCAGAAATTTGTTGCTACAT 2618
 QY 2161 TCTGGGAACGGGGCGAGGTGAGATAGTACGAGGATAGGCTTGAATGATGATG 2220
 DB 2619 TCTGGGAACGGGGCGAGGTGAGATAGTACGAGGATAGGCTTGAATGATGATG 2678
 QY 2221 ATGATTAATATGTGCGCGGGGTGCTTGCGATGAGACGGGGTGTATATGATGATG 2280
 DB 2679 ATGATTAATATGTGCGCGGGGTGCTTGCGATGAGACGGGGTGTATATGATGATG 2738
 QY 2281 TTTACTGCGCCCAATTTTACGCGGTACGCGTCTTCTGCGCAATACCACTTATCTCTAC 2340
 DB 2739 TTTACTGCGCCCAATTTTACGCGGTACGCGTCTTCTGCGCAATACCACTTATCTCTAC 2798
 QY 2341 GGGTGATGCTTCTATGCGTTTAAACAATACCTGTGTGGAAGCTTGACCGATGATGAGT 2400
 DB 2799 GGGTGATGCTTCTATGCGTTTAAACAATACCTGTGTGGAAGCTTGACCGATGATGAGT 2858
 QY 2401 CGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGTGCGCCCAAAAAGAGCGCT 2460
 DB 2859 CGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGTGCGCCCAAAAAGAGCGCT 2918
 QY 2461 TCAATTTAAGAAATGCTCTTTTGAAGGTGTACCTTTGGGTATCTGTCTGAGAGGTAACTCC 2520
 DB 2919 TCAATTTAAGAAATGCTCTTTTGAAGGTGTACCTTTGGGTATCTGTCTGAGAGGTAACTCC 2978
 QY 2521 AGGGGCGCCCAATGTGCGCTCCGACTGTGAGTGTCTTCAATGATGATGAGTGGCT 2580
 DB 2979 AGGGGCGCCCAATGTGCGCTCCGACTGTGAGTGTCTTCAATGATGATGAGTGGCT 3038
 QY 2581 GTGATTTAAGCATTAATGTGTGTGCAACTGTGCAAGAGAGCGGCTCTCAGATGTGAC 2640
 DB 3039 GTGATTTAAGCATTAATGTGTGTGCAACTGTGCAAGAGAGCGGCTCTCAGATGTGAC 3098

QY 2641 TGTCTGGAACGGCAACTGTCACTTCTGTAAGACATTTGACGTAAGCCAGCATCTTCCGAG 2700
 DB 3099 TGTCTGGAACGGCAACTGTCACTTCTGTAAGACATTTGACGTAAGCCAGCATCTTCCGAG 3158
 QY 2701 GCTTGGCAAGTGTGTGAGCATTAATCATCTGACCCGCTGTTCTTGCATTTGGGTAACAG 2760
 DB 3159 GCTTGGCAAGTGTGTGAGCATTAATCATCTGACCCGCTGTTCTTGCATTTGGGTAACAG 3218
 QY 2761 AGGGGGGTGTCTTCACTTACCTTAACATGCAATTTGAGTCACTAAGATATTTGAGGCC 2820
 DB 3219 AGGGGGGTGTCTTCACTTACCTTAACATGCAATTTGAGTCACTAAGATATTTGAGGCC 3278
 QY 2821 GAGAGCATGTCTCAAGGTGAACTTGAACGGGGTGTGATGATGACATGAAATCTTGAG 2880
 DB 3279 GAGAGCATGTCTCAAGGTGAACTTGAACGGGGTGTGATGATGACATGAAATCTTGAG 3338
 QY 2881 GTGCTGAGGTACATGAGAACCCGACCAAGGAGTGCAGACCTTGCAGTGTGGCGTAAACAT 2940
 DB 3339 GTGCTGAGGTACATGAGAACCCGACCAAGGAGTGCAGACCTTGCAGTGTGGCGTAAACAT 3398
 QY 2941 ATTAGAACCAGCCTGTGATGCTGATGTGACCCGAGAGCTGAGGCCGATCACTTGCTG 3000
 DB 3399 ATTAGAACCAGCCTGTGATGCTGATGTGACCCGAGAGCTGAGGCCGATCACTTGCTG 3458
 QY 3001 CTGGCTTGCACCCGCGCTGAGTGTGCTTATGCGATGAAATTAAGATTGAG 3052
 DB 3459 CTGGCTTGCACCCGCGCTGAGTGTGCTTATGCGATGAAATTAAGATTGAG 3510

RESULT 4
 AX084507
 LOCUS AX084507 34448 bp DNA linear PAT 28-FEB-2001
 DEFINITION Sequence 4 from Patent WO0104282.
 AX084507
 VERSION AX084507.1 GI:13185915
 KEYWORDS
 SOURCE human adenovirus C
 ORGANISM Human adenovirus C
 Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 REFERENCE 1
 Mould, W.S., Toth, K., Doronin, K. and Tollefson, A.E.
 AUTHORS Replication-competent anti-cancer vectors
 TITLE Patent: WO 0104282-A 4 18-JAN-2001;
 JOURNAL Saint Louis University (US)
 FEATURES
 source location/Qualifiers
 1..34448
 /organism="Human adenovirus C"
 /mol_type="unassigned DNA"
 /db_xref="taxon:129951"
 ORIGIN
 Query Match 100.0%; Score 3052; DB 6; Length 34448;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTGTAGTATTTTAAACCCGCTGAGTTCTCAAGAGCCACTTTGATGCCAGCGAGT 60
 DB 459 CGTGTAGTATTTTAAACCCGCTGAGTTCTCAAGAGCCACTTTGATGCCAGCGAGT 518
 QY 61 AGAATTTTCTCCGCGAGCGCTCCGACACCGGGAATGAAATAGACATATTATCTGCC 120
 DB 519 AGAATTTTCTCCGCGAGCGCTCCGACACCGGGAATGAAATAGACATATTATCTGCC 578
 QY 121 ACGGAGGTGTTATTACGGAAGAAATGCGCGCACTTTTGGACCAAGTGAATGAGAG 180
 DB 579 ACGGAGGTGTTATTACGGAAGAAATGCGCGCACTTTTGGACCAAGTGAATGAGAG 638
 QY 181 TACTGGCTGATATCTTCCACCTCTTACGCAATTTTGAACCACTTACGCACTGT 240
 DB 639 TACTGGCTGATATCTTCCACCTCTTACGCAATTTTGAACCACTTACGCACTGT 698
 QY 241 ATGATTTAAGAGTACGAGCGCCCGAAGATCCCAAGAGAGAGCGGTTTCGAGATTTTTC 300

Db 699 ATGATTTAGAGGTGACGCGCCCGGAAAGATCCCAACGAGAGGCGGTTTCGCAATTTTTC 758
Qy 301 CCGACTCTGTAAATGTGGCGGTGCGAGAAAGGATTGACTTACTCTTTTCCGCGGGGC 360
Db 759 CCGACTCTGTAAATGTGGCGGTGCGAGAAAGGATTGACTTACTCTTTTCCGCGGGGC 818
Qy 361 CCGGTTCTCCGAGCGGCTCACTTTTCCGAGCGCGAGCGCGAGAGAGAGCT 420
Db 819 CCGGTTCTCCGAGCGGCTCACTTTTCCGAGCGCGAGCGCGAGAGAGAGCT 878
Qy 421 TGGGTCGGGTTCTATGCGCAAACTTTGTAACCGAGGTATGATCTTACCTGCCAGAG 480
Db 879 TGGGTCGGGTTCTATGCGCAAACTTTGTAACCGAGGTATGATCTTACCTGCCAGAG 938
Qy 481 CTGGTTTCCACCGAGTACGACGAGGATGGAAGGGGTGAGAGATTGTTGTAAGTTATG 540
Db 939 CTGGTTTCCACCGAGTACGACGAGGATGGAAGGGGTGAGAGATTGTTGTAAGTTATG 998
Qy 541 TGGAGCACCCGCGGACGAGTTCAGAGTCTTGTCATTATCACCGAGAGAAATACGGGGGAC 600
Db 999 TGGAGCACCCGCGGACGAGTTCAGAGTCTTGTCATTATCACCGAGAGAAATACGGGGGAC 1058
Qy 601 CAGATATTATGTGTTGCTTGTCTATATAGAGACCTGTGGCAATGTTGTCTACAGTAAGT 660
Db 1059 CAGATATTATGTGTTGCTTGTCTATATAGAGACCTGTGGCAATGTTGTCTACAGTAAGT 1118
Qy 661 GAAATTTATGGGCAATGGGTGATATAGTGTGGGTTGTGTGTAATTTTTTTTTTAT 720
Db 1119 GAAATTTATGGGCAATGGGTGATATAGTGTGGGTTGTGTGTAATTTTTTTTTTAT 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGGCTGTGTC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGGCTGTGTC 1238
Qy 781 TGAACCTGAGCTGAGCGCCGAGCCAGAACCGAGGCTTGAAAGACTTCCCGCTCTAA 840
Db 1239 TGAACCTGAGCTGAGCGCCGAGCCAGAACCGAGGCTTGAAAGACTTCCCGCTCTAA 1298
Qy 841 AATGGCGCTGCTATCTGAGAGCGCCGACATCACTGTGTATAGAAATGCAATAGTAG 900
Db 1299 AATGGCGCTGCTATCTGAGAGCGCCGACATCACTGTGTATAGAAATGCAATAGTAG 1358
Qy 901 TACGATAGCTGTGACTCCGCTCTTCTTAACAACACTCTGAGATACACCGGTGCTCC 960
Db 1359 TACGATAGCTGTGACTCCGCTCTTCTTAACAACACTCTGAGATACACCGGTGCTCC 1418
Qy 961 GCTGTGCCCCATTAACAACAGATTCGCTGAGAGTGTGGGGCTGCCAGGCTGTGGAATG 1020
Db 1419 GCTGTGCCCCATTAACAACAGATTCGCTGAGAGTGTGGGGCTGCCAGGCTGTGGAATG 1478
Qy 1021 TATGAGGACTTGTCTTAACGAGCGCTGGGCAACTTTGACTTGAAGCTGTAAACGCCGAG 1080
Db 1479 TATGAGGACTTGTCTTAACGAGCGCTGGGCAACTTTGACTTGAAGCTGTAAACGCCGAG 1538
Qy 1081 GCCATTAAGGTGTAACCTGTGATTCGCTGTGTGTTAAACGCTTTTGTGTGATGAGT 1140
Db 1539 GCCATTAAGGTGTAACCTGTGATTCGCTGTGTGTTAAACGCTTTTGTGTGATGAGT 1598
Qy 1141 TGAATTAAGTTAATAAAGGCGAGATATGTTTAACTTGCATGCGCGTAAATGAGGC 1200
Db 1599 TGAATTAAGTTAATAAAGGCGAGATATGTTTAACTTGCATGCGCGTAAATGAGGC 1658
Qy 1201 GGGGCTTAAAGGCTTATATAGCGCGGTGGCTATCTTGTTGATCATGCACTCATGGA 1260
Db 1659 GGGGCTTAAAGGCTTATATAGCGCGGTGGCTATCTTGTTGATCATGCACTCATGGA 1718
Qy 1261 GGGCTTGGAGTGTGTAAGATTTTCTGCTGTGCTAACTTGGAACAGAGCTCTTA 1320
Db 1719 GGGCTTGGAGTGTGTAAGATTTTCTGCTGTGCTAACTTGGAACAGAGCTCTTA 1778
Qy 1321 CAGTACTCTTGGTTTGTGAGGTTTCTGTGGGCTCATCCAGGCAAAAGTTAGTGTGAG 1380
Db 1779 CAGTACTCTTGGTTTGTGAGGTTTCTGTGGGCTCATCCAGGCAAAAGTTAGTGTGAG 1838

Qy 1381 AATTAAAGAGATTACAGTGGGAATTTGAAGACTTTTGAATATCTGTGTGAGCTGT 1440
Db 1839 AATTAAAGAGATTACAGTGGGAATTTTGAAGACTTTTGAATATCTGTGTGAGCTGT 1898
Qy 1441 TGAATCTTGTGATCTGGGTCAACAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTGA 1500
Db 1899 TGAATCTTGTGATCTGGGTCAACAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTGA 1958
Qy 1501 TTTTTCACACCGGGGGCGGCTGCGCTGTGCTGCTTTTGTAGTTTAAAGATTA 1560
Db 1959 TTTTTCACACCGGGGGCGGCTGCGCTGTGCTGCTTTTGTAGTTTAAAGATTA 2018
Qy 1561 ATGAGGGAAGAAACCCATCTGAGCGGGGGGTACCTGTGATTTTCTGCGCATGCACT 1620
Db 2019 ATGAGGGAAGAAACCCATCTGAGCGGGGGGTACCTGTGATTTTCTGCGCATGCACT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGTCTACTGTGTCTTCCGTCGCGGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGTCTACTGTGTCTTCCGTCGCGGC 2138
Qy 1681 GATTAATCCGACCGAGAGAGCAGCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 2139 GATTAATCCGACCGAGAGAGCAGCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAG 2198
Qy 1741 GCAGAGCCCATGGAACCCGAGAGCGGCGCTGGAACCTCGGGAATGAAATGTTGACAGGTG 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCGGCGCTGGAACCTCGGGAATGAAATGTTGACAGGTG 2258
Qy 1801 GCTGAACCTGATCCAGAACTGAGACGCAATTTTGAATTAACAGAGATGGGACAGGCTA 1860
Db 2259 GCTGAACCTGATCCAGAACTGAGACGCAATTTTGAATTAACAGAGATGGGACAGGCTA 2318
Qy 1861 AAGGGGTTAAAGAGAGAGCGGGGGCTTGTGAGGCTTCAAGAGAGCTAAGAACTAGCT 1920
Db 2319 AAGGGGTTAAAGAGAGAGCGGGGGCTTGTGAGGCTTCAAGAGAGCTAAGAACTAGCT 2378
Qy 1921 TTTAGCTTTAATGACACAGACACCGCTGAGTGTATTAATTTTCAACAGATCAAGATAT 1980
Db 2379 TTTAGCTTTAATGACACAGACACCGCTGAGTGTATTAATTTTCAACAGATCAAGATAT 2438
Qy 1981 TGGCTAATGAGCTTGTATCTGTGGGCGAAGATATTCATAGAGCAGCTGACCACTTAC 2040
Db 2439 TGGCTAATGAGCTTGTATCTGTGGGCGAAGATATTCATAGAGCAGCTGACCACTTAC 2498
Qy 2041 TGGCTGACGCGAGGAGTATTTTGAAGGCTTATGAGGATATGCAAAAGGTGCACTT 2100
Db 2499 TGGCTGACGCGAGGAGTATTTTGAAGGCTTATGAGGATATGCAAAAGGTGCACTT 2558
Qy 2101 AGGCAAGTTGCAAGTACAGAGATCAGCAAACTTGAATATCAGGAAATGTTGCTACATT 2160
Db 2559 AGGCAAGTTGCAAGTACAGAGATCAGCAAACTTGAATATCAGGAAATGTTGCTACATT 2618
Qy 2161 TCTGGGAAACGGGCGCGAGGTGAGATATGAGAGATAGAGTGGCTTTAGATGAGC 2220
Db 2619 TCTGGGAAACGGGCGCGAGGTGAGATATGAGAGATAGAGTGGCTTTAGATGAGC 2678
Qy 2221 ATGATTAATATGAGCGCGGGGTGCTTGGCAATGAGCGGGGTGTTATTAAGATGAG 2280
Db 2679 ATGATTAATATGAGCGCGGGGTGCTTGGCAATGAGCGGGGTGTTATTAAGATGAG 2738
Qy 2281 TTTACTGGCCCCCAATTTTAAAGCGGTATTTCTGTGCAATACCAACTTATCTTACAC 2340
Db 2739 TTTACTGGCCCCCAATTTTAAAGCGGTATTTCTGTGCAATACCAACTTATCTTACAC 2798
Qy 2341 GGTGTAAAGCTTCTATAGGTTTAAACAATACTGTGTGAAAGCTGAGCCGATGTAAGGTT 2400
Db 2799 GGTGTAAAGCTTCTATAGGTTTAAACAATACTGTGTGAAAGCTGAGCCGATGTAAGGTT 2858
Qy 2401 CCGGGCTGTGCTTTTACTGCTGTGGAAGGGGCTGTGTCTCCGCCCAAAAGCAGGCT 2460
Db 2859 CCGGGCTGTGCTTTTACTGCTGTGGAAGGGGCTGTGTCTCCGCCCAAAAGCAGGCT 2918

Qy	2461	TCATTAAGAAATGCTCTTTGAAAGGTGTAACCTTGSGTATTCCTGTGAGGGTAACCTC	2520
Db	2919	TCATTAAGAAATGCTCTTTGAAAGGTGTAACCTTGSGTATTCCTGTGAGGGTAACCTC	2978
Qy	2521	AGGGGCGCCCAACATGTGGCCCTCCGACCTGTGGTTGCTTCATGCTAAGTAAAGGTGGCT	2580
Db	2979	AGGGTGGCCCAACATGTGGCCCTCCGACCTGTGGTTGCTTCATGCTAAGTAAAGGTGGCT	3038
Qy	2581	GTGATTAAGCATMACTGGTATGTGGCAACCTGCGAGACAGGGCTCTCAGATGCTGACC	2640
Db	3039	GTGATTAAGCATMACTGGTATGTGGCAACCTGCGAGACAGGGCTCTCAGATGCTGACC	3098
Qy	2641	TGCTTGAGACGGCAACTGTCACTCTGCTGAAGACATTCACTGAAGCCAGCCACTCTGCAAG	2700
Db	3099	TGCTTGAGACGGCAACTGTCACTCTGCTGAAGACATTCACTGAAGCCAGCCACTCTGCAAG	3158
Qy	2701	GCCTGGCCAGTGTGTTGAGCATTAACATCAACCCGCTGTCTTCCTTGATTTGGGTAAACAG	2760
Db	3159	GCCTGGCCAGTGTGTTGAGCATTAACATCAACCCGCTGTCTTCCTTGATTTGGGTAAACAG	3218
Qy	2761	AGGGGGGTGTTCTTCACTTACCAATGCAATTGTAGTCAACATAAGTATTTGCTTGAGCC	2820
Db	3219	AGGGGGGTGTTCTTCACTTACCAATGCAATTGTAGTCAACATAAGTATTTGCTTGAGCC	3278
Qy	2821	GAGACATGTCCAGAGTGAACCTGAACGGGGTGTTCATCATGACCATGAAGATCTGGAAG	2880
Db	3279	GAGACATGTCCAGAGTGAACCTGAACGGGGTGTTCATCATGACCATGAAGATCTGGAAG	3338
Qy	2881	GTGCTGAGATTAAGATGAAGACCCGACCAAGGTGACAGCCCTGCGATGTGGGGGTAAACAT	2940
Db	3339	GTGCTGAGATTAAGATGAAGACCCGACCAAGGTGACAGCCCTGCGATGTGGGGGTAAACAT	3398
Qy	2941	ATTAGGAACACAGCCTGTGATGTGAGTGTGACCGAGAGCTGAGGCCCGATCATTTGGTG	3000
Db	3399	ATTAGGAACACAGCCTGTGATGTGAGTGTGACCGAGAGCTGAGGCCCGATCATTTGGTG	3458
Qy	3001	CTGGCTTGACCCCGGCGCTGAGTTTGGCTCTTGACGATGAAGATTAAGATTGAG	3052
Db	3459	CTGGCTTGACCCCGGCGCTGAGTTTGGCTCTTGACGATGAAGATTAAGATTGAG	3510
RESULT 5			
LOCUS	AY339865	35934 bp	DNA linear VRL 13-Aug-2003
DEFINITION	Human adenovirus C serotype 5, complete genome.		
ACCESSION	AY339865		
VERSION	AY339865.1	GI:33465830	
KEYWORDS			
SOURCE	Human adenovirus C		
ORGANISM	Human adenovirus C		
REFERENCE	Viruses; daDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.		
AUTHORS	McAllister, D.L., Lu, F., Thomas, B.K., Hutchins, B.M. and Suganum, B.J.		
TITLE	Complete Nucleic Acid Sequence of the Adenovirus Type 5 Reference Material		
JOURNAL	Bioprocessing (2003) In press		
REFERENCE	2 (bases 1 to 35934)		
AUTHORS	Suganum, B.J., McAllister, D.L. and Hutchins, B.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-JUL-2003) Process Sciences, Canji Inc., Schering-Plough Corporation, 3525 John Hopkins Court, San Diego, CA 92121, USA		
FEATURES			
source	1..35934	location/Qualifiers	
	/organism="Human adenovirus C"		
	/vifion		
	/mol_type="genomic DNA"		
	/serotype="5"		
	/db_xref="taxon:129951"		
	1..103		
	/note="5' inverted terminal repeat"		
	/rpe_type="inverted		
	repeat_region		

gene 468. .1632
/gene="E1A"
TATA_signal 468. .475
/gene="E1A"
CDS join(560. .1112,1229. .1545)
/gene="E1A"
/note="derived from the E1A 13S mRNA"
/codon_start=1
/product="33 kDa protein"
/protein_id="AA019284.1"
/db_xref="GI:33465831"
/translation="MRHITCGGVITTEMAASLIDQILEVLANLPPPSHFPEPTLH
E1YDLDVPAEDPNEEAVSQIPDSVMAVOEGIDLTFPPAPSPBPPLHSRQEPD
EORALGPMPPLVEVIDLTCHEAGFPSPDEDEGEFVLDYVEHGHGCRCHYH
RNTDDPIMCSICYMRTCGMVYSPVSEPEPEPEPEPARPTRRPMAPALIRPPT
SVSECSNSTSCDSGSPSNTPEIHVPVPCIPKPAVVRGGRQAVECEDLNP
GQPLDSCRRPP"
join(560. .974,1229. .1545)
/gene="E1A"
/note="derived from the E1A 12S mRNA"
/codon_start=1
/product="27 kDa protein"
/protein_id="AA019285.1"
/db_xref="GI:33465832"
/translation="MRHITCGGVITTEMAASLIDQILEVLANLPPPSHFPEPTLH
E1YDLDVPAEDPNEEAVSQIPDSVMAVOEGIDLTFPPAPSPBPPLHSRQEPD
EORALGPMPPLVEVIDLTCHEAGFPSPDEDEGEFVSEPEPEPEPARPTRR
PMAPALIRPPTSVSECSNSTSCDSGSPSNTPEIHVPVPCIPKPAVVRGGRQ
AVECEDLNPGEPLDSCRRPP"
975. .1228
/gene="E1A"
/note="E1A 12S"
1113. .1228
/gene="E1B"
/note="E1A 13S"
1611. .1616
/gene="E1A"
1632
/gene="E1A"
1672. .3509
/gene="E1B"
1672. .1678
/gene="E1B"
1714. .2244
/gene="E1B"
/codon_start=1
/product="E1B 19k"
/protein_id="AA019286.1"
/db_xref="GI:33465833"
/translation="MEAWECLEDFSAVNLLEQSSNSTSMFWRFLMGSSQAKLVCRIK
EYKREPELILKSGEFLDSLNGHOLFQKVKITDFTSGPAAAVFLSIKDK
WSEFHLISGGVILDELIAHMLRAVVRKHNRLLLSVSRPAIPIPEEQOOOEEARRRR
QEQSWNRAGLIDPRE"
2019. .3509
/gene="E1B"
/codon_start=1
/product="E1B 55k"
/protein_id="AA019287.1"
/db_xref="GI:33465834"
/translation="MERNPSEBRCVPAGFSGHVASVEGCTQESPAIVFRPQDNTD
GGAALAAAGSOAALAAAGAPMESESRPGSGMNVVAVELYPELRILITTEDGGGLG
VREBGADEBEATEBANLAFSLMTRHREPCITFQOIKONCANEDLLAQKSIEDLTLY
WLOPDDDEEABE1RYAKVALRPOCKYIKSLVINRNCYSISGNAEVIDEDVAPR
CSIMIMWGVAVMGGVIMNVRFTGPNPSGTVFLANTNLIILHGVSFYGNNTCEAWT
DVRVNGCAYCCMGKGVVCRPSKASIKKCLPERFTTGLISBGNRVRYHVASDCCGM
LYKSAVYAKHNVGCNCEDRASQMLTSDGCHLKITIHVASHRKAMPVFEHNITLR
CSLHGNNRGVFLPYQCNLSHTKILLPBESSKVNILNGVDMTKIMKILRYDETTRR
CRPCECGKILRNQPVMLDVTIELRPHLVLACTRAREGSSDEBDT"
3551. .3556
/note="E1X TATA box"
3609. .4031
/note="protein 9"
/codon_start=1

/product="p1x"
/protein_id="AA019288.1"
/db_xref="gi:33465835"
/translation="MSTRSPGGSIVSSVLTTRMPNACVROWNGSSIDGEPVLPANS
TLTYEVSGTPTLTAASAAATAATRGVTAFPLSLAASAASSASRSARDKLT
LLAQDLSITRLNVAISOQLDLRQVSALKASSPNAV"
polya_signal
4038. . 4043
/note="E1B/protein 1x"
4070
/note="E1B/p1x"
/complement (join(4091. .5427,5706. .5718))
/product="E2B 1Va2"
/codon_start=1
/protein_id="AA019289.1"
/db_xref="gi:33465836"
/translation="MSTRGRRALQHQDQPOAHFGORARASAPLHRDPADEDA
PVEHDPGSGRAPPTAVQRKPPQAPKGDLDSDAVEQVTEMLDRLELQTLKSP
TADGKPLKPNASLOELSLQGERLADLVENNRVRDMLNEVAPLDRLELQTLKSP
QLOVIGVYPTGCGKQLRNLSQLISPTPEVFIAPQVMI PPSLAKAMQ
ICEGVYAGPDGTLIPQSGTLRPRVKMAVDLLEHNYDSDPRNTFAQAAAGPIA
IIMECMENLKGKGVSKFPAFPKSLDKPKCTGYTVVYLNNAPRDMAGPIA
LKISKMHLSIPRMHSQNLNFVVTYTKGLPLASLLKQDPRHHAORSCDMITNT
TPQEHALQWCTLHPDGLMPYLNINQSLYHVEKIKHTLNDRMSRAIRAKTPK"
4952
/note="compared to Ad2WT of NC_001405; his to gln change"
/replace="c"
4952
/note="compared to GenBank Accession Number M73260"
/replace="g"
/complement (5197. .8367)
/codon_start=1
/product="E2B 120K DNA polymerase"
/protein_id="AA019290.1"
/db_xref="gi:33465837"
/translation="MDSHLADVVIKLRPPADITWLSRGVVRSTVTPLEPDGQ
QAAVEHQPPPEGLKFLCPLVRGQVLDVDVANHCOYCARFKSQHCSAR
LRDYPFHINSHSNMWEIOFPFGSHPRTERLFVTVRTVYMGAFQOLVPMIL
VMKFGDEPLVTAAADLANGLMDEMDPTFYCTPEKNAIGROPTFEDHOML
ARDLMSFPVSNPLADWALSBEHGSBEELTEBELKLPKIGIPRLELYVGHNT
NGPREYIAAVINNRSEVPSPRITRPMRACKILFNDVTPALPNRSKRRDPL
WEGCGDDTDKTYQLKVNKDFALHTISLRKAQAALVEKGCAYQAVNPYIL
GSGSEADGFP1QEWKDRREFVNLRELKKGGDKDI IETLDYCALDVYAEVLV
NKLDSYASFVADAVGLDASFNFORPTLISNSHAIFRQVFAEOPARSNGLPDL
APSHEDYVASIRGRCYPTVYLGLPELVYDI CMYVSAALTHMPMPNPPLP
ETVCGACGADAVSPESVFLAPKLYALKSHGSCGASKGLRAKGAABGLDVTY
KCYLADOGREORPSTSRSLKRTLASAOGAHPVTYQTLTTRLTPMKMDTLAL
DEHRLPYSESRPNRNEICWEMP"
intron
complement (5428. .5705)
/note="for E2B 1Va2 mRNA"
6018. .6024
/note="major late mRNAs TATA box"
TATA_signal
complement (8583. .10544)
/note="putative precursor"
CDS
/codon_start=1
/product="E2B pTP 75K"
/protein_id="AA019291.1"
/db_xref="gi:33465838"
/translation="MHEPLPLRNTMNRVDRPPASTTAAGITWMSRYLYGHRMLD
LAPGAPLRLPPLRQPPHFLVGYQVTRCNQDVPSRAVSRVLTSLTELSPGHQVY
NMSWANCTYINTGAHARFVMDDFQSTLQVOQALIAEVNLDLQIMRGFTV
RMGGGRRLRPNASAAAIDARDAQEGBEEVEVERIMDOYDRLRCQMEAGMD
RLRQOAGKDMVLSTIRLRKTAIFYNII STSARNNPDRRLPPPAVLSLPDCDW
LDAPLEERSDVPDADLSLGGVPTOLLACIVASVLPHGSGPPTNRGMAVGG
LRPENGAAVETMRKRGEMIERVVDLTPRRRRRRPPPPPEEBEGALMBEEL
EEEBEAPVAFREVRDVAELIRLEBELTVSARNSQFNFVADPYEAMELEALGDI
NESTLRWVNFVFAEHTATTINYLFOELRYAVAFARVETNLQOVNARADAGGV
YSRWNEGGLNAFSQLMARISNDLAAIVERAGRGDLQEEETEQFMAETAYADNSGDVQ

variation
EILROAANDTEIDISVELSFRFLTGVEVETORRQIOEINRRVAVAFASNLRAQHQLLP
ARGADVLPPLPAGPEPPLPPGARPRRF"
8783
/note="compared to Ad2WT of NC_001405; leu to phe change"
/replace="a"
8783
/note="compared to GenBank Accession Number M73260"
/replace="g"
/codon_start=1
/product="L1 52, 55K"
/protein_id="AA019292.1"
/db_xref="gi:33465839"
/translation="MHPVLROMRPPPOQROEOEOROTCARPSPPPTSGATSADNA
ADGVEPRRRARHLYDLREGEGRLARLGPASPEHNPVOLKRDREAVPRONLFRD
EGEPRERMRKRKHAGRELHGNREBLLEEDPREPARGISAPARHVAADLVYAY
EQVNOEINFOKSFNNHVRTLVABEVAFLIMDVSALBOQNSPKPLMAQPLIV
QHSNDKAEFADLNLIVPEGRMLDLINLQSLIVERSLSDKVAALNYSLSIG
KFYAKLYHPYPIIDKEVKIEGYMMALKVLISDLDGYRNERJHKAVSRRSE
LSRELHSLORALAGSGSDREAESYFDAGADLRMAPSRRLAAGAAGPLAVAPAR
AGNVGVEYEDDEDEVEPEDGEY"
variation
11284
/note="compared to GenBank Accession Number M73260"
/replace="c"
variation
Query Match 100.0%; Score 3052; DB 14; Length 35934;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGTGTAGTATTTATTAACCCGGTAGTTCCTCAAGAGCCACTTTGATGCCAGCGAGT 60
Db 459 CGTGTAGTATTTATTAACCCGGTAGTTCCTCAAGAGCCACTTTGATGCCAGCGAGT 518
OY 61 AGATTTTCCCTCCGAGCCGCTCCGACACCGGGACGAAATAGACATTTATCTGCC 120
Db 519 AGATTTTCCCTCCGAGCCGCTCCGACACCGGGACGAAATAGACATTTATCTGCC 578
OY 121 ACGGAGGTGTTATTAACGAAAGAAATGCGCCGACGCTTTTGGACACAGCTGATCGAAGAG 180
Db 579 ACGGAGGTGTTATTAACGAAAGAAATGCGCCGACGCTTTTGGACACAGCTGATCGAAGAG 638
OY 181 TACTGCTGATATCTTCACTCTCTAGCACTTTTGAACCACTACCTTCAGCAACTGT 240
Db 639 TACTGCTGATATCTTCACTCTCTAGCACTTTTGAACCACTACCTTCAGCAACTGT 698
OY 241 ATGATTTAGACGTGACGGCCCCCGGAAATCCCAACGAGGAGCGGTTTCGAGATTTTTC 300
Db 699 ATGATTTAGACGTGACGGCCCCCGGAAATCCCAACGAGGAGCGGTTTCGAGATTTTTC 758
OY 301 CCGACTCTGATATGTTGGCGGTGAGAGAGGATTTGACTTACTCTTTCGCGCGCGC 360
Db 759 CCGACTCTGATATGTTGGCGGTGAGAGAGGATTTGACTTACTCTTTCGCGCGCGC 818
OY 361 CCGGTTCTCGGAGCGCGCTTCACTTTCGCGGACCGCGAGCCGAGAGAGAGCCT 420
Db 819 CCGGTTCTCGGAGCGCGCTTCACTTTCGCGGACCGCGAGCCGAGAGAGAGCCT 878
OY 421 TGGGTCCGTTTCTATACCAAACTTGTACCGGAGGTGATGATCTTACCTGCCACGAG 480
Db 879 TGGGTCCGTTTCTATACCAAACTTGTACCGGAGGTGATGATCTTACCTGCCACGAG 938
OY 481 CTGACTTTCACACGAGTACGACGAGATGAAGAGGTTGAGATTTGTGTAGATTATG 540
Db 939 CTGACTTTCACACGAGTACGACGAGATGAAGAGGTTGAGATTTGTGTAGATTATG 998
OY 541 TGAAGACCCCGGAGCGGTTGACGGTCTTGTCTATTTACCGGAGGAATACGGGGAGC 600
Db 999 TGAAGACCCCGGAGCGGTTGACGGTCTTGTCTATTTACCGGAGGAATACGGGGAGC 1058
OY 601 CAGATATTATGTGTGCTTGTGCTATATGAGACCTGTGCAATTTGTCTACAGTAACT 660
Db 1059 CAGATATTATGTGTGCTTGTGCTATATGAGACCTGTGCAATTTGTCTACAGTAACT 1118

QY	661	TAATAATATNTGGCAGTGGGTGTATAGAGTGTGGGTTTGCTGTGTGAATTTT	TTTTTAAAT	720
Db	1119	GAATAATATNTGGCAGTGGGTGTATAGAGTGTGGGTTTGCTGTGTGAATTTT	TTTTTAAAT	1178
QY	721	TTTTACAGTTTTGTGTGTTTAAAGAAATTTTGATTTGTTTAAAGAGCTGTGTNC		780
Db	1179	TTTTACAGTTTTGTGTGTTTAAAGAAATTTTGATTTTGATTTTAAAGAGCTGTGTNC		1233
QY	781	TGAACCTGAGCCTGAGCCCGAGCCAGAACCCGAGGCTTGCAAGACCTACCCGCGTCTPA		840
Db	1239	TGAACCTGAGCCTGAGCCCGAGCCAGAACCCGAGGCTTGCAAGACCTACCCGCGTCTPA		1298
QY	841	AATGGCGGCTGCTATTCCTGAGACGGCCGACATCACTGTGTCTATAGAAATGCAATAGTAG		900
Db	1289	AATGGCGGCTGCTATTCCTGAGACGGCCGACATCACTGTGTCTATAGAAATGCAATAGTAG		1358
QY	901	TACGATATAGCTGTGACTCCGGCTCTCTTAAACAACAACCTCTGAGATACACCGGATGTGCC		960
Db	1359	TACGATATAGCTGTGACTCCGGCTCTCTTAAACAACAACCTCTGAGATACACCGGATGTGCC		1418
QY	961	GCTGTGCCCATTTAAACAGTTGCCGTGAGATGTGGGCGTCCGACAGCTGTGGAATG		1020
Db	1419	GCTGTGCCCATTTAAACAGTTGCCGTGAGATGTGGGCGTCCGACAGCTGTGGAATG		1478
QY	1021	TATCGAGAGACTTGTCTTAAACGAGCCTGGGCAACCTTTGACTTGAAGCTTAAACGCCCAAG		1080
Db	1479	TATCGAGAGACTTGTCTTAAACGAGCCTGGGCAACCTTTGACTTGAAGCTTAAACGCCCAAG		1538
QY	1081	GCCATTAAGGTGTAAACCTGTGATTCGATGTGTGTTAACGCTTGTGTGCGAATGAGT		1140
Db	1539	GCCATTAAGGTGTAAACCTGTGATTCGATGTGTGTTAACGCTTGTGTGCGAATGAGT		1598
QY	1141	TGATGTAAAGTTAATAAAGGGTGAAGTAACTTTAACTTGATGAGCGGTAAATGGAGGC		1200
Db	1599	TGATGTAAAGTTAATAAAGGGTGAAGTAACTTTAACTTGATGAGCGGTAAATGGAGGC		1658
QY	1201	GGGCGCTTAAGAGGTATATATATGCCCGGTGGGCTAATCTTGTTACATCTGACCTTCATGGA		1260
Db	1659	GGGCGCTTAAGAGGTATATATATATGCCCGGTGGGCTAATCTTGTTACATCTGACCTTCATGGA		1718
QY	1261	GGCTTTGGAGTGTGTGGAAGATTTTCTGCTGTGTGTGAACCTTGCTGGAACAGAGCTCTAA		1320
Db	1719	GGCTTTGGAGTGTGTGGAAGATTTTCTGCTGTGTGTGAACCTTGCTGGAACAGAGCTCTAA		1778
QY	1321	CAGTACCTCTTGTTTTGAGGTTTCTGTGTGGGCTCATCCAGGCAAAAGTATGCTCGAG		1380
Db	1779	CAGTACCTCTTGTTTTGAGGTTTCTGTGTGGGCTCATCCAGGCAAAAGTATGCTCGAG		1838
QY	1381	AATTAAAGAGAGATTACAAGTGGGAATTTGAAGAGCTTTTGAATTCCTGTGTGAGCTGTT		1440
Db	1839	AATTAAAGAGAGATTACAAGTGGGAATTTGAAGAGCTTTTGAATTCCTGTGTGAGCTGTT		1898
QY	1441	TGATTTCTTTGAATCTCGGGTCAACAGGGGCTTTTCCAGAGAAAGTCAATCAAGACTTTTGA		1500
Db	1899	TGATTTCTTTGAATCTCGGGTCAACAGGGGCTTTTCCAGAGAAAGTCAATCAAGACTTTTGA		1958
QY	1501	TTTTTCCACACCGGGGCGCGCTGGCGCTGCTGTTTGTGATTTTAAAGATTA		1560
Db	1959	TTTTTCCACACCGGGGCGCGCTGGCGCTGCTGTTTGTGATTTTAAAGATTA		2018
QY	1561	ATGAGAGGAAGAAACCAATCTGAGCGGGGGGTACCTGTGAGATTTTCTGGCCATGATCT		1620
Db	2019	ATGAGAGGAAGAAACCAATCTGAGCGGGGGGTACCTGTGAGATTTTCTGGCCATGATCT		2078
QY	1621	GTGAGAGCGGTTTGTGAGACAACAAGATTCGGCTGTACTGTGTCTTCCGTCCGCGCGC		1680
Db	2079	GTGAGAGCGGTTTGTGAGACAACAAGATTCGGCTGTACTGTGTCTTCCGTCCGCGCGC		2138
QY	1681	GATTAATACCGAGCGAGAGACAGACAGACACAGAGAGAACCCAGGCGGCGGCGACAGA		1740
Db	2139	GATTAATACCGAGCGAGAGACAGACAGACAGACAGAGAGAACCCAGGCGGCGGCGACAGA		2198
QY	1741	GCAGAGCCCATGGAACCCGAGAGCCGGCCTTGGAACCTTCGGGAATGAATGTTGTACAGGTG		1800

Db	2199	GCAGAGCCCAATGGAAACCCGAGAGCCGCGCTCGACCTTCGGGAATGAATGTGTGACAGGTG	2258
OY	1801	GCTGAACCTGTATCCAGAACTGAGACGCATTTTGTGCAATTTACAGAGGATATGGCCAGGGGCTA	1866
Db	2259	GCTGAACCTGTATCCAGAACTGAGACGCATTTTGTGCAATTTACAGAGGATATGGCCAGGGGCTA	2318
OY	1861	AAGGGGATAAAGAGGAGACGGGGGGCTTGTGAGGCTACAGAGGAGGCTAGGAACTTAGCT	1920
Db	2319	AAGGGGATAAAGAGGAGACGGGGGGCTTGTGAGGCTACAGAGGAGGCTAGGAACTTAGCT	2378
OY	1921	TTTAGCTTAATGACCAACACCCGTCCTGAGTGTATTACTTTTCAACAGATCAAGATATAT	1980
Db	2379	TTTAGCTTAATGACCAACACCCGTCCTGAGTGTATTACTTTTCAACAGATCAAGATATAT	2438
OY	1981	TGCGCTAATGAGCTTGATCTGCTGGCGCAGAAAGTATCCATAGAGCAGCTGACCACTTAC	2040
Db	2439	TGCGCTAATGAGCTTGATCTGCTGGCGCAGAAAGTATCCATAGAGCAGCTGACCACTTAC	2498
OY	2041	TGGCTGACGACGAGGGAGATTTTGTAGAGGAGCTTATAGGATATAGCAAAAGTGGCACTT	2100
Db	2499	TGGCTGACGACGAGGGAGATTTTGTAGAGGAGCTTATAGGATATAGCAAAAGTGGCACTT	2558
OY	2101	AGGCCAGATTGCAGATACAGAGATCAGCAAACTTGTAATATCAGGAAATGTGCTCAATT	2160
Db	2559	AGGCCAGATTGCAGATACAGAGATCAGCAAACTTGTAATATCAGGAAATGTGCTCAATT	2618
OY	2161	TCTGGAAACGGGGGCGAGGTGGAGATAGATACGAGAGATAGGGGTGCTTATAGATGATAC	2220
Db	2619	TCTGGAAACGGGGGCGAGGTGGAGATAGATACGAGAGATAGGGGTGCTTATAGATGATAC	2678
OY	2221	ATGATTAATATATGTGGCGCGGGGTGCTTGGCATGAGACGGGGGTGTTATTAAGATGATAG	2280
Db	2679	ATGATTAATATATGTGGCGCGGGGTGCTTGGCATGAGACGGGGGTGTTATTAAGATGATAG	2738
OY	2281	TTTACTGGCCCCAATTTTAAAGCGGTACGATTTTCTGGCCAAATACCAACTTATCTTACAC	2340
Db	2739	TTTACTGGCCCCAATTTTAAAGCGGTACGATTTTCTGGCCAAATACCAACTTATCTTACAC	2798
OY	2341	GGTGTAAAGCTCTATGGGTTTAAACAATCCGTGTGGAACCTGGAGCCGATGTAAAGGTT	2400
Db	2799	GGTGTAAAGCTCTATGGGTTTAAACAATCCGTGTGGAACCTGGAGCCGATGTAAAGGTT	2858
OY	2401	CGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT	2460
Db	2859	CGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT	2918
OY	2461	TCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGGTATCTGTGTGAGGTTAATCC	2520
Db	2919	TCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGGTATCTGTGTGAGGTTAATCC	2978
OY	2521	AGGGTGGGCCCAATATGGGCTCCGACCTGTGTGTCTTACATGCTAATGTAAGAAAGGTGGCT	2580
Db	2979	AGGGTGGGCCCAATATGGGCTCCGACCTGTGTGTCTTACATGCTAATGTAAGAAAGGTGGCT	3038
OY	2581	GTCATTAAGCATTAACATGATGTATGGGCAACGCGAGAGCAGGGGCTTCCAGATGCTBACC	2640
Db	3039	GTCATTAAGCATTAACATGATGTATGGGCAACGCGAGAGCAGGGGCTTCCAGATGCTBACC	3098
OY	2641	TGCTCGAGCGCAACTGTCACTGTCTGAAGACCAATTACGTAAGCCAGCCACTCTCGCAG	2700
Db	3099	TGCTCGAGCGCAACTGTCACTGTCTGAAGACCAATTACGTAAGCCAGCCACTCTCGCAG	3158
OY	2701	GCCCTGGCAGTGTATTGAGCATTAACATCTACACCCGCTGTCTTTCGATTTGGGGTAACAG	2760
Db	3159	GCCCTGGCAGTGTATTGAGCATTAACATCTACACCCGCTGTCTTTCGATTTGGGGTAACAG	3218
OY	2761	AGGGGGGTGTTCCTACCTTACCAATGCAATTTTGAAGTACACTTAAGATATTTGCTTGAAGCC	2820
Db	3219	AGGGGGGTGTTCCTACCTTACCAATGCAATTTTGAAGTACACTTAAGATATTTGCTTGAAGCC	3278
OY	2821	GAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGTAACATGACCAATGAAGATCTGGAAG	2880

Db 3279 GAGAGCATGTCCAAAGSTGAACCTGAACGGGGGTGTTTGACATGATGACCATGAAGATCTGNAAG 3338
Qy 2881 GTGCTGAGSTACGATGAGAACCCCGACCGAGTGCAGACCCCTGCGAGTGTGGGGTAAACAT 2940
Db 3339 GTGCTGAGSTACGATGAGAACCCCGACCGAGTGCAGACCCCTGCGAGTGTGGGGTAAACAT 3398
Qy 2941 ATTAGGAACCAAGCCGTGTGATCTGATGTGACCCGAGAGCTGAGAGCCCGATCATTGGGTG 3000
Db 3399 ATTAGGAACCAAGCCGTGTGATCTGATGTGACCCGAGAGCTGAGAGCCCGATCATTGGGTG 3458
Qy 3001 CTGGCTTCACCCCGCGCTGAGTGGCTCTACGAGTGAAGATACGATTGAG 3052
Db 3459 CTGGCTTCACCCCGCGCTGAGTGGCTCTACGAGTGAAGATACGATTGAG 3510

RESULT 6
LOCUS AR091533 35935 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5994132.
ACCESSION AR091533
VERSION AR091533.1 GI:10018288
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35935)
AUTHORS Chamberlain,J.S. and Kumar-Singh,R.
TITLE Adenovirus vectors
JOURNAL Patent: US 5994132-A 1 30-NOV-1999;
FEATURES
Location/Qualifiers
1..35935
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 3052; DB 6; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTGTAGTGTATTATACCCGGTGAATTCCTCAAGAGCCACTCTTGTAGTCCGACGGAGT 60
Db 459 CGTGTAGTGTATTATACCCGGTGAATTCCTCAAGAGCCACTCTTGTAGTCCGACGGAGT 518
Qy 61 AGAGTTTCTCCTCCGAGCCGCTCCGACACCGGAGCTGAAATGAGACATATATCTGCC 120
Db 519 AGAGTTTCTCCTCCGAGCCGCTCCGACACCGGAGCTGAAATGAGACATATATCTGCC 578
Qy 121 ACGGAGGTGTATTATCCGAAGAAATGCGCGCCAGTCTTTTGGACCAAGCTGATCGAAGAG 180
Db 579 ACGGAGGTGTATTATCCGAAGAAATGCGCGCCAGTCTTTTGGACCAAGCTGATCGAAGAG 638
Qy 181 TACTGGCTGATATTTTCACTCTAGCCATTTTGAACCACTTACCTTCCGACGAACTGT 240
Db 639 TACTGGCTGATATTTTCACTCTAGCCATTTTGAACCACTTACCTTCCGACGAACTGT 698
Qy 241 ATGATTAGAGTGACGGCCCCCGAAGATCCCAAGAGAGCGGTTTCGCGAGTTTTC 300
Db 699 ATGATTAGAGTGACGGCCCCCGAAGATCCCAAGAGAGCGGTTTCGCGAGTTTTC 758
Qy 301 CCGACTCTGTATGTGGCGGTGACAGAAAGGATTTGACTTCACTTTCCGCGCGCGC 360
Db 759 CCGACTCTGTATGTGGCGGTGACAGAAAGGATTTGACTTCACTTTCCGCGCGCGC 818
Qy 361 CCGGTTTTCGAGAGCCGCTCACTTTCCGCGACCCGAGACCGCGAGACGAGAGCT 420
Db 819 CCGGTTTTCGAGAGCCGCTCACTTTCCGCGACCCGAGACCGCGAGACGAGAGCT 878
Qy 421 TGGGTCGAGTTTCTATGCGCAACCTTGTACCGAGAGTGTGATCTTTCCTGGCGAGAG 480
Db 879 TGGGTCGAGTTTCTATGCGCAACCTTGTACCGAGAGTGTGATCTTTCCTGGCGAGAG 938
Qy 481 CTGGCTTTCACCCAGTGAAGAGATGAAGAGGCTGAGAGTGTGTGATTTATG 540

Db 939 CTGGCTTTCACCCAGTGAAGCAGAGAGTGAAGAGGCTGAGAGTGTGTGATTTATG 998
Qy 541 TGAAGCAACCCCGGACAGGTTTGAAGGCTTGTCAATTATCAACCGAGGAATPACGGGGAGC 600
Db 999 TGAAGCAACCCCGGACAGGTTTGAAGGCTTGTCAATTATCAACCGAGGAATPACGGGGAGC 1058
Qy 601 CAGATATTATGTGTTCGCTTGTCTATATGAGACCTGTGGCATTTTGTCTACAGTAAGT 660
Db 1059 CAGATATTATGTGTTCGCTTGTCTATATGAGACCTGTGGCATTTTGTCTACAGTAAGT 1118
Qy 661 GAAATTTATGGGACGTGGGTGATAGAGTGGTGTGGTGTGTGATTTTTTTTTTAAAT 720
Db 1119 GAAATTTATGGGACGTGGGTGATAGAGTGGTGTGGTGTGTGATTTTTTTTTTAAAT 1178
Qy 721 TTTTACAGTTTGTGTGTTTAAAGAAATTTGTATGTGATTTTTTAAAGGTCCTGTGC 780
Db 1179 TTTTACAGTTTGTGTGTTTAAAGAAATTTGTATGTGATTTTTTAAAGGTCCTGTGTGC 1228
Qy 781 TGAACCTGAGCTGAGCCGACGAGCCGAGACCTGCAAGACCTTACCCTGCTTAA 840
Db 1239 TGAACCTGAGCTGAGCCGACGAGCCGAGACCTGCAAGACCTTACCCTGCTTAA 1298
Qy 841 AATGGCCCTGTCTATCTGAGACGCGCCGACATCACTGTGTCTTGAAGATGCAATAGTAG 900
Db 1299 AATGGCCCTGTCTATCTGAGACGCGCCGACATCACTGTGTCTTGAAGATGCAATAGTAG 1358
Qy 901 TACGATAGCTGTGACCTCCGCTCTTAAACACACCTCTGAGATPACACCCGGTGTCC 960
Db 1359 TACGATAGCTGTGACCTCCGCTCTTAAACACACCTCTGAGATPACACCCGGTGTCC 1418
Qy 961 GCTGTGCCCATTTAAACAGTTGCGGTGAGAGTGTGGCGGTGCCAGGCTGTGGAATG 1020
Db 1419 GCTGTGCCCATTTAAACAGTTGCGGTGAGAGTGTGGCGGTGCCAGGCTGTGGAATG 1478
Qy 1021 TATGAGAGCTTGTCTTAAACGACCTGGGCAACTTTTGAAGCTTGAAGCTTAAACGCCCTAG 1080
Db 1479 TATGAGAGCTTGTCTTAAACGACCTGGGCAACTTTTGAAGCTTGAAGCTTAAACGCCCTAG 1538
Qy 1081 GCCATTAAGGTGTAAACCTGTGATTCGAGTGTGGTGTAAACGCTTGTGTGTGATGATGAT 1140
Db 1539 GCCATTAAGGTGTAAACCTGTGATTCGAGTGTGGTGTAAACGCTTGTGTGTGATGATGAT 1598
Qy 1141 TGATGTAAATTAAAGGTGAGATATGTTTAACTTGCATGGCGGTTTAAATGGGCG 1200
Db 1599 TGATGTAAATTAAAGGTGAGATATGTTTAACTTGCATGGCGGTTTAAATGGGCG 1658
Qy 1201 GGGGCTTAAAGGTTATATATGCGCGCTGCTATCTGTGTATCATCTGACCTCATGGA 1260
Db 1659 GGGGCTTAAAGGTTATATATGCGCGCTGCTATCTGTGTATCATCTGACCTCATGGA 1718
Qy 1261 GGGTGGGAGTGTGGAAGATTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTTAA 1320
Db 1719 GGGTGGGAGTGTGGAAGATTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTTAA 1778
Qy 1321 CAGTACCTCTTGTGTTGAGAGTTCGTGGGCTCATCCGAGCAAAATTAGCTGAG 1380
Db 1779 CAGTACCTCTTGTGTTGAGAGTTCGTGGGCTCATCCGAGCAAAATTAGCTGAG 1838
Qy 1381 AATTAAAGAGATTAAAGTGGGAATTTGAAGACTTTTGAATTCCTGTGGTGAAGCTTT 1440
Db 1839 AATTAAAGAGATTAAAGTGGGAATTTGAAGACTTTTGAATTCCTGTGGTGAAGCTTT 1898
Qy 1441 TGATTTCTTGAATCGGGTCCAGGGGCTTTTCAAGAGAAAGTCAATCAAGACTTTGGA 1500
Db 1899 TGATTTCTTGAATCGGGTCCAGGGGCTTTTCAAGAGAAAGTCAATCAAGACTTTGGA 1958
Qy 1501 TTTTTCACACCGGGGGCGGCTGCGGCTGTGCTTTTGTGATTTTATPAAAGATTA 1560
Db 1959 TTTTTCACACCGGGGGCGGCTGCGGCTGTGCTTTTGTGATTTTATPAAAGATTA 2018
Qy 1561 ATGAGCGAAGAAACCATCTGAGCGGGGGGTACTGCTGGAATTTTCTGCGCAATGATCT 1620
Db 2019 ATGAGCGAAGAAACCATCTGAGCGGGGGGTACTGCTGGAATTTTCTGCGCAATGATCT 2078

QY 1621 GTGAGAGCGGTTGTGAGACACAGAAATCGCTCTACTGTTGTTCTTCCGTCCGCCGCC 1680
 DB GTGAGAGCGGTTGTGAGACACAGAAATCGCTCTACTGTTGTTCTTCCGTCCGCCGCC 2138
 QY 1681 GATTAATCCGACGAGAGAGCAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
 DB GATTAATCCGACGAG 2198
 QY 1741 GCAGAGCCCATGGAACCCGAGAGCCGCTGGAACCTTCGAGATGAAATGTTGTAACAGGTG 1800
 DB GCAGAGCCCATGGAACCCGAGAGCCGCTGGAACCTTCGAGATGAAATGTTGTAACAGGTG 2258
 QY 1801 GCTGAATCTGATCCAGAACTGAGACGCAATTTTGACAAATTCAGAGATGGCAGAGGCTTA 1860
 DB GCTGAATCTGATCCAGAACTGAGACGCAATTTTGACAAATTCAGAGATGGCAGAGGCTTA 2318
 QY 1861 AAGGGGGTAAAG 1920
 DB AAGGGGGTAAAG 2319
 QY 1921 TTTAGCTTAATGACAGACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
 DB TTTAGCTTAATGACAGACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
 QY 1981 TGCCCTAATGAGCTTGTCTGCTGCGCAGAAATTCATAGACAGCTGACCACTTAC 2040
 DB TGCCCTAATGAGCTTGTCTGCTGCGCAGAAATTCATAGACAGCTGACCACTTAC 2439
 QY 2041 TGCGTGCAGACGAGGAGATGATTTTGAAGAGGCTATTGAGGATATGCAAGAGGAGCACTT 2100
 DB TGCGTGCAGACGAGGAGATGATTTTGAAGAGGCTATTGAGGATATGCAAGAGGAGCACTT 2499
 QY 2101 AGGCCAGATTGCAAGTACAGAGTACAGAACTTGTAAATATCAGAAATTTGTTGCTACATT 2160
 DB AGGCCAGATTGCAAGTACAGAGTACAGAACTTGTAAATATCAGAAATTTGTTGCTACATT 2559
 QY 2161 TCTGGAGAACGGGGCCGAGAGTGAATAGATCGAGAGATAGGGTGGCTTTAGATGTAAGC 2220
 DB TCTGGAGAACGGGGCCGAGAGTGAATAGATCGAGAGATAGGGTGGCTTTAGATGTAAGC 2619
 QY 2221 ATGATTAATATGTGGCGGGGGTCTTGGCATGAGACGGGGGTGTTATTAATGATGTAAG 2280
 DB ATGATTAATATGTGGCGGGGGTCTTGGCATGAGACGGGGGTGTTATTAATGATGTAAG 2679
 QY 2281 TTTACTGGCCCCAATTTTAAAGCGTATCGGTTTCTGGCCAAATCAACCTTATCTTACAC 2340
 DB TTTACTGGCCCCAATTTTAAAGCGTATCGGTTTCTGGCCAAATCAACCTTATCTTACAC 2739
 QY 2341 GGTGTAAAGCTTCTATGGGTTTAAACAATCTGTGTGGAAGCTTGAGCCGATGTAAGGTT 2400
 DB GGTGTAAAGCTTCTATGGGTTTAAACAATCTGTGTGGAAGCTTGAGCCGATGTAAGGTT 2799
 QY 2401 CGGGGCTGTGCTTTTACTGCTGAGAAAGGGGTGTGTCGCCCAAAAGAGAGGCT 2460
 DB CGGGGCTGTGCTTTTACTGCTGAGAAAGGGGTGTGTCGCCCAAAAGAGAGGCT 2859
 QY 2461 TCAATTAAGAAATGCTCTTTGAAAGGTATCTTGGGTATCTGTCTGAGAGGTATCTCC 2520
 DB TCAATTAAGAAATGCTCTTTGAAAGGTATCTTGGGTATCTGTCTGAGAGGTATCTCC 2919
 QY 2521 AGGGTGGCCCAATGTGGCTCCGACGTGTGTGTTCTTATGCTATGTAAGAAAGGTGCT 2580
 DB AGGGTGGCCCAATGTGGCTCCGACGTGTGTGTTCTTATGCTATGTAAGAAAGGTGCT 2979
 QY 2581 GTGATTAAGCATATCATGTATGTGGCAATGCGAGAGACAGGGGCTCTCAGATCTGAC 2640
 DB GTGATTAAGCATATCATGTATGTGGCAATGCGAGAGACAGGGGCTCTCAGATCTGAC 3039
 QY 2641 TGCTCGGACGGCACTGTCACTGTCTGTAAGCAATTCAGTACGAGCAGCACTCTCGCAG 2700
 DB TGCTCGGACGGCACTGTCACTGTCTGTAAGCAATTCAGTACGAGCAGCACTCTCGCAG 3099

QY 2701 GCCTGGCCAGTGTGTTGAGCATATACATCTGACCCGCTGTTCTTGTGCAATTTGGGTAACAG 2760
 DB GCCTGGCCAGTGTGTTGAGCATATACATCTGACCCGCTGTTCTTGTGCAATTTGGGTAACAG 3159
 QY 2761 AGGGGGGTGTTCTTCACTTACCAATGCAATTTAGTCACTAAGATATTGCTGAGCCC 2820
 DB AGGGGGGTGTTCTTCACTTACCAATGCAATTTAGTCACTAAGATATTGCTGAGCCC 3219
 QY 2821 GAGAGATGTCCAGAGTGAACCTGGAACGGGGTGTGTTGACATGACATGAAGATCTGGAAG 2880
 DB GAGAGATGTCCAGAGTGAACCTGGAACGGGGTGTGTTGACATGACATGAAGATCTGGAAG 3279
 QY 2881 GTGCTGAGTACCATGAGACCCGACCAAGGTGACAGACCTTGGAGTGTGGCGGTAAACAT 2940
 DB GTGCTGAGTACCATGAGACCCGACCAAGGTGACAGACCTTGGAGTGTGGCGGTAAACAT 3339
 QY 2941 ATTAGAACAGACCTGTGATGCTGATGTGACCGAGAGAGCTGAGAGCCCATCTTGGTG 3000
 DB ATTAGAACAGACCTGTGATGCTGATGTGACCGAGAGAGCTGAGAGCCCATCTTGGTG 3399
 QY 3001 CTGGCTGACACCGCGCTGAGATTGCTGCTTACGCGATGAAGATACAGATTGAG 3052
 DB CTGGCTGACACCGCGCTGAGATTGCTGCTTACGCGATGAAGATACAGATTGAG 3459
 RESULT 7
 AR102226
 LOCUS AR102226 35935 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 1 from patent US 6083750.
 ACCESSION AR102226
 VERSION AR102226.1 GI:12813024
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 35935)
 AUTHORS Chamberlain, J.S. and Kumar-Singh, R.
 TITLE Adenovirus vectors
 JOURNAL Patent: US 6083750-A 1 04-JUL-2000;
 FEATURES
 source 1..35935
 /organism="Unknown"
 /mol_type="unassigned DNA"
 ORIGIN
 Query Match 100.0%; Score 3052; DB 6; Length 35935;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTGTAGTATTAATACCCGGTGAAGTTCTTCAAGAGGCCACTTGTAGTGCACGCCAGT 60
 DB CGTGTAGTATTAATACCCGGTGAAGTTCTTCAAGAGGCCACTTGTAGTGCACGCCAGT 518
 QY 61 AGAGTTTCTCCCTCCGAGCGGCTCCGACACGGGACGTAAGAAATGACATATTATCTGCC 120
 DB AGAGTTTCTCCCTCCGAGCGGCTCCGACACGGGACGTAAGAAATGACATATTATCTGCC 578
 QY 519 AGAGTTTCTCCCTCCGAGCGGCTCCGACACGGGACGTAAGAAATGACATATTATCTGCC 578
 DB AGAGTTTCTCCCTCCGAGCGGCTCCGACACGGGACGTAAGAAATGACATATTATCTGCC 578
 QY 121 ACGGAGGTGTTATTAACGAAGAAATGAGCGGCACTTTTGAACACAGCTGATCGAAGAG 180
 DB ACGGAGGTGTTATTAACGAAGAAATGAGCGGCACTTTTGAACACAGCTGATCGAAGAG 638
 QY 579 ACGGAGGTGTTATTAACGAAGAAATGAGCGGCACTTTTGAACACAGCTGATCGAAGAG 638
 DB ACGGAGGTGTTATTAACGAAGAAATGAGCGGCACTTTTGAACACAGCTGATCGAAGAG 638
 QY 181 TACTGGCTGTAATCTTCCACCTCTAGCCATTTTGAACACCACTTCAAGAACTGT 240
 DB TACTGGCTGTAATCTTCCACCTCTAGCCATTTTGAACACCACTTCAAGAACTGT 698
 QY 241 ATGATTTAGACGTGACGGGCCCGCAAGATCCCAACGAGAGAGCGGTTTGCAGATTTTTC 300
 DB ATGATTTAGACGTGACGGGCCCGCAAGATCCCAACGAGAGAGCGGTTTGCAGATTTTTC 758
 QY 699 ATGATTTAGACGTGACGGGCCCGCAAGATCCCAACGAGAGAGCGGTTTGCAGATTTTTC 758
 DB ATGATTTAGACGTGACGGGCCCGCAAGATCCCAACGAGAGAGCGGTTTGCAGATTTTTC 758
 QY 301 CCGACTCTGTAATGTTGGCGGTGACGAGAGGATTTGACTTACTCACTTTTCCGCCGCC 360
 DB CCGACTCTGTAATGTTGGCGGTGACGAGAGGATTTGACTTACTCACTTTTCCGCCGCC 818

QY 361 CCGGTTCTCGGAGCGGCTGACACCTTTCCGGGACGCCGAGACGCCGGAGAGAGGCT 420
Db 819 CCGGTTCTCGGAGCGGCTGACACCTTTCCGGGACGCCGAGACGCCGAGAGAGGCT 878
QY 421 TGGGTCGGGTTTCTATGCAAACTTGTACCGGAGTGATGATCTTAACCTTGCAACGAG 480
Db 879 TGGGTCGGGTTTCTATGCAAACTTGTACCGGAGTGATGATGATCTTAACCTTGCAACGAG 938
QY 481 CTGGCTTTCCACCCAGTACGACGAGATGAAAGGGTGAGAGATTTGTGTTAATTTATG 540
Db 939 CTGGCTTTCCACCCAGTACGACGAGATGAAAGGGTGAGAGATTTGTGTTAATTTATG 998
QY 541 TGAAGACACCCGGGACGGTTGACAGTCTTGTCAATTAACCGAGAGAAATACGGGGAGC 600
Db 999 TGAAGACACCCGGGACGGTTGACAGTCTTGTCAATTAACCGAGAGAAATACGGGGAGC 1058
QY 601 CAGATATTATGTTGCTTGTGCTATATAGAGACCTGTGACATGTTGTCTACAGTAAGT 660
Db 1059 CAGATATTATGTTGCTTGTGCTATATAGAGACCTGTGACATGTTGTCTACAGTAAGT 1118
QY 661 GAAATTTATGGGCACTGGGTGATAGAGTGTTGGGTTTGGTGTGTTAATTTTTTTTAA 720
Db 1119 GAAATTTATGGGCACTGGGTGATAGAGTGTTGGGTTTGGTGTGTTAATTTTTTTTAA 1178
QY 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATTGTGATTTTTTTTAAAGGCTCTGTGC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATTGTGATTTTTTTTAAAGGCTCTGTGC 1238
QY 781 TGAACCTGAGCTGAGCCGAGCCGAGAAACGGAGCTTGCAAGACCTACCCGCTCTAA 840
Db 1239 TGAACCTGAGCTGAGCCGAGCCGAGAAACGGAGCTTGCAAGACCTACCCGCTCTAA 1298
QY 841 AATGGCCGCTGCTATCCCTGAGAACGCCGACATGACCTGTGCTAGAGAAATGCAATAGTAG 900
Db 1299 AATGGCCGCTGCTATCCCTGAGAACGCCGACATGACCTGTGCTAGAGAAATGCAATAGTAG 1358
QY 901 TACGGAATGCTGTGACTCCGGTCTTCTAACAACCTCTGAGATACACCGGAGTCTCC 960
Db 1359 TACGGAATGCTGTGACTCCGGTCTTCTAACAACCTCTGAGATACACCGGAGTCTCC 1418
QY 961 GCTGTGCCCATTTAAACCAAGTTGCCGTGAGAGTTGGTGGGCGTCCGACGGCTGTGGAATG 1020
Db 1419 GCTGTGCCCATTTAAACCAAGTTGCCGTGAGAGTTGGTGGGCGTCCGACGGCTGTGGAATG 1478
QY 1021 TATGAGAGACTTGTCTTAACGAGCCCTGGGCAACCTTTGGAACCTTGAGCTTAAACGCCAG 1080
Db 1479 TATGAGAGACTTGTCTTAACGAGCCCTGGGCAACCTTTGGAACCTTGAGCTTAAACGCCAG 1538
QY 1081 GCCATTAAGGTAAACCTGTGATTGCGTGTGTTAACGCCCTTGTGTTGCTGAATGAGT 1140
Db 1539 GCCATTAAGGTAAACCTGTGATTGCGTGTGTTAACGCCCTTGTGTTGCTGAATGAGT 1598
QY 1141 TGATGTAAATTTAATAAAGGTGAGATATGTTTAACTTGCAATGCGTGTAAATGGGCG 1200
Db 1599 TGATGTAAATTTAATAAAGGTGAGATATGTTTAACTTGCAATGCGTGTAAATGGGCG 1658
QY 1201 GGGGCTTAAAGGATATATAGCGCGCGGGGCTAATCTTGTTACATGTCGATCGATGGA 1260
Db 1659 GGGGCTTAAAGGATATATAGCGCGCGGGGCTAATCTTGTTACATGTCGATCGATGGA 1718
QY 1261 GCGTTGGAGAGTGTGGAAGATTTTTCTGCTGTGCGTAACCTTGCGAAGAGAGCTCTAA 1320
Db 1719 GCGTTGGAGAGTGTGGAAGATTTTTCTGCTGTGCGTAACCTTGCGAAGAGAGCTCTAA 1778
QY 1321 CAGTACTCTTGTGTTGGAAGTCTGTGGGCGCTCATCCGAGGAAAGTTAAGTCTGAG 1380
Db 1779 CAGTACTCTTGTGTTGGAAGTCTGTGGGCGCTCATCCGAGGAAAGTTAAGTCTGAG 1838
QY 1381 AATTTAAGAGATTAACAAGTGGGAAATTTGGAAGAGCTTTGAAATCTGTGAGTGAAGCTT 1440
Db 1839 AATTTAAGAGATTAACAAGTGGGAAATTTGGAAGAGCTTTGAAATCTGTGAGTGAAGCTT 1898
QY 1441 TGATTTCTTTGAATCGGTGACACAGGCGCTTTTCCAAAGAGAAAGTCAAGAAGCTTTGGA 1500

Db 1899 TGATTTCTTTGAATCTGGGTACACAGGCGCTTTTCCAAAGAGAAAGTCAAGAAGCTTTGGA 1958
QY 1501 TTTTTCACACCCGGGCGCGCTGTGCGTCTTGTGTTTGAAGTTTAAAGATTA 1560
Db 1959 TTTTTCACACCCGGGCGCGCTGTGCGTCTTGTGTTTGAAGTTTAAAGATTA 2018
QY 1561 ATGAGGGAAGAAACCATCTGAGCGGGGGGTACCTGTGGAATTTTCTGGCAGATCT 1620
Db 2019 ATGAGGGAAGAAACCATCTGAGCGGGGGGTACCTGTGGAATTTTCTGGCAGATCT 2078
QY 1621 GTGAGAGCGGTTGTGAGACAAAGAAATGCTGTCTACTGTGTCTTCCGTCCGCCCGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACAAAGAAATGCTGTCTACTGTGTCTTCCGTCCGCCCGC 2138
QY 1681 GATTAATACCGACGGAGAGACGACGACGACGACGAGAGAAAGCCAGCGCGCGGACGGA 1740
Db 2139 GATTAATACCGACGGAGAGACGACGACGACGAGAGAGAAAGCCAGCGCGCGGACGGA 2198
QY 1741 GCAGAGCCATGGAACCGGAGCGCGGCTGGAACCTCGGGAAATGAATGTTGACAGGTG 1800
Db 2199 GCAGAGCCATGGAACCGGAGCGCGGCTGGAACCTCGGGAAATGAATGTTGTTCAAGGTG 2258
QY 1801 GCTGAACCTGATCCAGAACTGAGACGCAATTTTGACAAATTAACAGAGATGGGCAAGGCTA 1860
Db 2259 GCTGAACCTGATCCAGAACTGAGACGCAATTTTGACAAATTAACAGAGATGGGCAAGGCTA 2318
QY 1861 AAGGGGTTAAAGAGGAGCGGGGGGCTTTGAGAGCTACAGAGAGGCTAAGAAATCTAGCT 1920
Db 2319 AAGGGGTTAAAGAGGAGCGGGGGGCTTTGAGAGCTACAGAGAGGCTAAGAAATCTAGCT 2378
QY 1921 TTTAGCTTAATGACCAACAACCGTCTGAGAGTATTACTTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACCAACAACCGTCTGAGAGTATTACTTTTCAACAGATCAAGATTAAT 2438
QY 1981 TGCCTAATGAGCTTGAATCTGTGCGCAGAAAGATTTCAATAGACAGCTGACCACTTAC 2040
Db 2439 TGCCTAATGAGCTTGAATCTGTGCGCAGAAAGATTTCAATAGACAGCTGACCACTTAC 2498
QY 2041 TGGCTGACGCCAGGGGATGATTTTGAAGAGGCTATTAGGGTATATGCAAGGTGGCACTT 2100
Db 2499 TGGCTGACGCCAGGGGATGATTTTGAAGAGGCTATTAGGGTATATGCAAGGTGGCACTT 2558
QY 2101 AGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGAAATGTTGTCTACATT 2160
Db 2559 AGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGAAATGTTGTCTACATT 2618
QY 2161 TCTGGGAAACGGGCGCAGAGTGAAGATTAACGAGGATAGGGTGGCTTTAGATGTAAGC 2220
Db 2619 TCTGGGAAACGGGCGCAGAGTGAAGATTAACGAGGATAGGGTGGCTTTAGATGTAAGC 2678
QY 2221 ATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAACGGGGTGTATTAAGAAATGTAAG 2280
Db 2679 ATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAACGGGGTGTATTAAGAAATGTAAG 2738
QY 2281 TTTACTGGCCCAATTTTAAAGGATACGATTTTCTGTGCAATAACCAACTTATCTTACAC 2340
Db 2739 TTTACTGGCCCAATTTTAAAGGATACGATTTTCTGTGCAATAACCAACTTATCTTACAC 2798
QY 2341 GGTGTAAAGCTTATATGGGTTTAAACAATACCTGTGTGAAGCTGAGCCGATGTAAAGGTT 2400
Db 2799 GGTGTAAAGCTTATATGGGTTTAAACAATACCTGTGTGAAGCTGAGCCGATGTAAAGGTT 2858
QY 2401 CGGGCGTGTGCTTTTACTGTGCTGGAAGGGGGTGTGTGTCGCCCCCAAAAGCAGGGCT 2460
Db 2859 CGGGCGTGTGCTTTTACTGTGCTGGAAGGGGGTGTGTGTCGCCCCCAAAAGCAGGGCT 2918
QY 2461 TCAATTTAAGAAATGCTCTTTTGAAGGATTAACCTTGGGATATCTGTCTGAGGATTAAGCTCC 2520
Db 2919 TCAATTTAAGAAATGCTCTTTTGAAGGATTAACCTTGGGATATCTGTCTGAGGATTAAGCTCC 2978
QY 2521 AGGGTGGCCCAAAATGTGGCTCCGACTGTGTGCTTCAATGCTAGTGAAGAAAGCTGTGCT 2580

Db 2979 AGGGTCCGCCAATGTGGCCCTCCGACTGTGTGTTCTTCATGTAGTGAAGGCTGCT 3038
Qy 2581 GTGATTAAACATTAACATGTATGTGGCAACTGCGAGACAAGGCGCTCTCAATGTCTGACC 2640
Db 3039 GTGATTAAACATTAACATGTATGTGGCAACTGCGAGACAAGGCGCTCTCAATGTCTGACC 3098
Qy 2641 TGTCTCGGACGGCAATGTCACTGTGTGAAGACCAATTCAGTACGACCACTCTTGCGAAG 2700
Db 3099 TGTCTCGGACGGCAATGTCACTGTGTGAAGACCAATTCAGTACGACCACTCTTGCGAAG 3158
Qy 2701 GCCTGGCCAGTGTGTGACATTAACATGACACCGCTGTCTTCTGATTTGGGTAAACAG 2760
Db 3159 GCCTGGCCAGTGTGTGACATTAACATGACACCGCTGTCTTCTGATTTGGGTAAACAG 3218
Qy 2761 AGGGGGGTGTCTTCACTTACCAATGCAATTTAGTCAACACTAAGATATTCCTTGAGCCC 2820
Db 3219 AGGGGGGTGTCTTCACTTACCAATGCAATTTAGTCAACACTAAGATATTCCTTGAGCCC 3278
Qy 2821 GAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGACATGACCAATGAATCTGGAAG 2880
Db 3279 GAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGACATGACCAATGAATCTGGAAG 3338
Qy 2881 GTGCTGAGGTACGATGAGACCCGACACAGTGCAGACCTGCGAGTGTGGCGTAAACAT 2940
Db 3339 GTGCTGAGGTACGATGAGACCCGACACAGTGCAGACCTGCGAGTGTGGCGTAAACAT 3398
Qy 2941 ATTAGGAACCAAGCTGTGATGTGTGATGTGACCGAGAGCTGAGGCCCGATCACTTGCTG 3000
Db 3399 ATTAGGAACCAAGCTGTGATGTGTGATGTGACCGAGAGCTGAGGCCCGATCACTTGCTG 3458
Qy 3001 CTGGCCCTGCACCCCGCTGAGATTTGGCTCTGAGCCATGAAGATACGATTTGAG 3052
Db 3459 CTGGCCCTGCACCCCGCTGAGATTTGGCTCTGAGCCATGAAGATACGATTTGAG 3510

RESULT 8
LOCUS AR116313 35935 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 43 from patent US 6133028.
ACCESSION AR116313
VERSION AR116313.1 GI:14096635
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 35935)
AUTHORS Imber,J.-L., Mchali,M. and Paviran,I.
TITLE Defective adenoviruses and corresponding complementation lines
JOURNAL Patent: US 6133028-A 43 17-OCT-2000;
FEATURES
Location/Qualifiers
1..35935
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 3052; DB 6; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTGTAGTATTTATACCGGAGTGTCTCAAGAGGCCACTGTGATGCGCAGCGAGT 60
Db 459 CGTGTAGTATTTATACCGGAGTGTCTCAAGAGGCCACTGTGATGCGCAGCGAGT 518
Qy 61 AGAGTTTCTCTCGACGCGCTCGACACCGGAGCTGAATAATGACATATTAATCTGCC 120
Db 519 AGAGTTTCTCTCGACGCGCTCGACACCGGAGCTGAATAATGACATATTAATCTGCC 578
Qy 121 ACGGAGGTATTAACCAAGAAATGCGCGCAGTCTTTTGACCAAGCTGATCGAAGAG 180
Db 579 ACGGAGGTATTAACCAAGAAATGCGCGCAGTCTTTTGACCAAGCTGATCGAAGAG 638
Qy 181 TACTGGCTGATATCTTCCACCTCTAGCGATTTTGAAACAATACTTACGAACTGT 240

Db 639 TACTGGCTGATATCTTCCACCTCTAGCGATTTTGAAACAATACTTACGAACTGT 698
Qy 241 ATGATTAGACGTGACGCGCCCCCAAGATCCCAACGAGAGCGGTTTCGAGATTTTTC 300
Db 699 ATGATTAGACGTGACGCGCCCCCAAGATCCCAACGAGAGCGGTTTCGAGATTTTTC 758
Qy 301 CCGACTCTGTAAATGTGGCGGTGACGAAGAGGATTTGACTTACTCATCTTTCCCGCGGCG 360
Db 759 CCGACTCTGTAAATGTGGCGGTGACGAAGAGGATTTGACTTACTCATCTTTCCCGCGGCG 818
Qy 361 CCGGTTCTCCGAGCGCGCTCACCTTTCCCGGACGCCGAGACGCCGAGAGAGGCT 420
Db 819 CCGGTTCTCCGAGCGCGCTCACCTTTCCCGGACGCCGAGACGCCGAGAGGCT 878
Qy 421 TGGGTCCGGTTTCTATGCGCAACCTTGTACCGAGGTGATGATCTTACCTGCCAGAG 480
Db 879 TGGGTCCGGTTTCTATGCGCAACCTTGTACCGAGGTGATGATCTTACCTGCCAGAG 938
Qy 481 CTGGCTTTCCACCCAGTGAACAAGGATGAAGAGGTGAGAGATTTGTATGATTAATG 540
Db 939 CTGGCTTTCCACCCAGTGAACAAGGATGAAGAGGTGAGAGATTTGTATGATTAATG 998
Qy 541 TGAAGCACCCCGGAGACGGTTGACAGTCTTGTCAATTAACCGGAGAAATACGGGGAGCC 600
Db 999 TGAAGCACCCCGGAGACGGTTGACAGTCTTGTCAATTAACCGGAGAAATACGGGGAGCC 1058
Qy 601 CAGATATTATGTGTGCTTGTCTATATGAGAACCTGTGACATGTTGTCTACAGTAAGT 660
Db 1059 CAGATATTATGTGTGCTTGTCTATATGAGAACCTGTGACATGTTGTCTACAGTAAGT 1118
Qy 661 GAAATATATGGGACGTGGGTATATGAGTGTGGTGTGGTGTGATTTTTTTTAT 720
Db 1119 GAAATATATGGGACGTGGGTATATGAGTGTGGTGTGGTGTGATTTTTTTTAT 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGATTTTGTATTTGATTTTAAAGGTCCTGTGTC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGATTTTGTATTTGTATTTTAAAGGTCCTGTGTC 1238
Qy 781 TGAACCTGAGCCTGAGCCGACCGAGCAACCGAGCCTGCAAGACCTACCCGCTCTTAA 840
Db 1239 TGAACCTGAGCCTGAGCCGACCGAGCAACCGAGCCTGCAAGACCTACCCGCTCTTAA 1298
Qy 841 AATGGCCCTCTCTATCTCTGAGACGCCCGGACATCACTGTGTCTTGAAGATGCAATATGAG 900
Db 1299 AATGGCCCTCTCTATCTCTGAGACGCCCGGACATCACTGTGTCTTGAAGATGCAATATGAG 1358
Qy 901 TACGATAGCTGTACTCCGGTCTTCTTACACACCTCTGAGATCAACCCGGTGTCTCC 960
Db 1359 TACGATAGCTGTACTCCGGTCTTCTTACACACCTCTGAGATCAACCCGGTGTCTCC 1418
Qy 961 GCTGTGCCCATTTAAACCAAGTTGCGGTGAGAGTGTGGCGGTGCGCAGGCTGTGGAATG 1020
Db 1419 GCTGTGCCCATTTAAACCAAGTTGCGGTGAGAGTGTGGCGGTGCGCAGGCTGTGGAATG 1478
Qy 1021 TATCAGAGACTTGTCTTAAACGAGCTGTGGCAACCTTTGACCTTGAAGCTTAAACGCCCCAG 1080
Db 1479 TATCAGAGACTTGTCTTAAACGAGCTGTGGCAACCTTTGACCTTGAAGCTTAAACGCCCCAG 1538
Qy 1081 GCCATTAAGGTGTAACCTGTGATTTGCGGTGTGTTAAGCGCTTGTGTGCTGATGAGT 1140
Db 1539 GCCATTAAGGTGTAACCTGTGATTTGCGGTGTGTTAAGCGCTTGTGTGCTGATGAGT 1598
Qy 1141 TGATGTAAAGTTTAAAGGTGAGATATGTTTAACTTGCATGAGCGGTAAATGGGGC 1200
Db 1599 TGATGTAAAGTTTAAAGGTGAGATATGTTTAACTTGCATGAGCGGTAAATGGGGC 1658
Qy 1201 GGGGCTTAAAGGTATTAATGCGCGGTGGGCTTAACTTGTGTTACATCTGACCTCATGAGA 1260
Db 1659 GGGGCTTAAAGGTATTAATGCGCGGTGGGCTTAACTTGTGTTACATCTGACCTCATGAGA 1718
Qy 1261 GGCTTGGAGAGTGTGGAAGATTTTCTGCTGTGCGTAACTTGTGGAACGAGACTCTTAA 1320
Db 1719 GGCTTGGAGAGTGTGGAAGATTTTCTGCTGTGCGTAACTTGTGGAACGAGACTCTTAA 1778

QY 1321 CAGTACCTCTGTTTGGAGGTTCTGTGGGGCTCATCCAGGAAAGTTAGTCTGAG 1380
DB 1779 CAGTACCTCTGTTTGGAGGTTCTGTGGGGCTCATCCAGGAAAGTTAGTCTGAG 1838
QY 1381 AATTAGAGAGATTACAGTGGGAATTGGAAGCTTTGAAATCTGTGGTGAAGCTTT 1440
DB 1839 AATTAGAGAGATTACAGTGGGAATTGGAAGCTTTGAAATCTGTGGTGAAGCTTT 1898
QY 1441 TGATCTTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCAAGACTTTGGA 1500
DB 1899 TGATCTTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCAAGACTTTGGA 1958
QY 1501 TTTTTCACACCGGGGGCGGCTGCGCTGTCTGTTTGAAGTTTATTAAGAAATA 1560
DB 1959 TTTTTCACACCGGGGGCGGCTGCGCTGTCTGTTTGAAGTTTATTAAGAAATA 2018
QY 1561 ATGAGCGAAGAAACCCATCTGAAGCGGGGGTACCTGTGATTTTCTGGCCATGCT 1620
DB 2019 ATGAGCGAAGAAACCCATCTGAAGCGGGGGTACCTGTGATTTTCTGGCCATGCT 2078
QY 1621 GTGAGAGCGGTTGTGAACACAGAAATGCGCTGCTACTGTGTCTTCCGTCCGCGGC 1680
DB 2079 GTGAGAGCGGTTGTGAACACAGAAATGCGCTGCTACTGTGTCTTCCGTCCGCGGC 2138
QY 1681 GATAATTACGACGAGAGAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 2139 GATAATTACGACGAGAGAGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2198
QY 1741 GCAGAGCCCATGGAACCCGAGAGCGGCGCTGGAACCTCGGAGATGATTTGACAGGTG 1800
DB 2199 GCAGAGCCCATGGAACCCGAGAGCGGCGCTGGAACCTCGGAGATGATTTGACAGGTG 2258
QY 1801 GCTGAACCTGTATCCGAACTGAGACGCAATTTGACAAATTAACAGAGATGGCGGCTTA 1860
DB 2259 GCTGAACCTGTATCCGAACTGAGACGCAATTTGACAAATTAACAGAGATGGCGGCTTA 2318
QY 1861 AAGGGGGTAAAG 1920
DB 2319 AAGGGGGTAAAG 2378
QY 1921 TTTAGCTTAATGACACAGACCGCTCTGAGTGTATTAATCTTTCAACAGATCAAGATTAAT 1980
DB 2379 TTTAGCTTAATGACACAGACCGCTCTGAGTGTATTAATCTTTCAACAGATCAAGATTAAT 2438
QY 1981 TGGCTTAATGAGCTTGAATCTGTGGCGCAGAAATTTCCATAGAGACGTAACCACTTAC 2040
DB 2439 TGGCTTAATGAGCTTGAATCTGTGGCGCAGAAATTTCCATAGAGACGTAACCACTTAC 2498
QY 2041 TGGCTGACAG 2100
DB 2499 TGGCTGACAG 2558
QY 2101 AGGCCAGATTGCAAGTACAGAACTTGTAAATATCAGAAATTTGTTGCTACATT 2160
DB 2559 AGGCCAGATTGCAAGTACAGAACTTGTAAATATCAGAAATTTGTTGCTACATT 2618
QY 2161 TCTGGGAACGGGGCCGAGGTGAGATTAATACGAGAGATAGGGTGGCTTTAGATGAGC 2220
DB 2619 TCTGGGAACGGGGCCGAGGTGAGATTAATACGAGAGATAGGGTGGCTTTAGATGAGC 2678
QY 2221 ATGATTAATATGTGCGCGGGGGTGTGGCAATGACGCGGGGTGTTAATATGAATGAAG 2280
DB 2679 ATGATTAATATGTGCGCGGGGGTGTGGCAATGACGCGGGGTGTTAATATGAATGAAG 2738
QY 2281 TTTACTGGCCCCCAATTTTAGCGGTAACGATTTCTGCGCAATACCAACTTATCTTACAC 2340
DB 2739 TTTACTGGCCCCCAATTTTAGCGGTAACGATTTCTGCGCAATACCAACTTATCTTACAC 2798
QY 2341 GGTGTAACCTTCTATAGGGTTTAACAATACCTGTGTGGAAGAGCTTGAACGATGAAGGTT 2400
DB 2799 GGTGTAACCTTCTATAGGGTTTAACAATACCTGTGTGGAAGAGCTTGAACGATGAAGGTT 2858

QY 2401 CGGGGCTGTGCTTTTATCTGCTGCTGGAGAGGGGGGTGGTGTGCGCCCCAAAGAGGGCT 2460
DB 2859 CGGGGCTGTGCTTTTATCTGCTGCTGGAGAGGGGGGTGGTGTGCGCCCCAAAGAGGGCT 2918
QY 2461 TCAATTAAGAAATGCTCTTTGAAAGGTGTAACCTTGGGTATCTGTGTGAGGGTAACTCC 2520
DB 2919 TCAATTAAGAAATGCTCTTTGAAAGGTGTAACCTTGGGTATCTGTGTGAGGGTAACTCC 2978
QY 2521 AGGGTGGCCCAATGTGGCTCCGACTGTGGTGTGCTTCAAGTCAAGTAAAGAGTGGCT 2580
DB 2979 AGGGTGGCCCAATGTGGCTCCGACTGTGGTGTGCTTCAAGTCAAGTAAAGAGTGGCT 3038
QY 2581 GTGATTAAGCATATCATGTGTGTGCAACCTGACAGAGACAGGGGCTCTCAGATGCTGACC 2640
DB 3039 GTGATTAAGCATATCATGTGTGTGCAACCTGACAGAGACAGGGGCTCTCAGATGCTGACC 3098
QY 2641 TGCTCGGACGGCAACTGTCACTGCTGAGAGACATTCACGTAGCCAGCACTCTGCAAG 2700
DB 3099 TGCTCGGACGGCAACTGTCACTGCTGAGAGACATTCACGTAGCCAGCACTCTGCAAG 3158
QY 2701 GCTGCGCAAGTGTGAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2760
DB 3159 GCTGCGCAAGTGTGAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3218
QY 2761 AGGGGGGTGCTCTTACCTTAACATGCAATTTAGTCACTAAGATATTTGCTTGAAGCC 2820
DB 3219 AGGGGGGTGCTCTTACCTTAACATGCAATTTAGTCACTAAGATATTTGCTTGAAGCC 3278
QY 2821 GAGAGCATGTCCAAAGTGAACCTGAACCGGGGTGTTGACATGACCATGAAGATCTGAA 2880
DB 3279 GAGAGCATGTCCAAAGTGAACCTGAACCGGGGTGTTGACATGACCATGAAGATCTGAA 3338
QY 2881 GTGCTGAGTACATGAGACCCGACCAAGAGTGCAGACCTTGGAGTGGGGGTAAATAT 2940
DB 3339 GTGCTGAGTACATGAGACCCGACCAAGAGTGCAGACCTTGGAGTGGGGGTAAATAT 3398
QY 2941 ATTAGAAACAGCCTGTGATGCTGATGTGACCGAGAGTGTGAGCCGATCACTTGGTG 3000
DB 3399 ATTAGAAACAGCCTGTGATGCTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 3458
QY 3001 CTGGCTGACACCGCGCTGAGTTGGCTTACGATGAAGATTAAGATTTGAG 3052
DB 3459 CTGGCTGACACCGCGCTGAGTTGGCTTACGATGAAGATTAAGATTTGAG 3510

RESULT 9
CQ854907
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .35935
/organism="unidentified adenovirus"
/mol_type="unasigned DNA"
/db_xref="taxon:10535"

ORIGIN
Query Match 100.0%; Score 3052; DB 6; Length 35935;
Best local similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTGTAGTATTTATACCCGCTGAGTTCTCAAGAGCCACTTGTAGTCCAGCGAGT 60
|||||

Db 459 CGTGTAGTATTTATACCGGGTAGTTCCTCAAGAGGCACTCTTGAGTCAGCGAGT 518
Qy 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGGACTGAAATGAGATATTTATCTGCC 120
Db 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGGACTGAAATGAGATATTTATCTGCC 578
Qy 121 ACGGAGGTGTTATACGGAAGAAATGGCCGACGCTTTTGAACAGCTGATGGAAGG 180
Db 579 ACGGAGGTGTTATACGGAAGAAATGGCCGACGCTTTTGAACAGCTGATGGAAGG 638
Qy 181 TACTGCTGATATCTTCCACTCTAGCCATTTTGAACACACTACCTTCCAGCACTGT 240
Db 639 TACTGCTGATATCTTCCACTCTAGCCATTTTGAACACACTACCTTCCAGCACTGT 698
Qy 241 ATGATTTAGAGTACGGCCCCCGAAGATCCCAAGAGAGCGGTTTCCGAGATTTTTC 300
Db 699 ATGATTTAGAGTACGGCCCCCGAAGATCCCAAGAGAGCGGTTTCCGAGATTTTTC 758
Qy 301 CCGACTCTGTAATGTTGGCGGTGAGAGAGGATTTGACTTACTGACTTTTCCGCGCGC 360
Db 759 CCGACTCTGTAATGTTGGCGGTGAGAGAGGATTTGACTTACTGACTTTTCCGCGCGC 818
Qy 361 CCGGTTCTCCGAGCCGCTCACTTCCCGGACCCGAGCAGCCGAGCAGAGAGCT 420
Db 819 CCGGTTCTCCGAGCCGCTCACTTCCCGGAGCCCGAGCAGCCGAGCAGAGAGCT 878
Qy 421 TGGGTCGGGTTCTATGCAAACTTTGTAACCGAGGTGATGATCTTACTCTGCCAGAG 480
Db 879 TGGGTCGGGTTCTATGCAAACTTTGTAACCGAGGTGATGATCTTACTCTGCCAGAG 938
Qy 481 CTGGCTTCCACCGAGTGAAGAGATGGAAGGGTGAAGAGATTTGTGTAATATATG 540
Db 939 CTGGCTTCCACCGAGTGAAGAGATGGAAGGGTGAAGAGATTTGTGTAATATATG 998
Qy 541 TGAAGACCCCGGACAGGTTGACAGTCTTGTCAATTAACAACGAGAAATACGGGGAGC 600
Db 999 TGAAGACCCCGGACAGGTTGACAGTCTTGTCAATTAACAACGAGAAATACGGGGAGC 1058
Qy 601 CAGATATATGTGTTCCGTTTGTATATGAGAACCTTGSCATGTTTGTCTACAGTAAGT 660
Db 1059 CAGATATATGTGTTCCGTTTGTATATGAGAACCTTGSCATGTTTGTCTACAGTAAGT 1118
Qy 661 GAAATATGSGGAGGTGATAGAGTGTGGGTTGTGTGTAATTTTTTTTTTAAAT 720
Db 1119 GAAATATGSGGAGGTGATAGAGTGTGGGTTGTGTGTAATTTTTTTTTTAAAT 1178
Qy 721 TTTTACAGTTTGTGTTAAAGAAATTTGTATTTGATTTTTTAAAGGTCCTGTGTC 780
Db 1179 TTTTACAGTTTGTGTTAAAGAAATTTGTATTTGATTTTTTAAAGGTCCTGTGTC 1238
Qy 781 TGAACCTGAGCCTGAGCCCGAGCAGAACCGGAGCTTGCAAGACTTACCCTCTCTAA 840
Db 1239 TGAACCTGAGCCTGAGCCCGAGCAGAACCGGAGCTTGCAAGACTTACCCTCTCTAA 1298
Qy 841 AATGGCCCTGCTATCTCTGAGACGCCCGCACTACCTGTGTCTAGAGAAATCAATAGTAG 900
Db 1299 AATGGCCCTGCTATCTCTGAGACGCCCGCACTACCTGTGTCTAGAGAAATCAATAGTAG 1358
Qy 901 TACGATAGCTGTGACTCCGGTCTTCTTACACACTCTGAGATACACCGGAGTGTCCC 960
Db 1359 TACGATAGCTGTGACTCCGGTCTTCTTACACACTCTGAGATACACCGGAGTGTCCC 1418
Qy 961 GCTGTGCCCATTAACCAAGTTGCTGTAGAGTTGTGTGGGCTGTGCAAGTGTGAATG 1020
Db 1419 GCTGTGCCCATTAACCAAGTTGCTGTAGAGTTGTGTGGGCTGTGCAAGTGTGAATG 1478
Qy 1021 TATGAGAGACTTGTCTTAAACGAGCCTTGCAACACTTGAATCTTGAACCTTGAACGCCCCAG 1080
Db 1479 TATGAGAGACTTGTCTTAAACGAGCCTTGCAACACTTGAATCTTGAACGCCCCAG 1538
Qy 1081 GCATTAAGGTATAACCTGTATGCGTGTGTGTTAAGCCTTGTGTTGCTGATAGT 1140
Db 1539 GCATTAAGGTATAACCTGTATGCGTGTGTGTTAAGCCTTGTGTTGCTGATAGT 1598

Qy 1141 TGATGTAGTTTAAATAAGGTGAGATATGTTTAACTTGATGCGGTGTTAAATGGGGC 1200
Db 1599 TGATGTAGTTTAAATAAGGTGAGATATGTTTAACTTGATGCGGTGTTAAATGGGGC 1658
Qy 1201 GGGGCTTAAAGGATATTAATGCGCGTGGGCTTAATCTTGGTTACATCTGACTCATGGA 1260
Db 1659 GGGGCTTAAAGGATATTAATGCGCGTGGGCTTAATCTTGGTTACATCTGACTCATGGA 1718
Qy 1261 GGCCTTGGAGTGTGGAAGATTTTCTGTGTCGTAACTTGTCTGGAACAGAGCTCTAA 1330
Db 1719 GGCCTTGGAGTGTGGAAGATTTTCTGTGTCGTAACTTGTCTGGAACAGAGCTCTAA 1778
Qy 1321 CAGTACTCTTGGTTTGAAGGTTCTGTGGGCTCATCCAGGCAAAAGTTAGTCTGAG 1380
Db 1779 CAGTACTCTTGGTTTGAAGGTTCTGTGGGCTCATCCAGGCAAAAGTTAGTCTGAG 1838
Qy 1381 AATTAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGGTAGCTGTT 1440
Db 1839 AATTAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGGTAGCTGTT 1898
Qy 1441 TGATTTCTTGAATCTGGGTCAACAGGCTTTTCCAAAGAGGTCAACAAGCTTTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACAGGCTTTTCCAAAGAGGTCAACAAGCTTTTGA 1958
Qy 1501 TTTTTCACACCGGGGCGCGCTGCGCTGCTGTGCTTTTGAAGTTTATTAAGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGCTGCTGTGCTTTTGAAGTTTATTAAGATTA 2018
Qy 1561 ATGAGAGGAAGAAACCATCTGAGCGGGGGGTACCTGTGGAATTTTCCGCGCATGCT 1620
Db 2019 ATGAGAGGAAGAAACCATCTGAGCGGGGGGTACCTGTGGAATTTTCCGCGCATGCT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACACAAGATTCGCTGCTACTGTGTCTTCCGTCCGCCGCG 1680
Db 2079 GTGAGAGCGGTTGTGAGACACAAGATTCGCTGCTACTGTGTCTTCCGTCCGCCGCG 2138
Qy 1681 GATTAATCCGACGGAGAGACAGCAGCAGCAGAGAGAAACCGCGCGCGCAGGA 1740
Db 2139 GATTAATCCGACGGAGAGACAGCAGCAGCAGAGAGAAACCGCGCGCGCAGGA 2198
Qy 1741 GCAGAGCCATGGAACCGGAGCGGCTGGAACCTTCGGGAATGAATGTTGACAGTG 1800
Db 2199 GCAGAGCCATGGAACCGGAGCGGCTGGAACCTTCGGGAATGAATGTTGACAGTG 2258
Qy 1801 GCTGAACGTATCCAGAACTGAGACGCAATTTGCAATTAACAAGATGGCAGGGCTA 1860
Db 2259 GCTGAACGTATCCAGAACTGAGACGCAATTTGCAATTAACAAGATGGCAGGGCTA 2318
Qy 1861 AAGGGGTAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT 1920
Db 2319 AAGGGGTAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT 2378
Qy 1921 TTTAGCTTAATGACCAACACCGCTGAGGTATTTACTTTCAACAGATCAAGGATAT 1980
Db 2379 TTTAGCTTAATGACCAACACCGCTGAGGTATTTACTTTCAACAGATCAAGGATAT 2438
Qy 1981 TGCGCTAATGAGCTTGTCTGCGCGCAGAAAGTATTCATAGAGAGCTGACCACTTAC 2040
Db 2439 TGCGCTAATGAGCTTGTCTGCGCGCAGAAAGTATTCATAGAGAGCTGACCACTTAC 2498
Qy 2041 TGGCTGAGCCAGGGGATGATTTTGAAGAGGCTATTAGGGTATATGCAAGGTGCACTT 2100
Db 2499 TGGCTGAGCCAGGGGATGATTTTGAAGAGGCTATTAGGGTATATGCAAGGTGCACTT 2558
Qy 2101 AGGCGAATTTGCAAGTACAGATCAGCAAACTTSTAATATACAGAAATGTTGCTACATT 2160
Db 2559 AGGCGAATTTGCAAGTACAGATCAGCAAACTTSTAATATACAGAAATGTTGCTACATT 2618
Qy 2161 TCTGGAAACGGGGCGAGGTGAGATAGATAACGAGATAGGGTGGCTTTAGATGTAAGC 2220
Db 2619 TCTGGAAACGGGGCGAGGTGAGATAGATAACGAGATAGGGTGGCTTTAGATGTAAGC 2678

2221 ATGATTAATATATGGCCGGGGGGTCTTGACATGACCGGGGTGTTATTATGATGTAAG 2280
2679 ATGATTAATATATGGCCGGGGGGTCTTGACATGACCGGGGTGTTATTATGATGTAAG 2738
2281 TTTACTGGCCCCCAATTTTAAAGCGGTATCGGTTTCTTGCCCAATACCACTTATCTTACAC 2340
2739 TTTACTGGCCCCCAATTTTAAAGCGGTATCGGTTTCTTGCCCAATACCACTTATCTTACAC 2798
2341 GGTGTAAGCTCTTAATGAGTTTAAACAATACCTGTGTGGAAGCTGTGACCGATGTAAAGGTT 2400
2799 GGTGTAAGCTCTTAATGAGTTTAAACAATACCTGTGTGGAAGCTGTGACCGATGTAAAGGTT 2858
2401 CGGGGCTGTGCTTTTAACTGCTGTAAGAGGGGTGTGTGTGCGCCCAAAAGCAGGCT 2460
2859 CGGGGCTGTGCTTTTAACTGCTGTAAGAGGGGTGTGTGTGCGCCCAAAAGCAGGCT 2918
2461 TCAATTTAAGAAATGCTCTTTGAAAAGGTATACCTTGGGTATCTGTCTGAGGGTAACTCC 2520
2919 TCAATTTAAGAAATGCTCTTTGAAAAGGTATACCTTGGGTATCTGTCTGAGGGTAACTCC 2978
2521 AGGGTGGCCCAATATGTCCTCCGACTGTGTTGCTTCACTGTAATGTAAGAGGCTGCT 2580
2979 AGGGTGGCCCAATATGTCCTCCGACTGTGTTGCTTCACTGTAATGTAAGAGGCTGCT 3038
2581 GTGATTTAAGCATTAATGATGTGTGCAACTGCGAGACAGGAGGCTCTCAGATGCTGACC 2640
3039 GTGATTTAAGCATTAATGATGTGTGCAACTGCGAGACAGGAGGCTCTCAGATGCTGACC 3098
2641 TGCTCGAGCGCAACTGTACCTGTGAAAGCAATTCAGTAGCCAGCCTCTTGCAGG 2700
3099 TGCTCGAGCGCAACTGTACCTGTGAAAGCAATTCAGTAGCCAGCCTCTTGCAGG 3158
2701 GCTCGGCGCAAGTGTGACATTAACAATACTGACCGCGTGTCTTGGTGAATTTGGTAAACAG 2760
3159 GCTCGGCGCAAGTGTGACATTAACAATACTGACCGCGTGTCTTGGTGAATTTGGTAAACAG 3218
2761 AGGGGGGTGTTCTTAACCTTACCAATGCAATTTGAGTCACTAAGATTTGCTTGAAGGCC 2820
3219 AGGGGGGTGTTCTTAACCTTACCAATGCAATTTGAGTCACTAAGATTTGCTTGAAGGCC 3278
2821 GAGAGCATGTCCAAAGGTGACCTGACCGGGGTGTTGACATGACCATGAAGATCTGGAAG 2880
3279 GAGAGCATGTCCAAAGGTGACCTGACCGGGGTGTTGACATGACCATGAAGATCTGGAAG 3338
2881 GTGCTGAGGTACGATGAGACCCGACCGAGTGCAGACCTGTGAGTGTGGGGGTAAATAT 2940
3339 GTGCTGAGGTACGATGAGACCCGACCGAGTGCAGACCTGTGAGTGTGGGGGTAAATAT 3398
2941 ATTAGAACAACCTGTGATCTGATGTGACCGAGAGCTGAGGCGCGATCACTTGGTGT 3000
3399 ATTAGAACAACCTGTGATCTGATGTGACCGAGAGCTGAGGCGCGATCACTTGGTGT 3458
3001 CTGGCTGACACCGCGCTGAGTTTGGCTCTACGATGAAGATACAGATTGAG 3052
3459 CTGGCTGACACCGCGCTGAGTTTGGCTCTACGATGAAGATACAGATTGAG 3510

RESULT 10
LOCUS AR230724 35935 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6451596.
ACCESSION AR230724
VERSION AR230724.1 GI:27271505
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35935)
AUTHORS Chamberlain,J.S., Amalfitano,A., Hauser,M.A., Kumar-Singh,R. and
Hartigan-O'Connor,D.J.
TITLE Helper adenovirus vector
JOURNAL Patent: US 6451596-A 1 17-SEP-2002;
FEATURES Location/Qualifiers

source 1..35935
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 3052; DB 6; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

1 CGTGTAGTATTTTAAACCCGAGTTCCTCAAGAGCCACTTGTAGTCCAGCGAGT 60
459 CGTGTAGTATTTTAAACCCGAGTTCCTCAAGAGCCACTTGTAGTCCAGCGAGT 518
61 AGATTTTTCCTCCGAGCCGCTCCGACACCGGGAATGAAATGACATTTATCTGCC 120
519 AGATTTTTCCTCCGAGCCGCTCCGACACCGGGAATGAAATGACATTTATCTGCC 578
121 ACGAGGTGTTATTAACGAATAATGACCGCACTTTTGAACCACTGATCGAAGAG 180
579 ACGAGGTGTTATTAACGAATAATGACCGCACTTTTGAACCACTGATCGAAGAG 638
181 TACTGCTGATTAATCTTCCACTTCACTTGAACCACTTGAACCACTTCAAGAACTGT 240
639 TACTGCTGATTAATCTTCCACTTCACTTGAACCACTTGAACCACTTCAAGAACTGT 698
241 ATGATTTAAGACGTACCGCCCGCAAGATCCCAACGAGAGGCGGTTTCGGAATTTTC 300
699 ATGATTTAAGACGTACCGCCCGCAAGATCCCAACGAGAGGCGGTTTCGGAATTTTC 758
301 CCGACTCTGTAATGTTGGCGGTGAGAGAGGATTTGACTACTTTCGCGCGCGC 360
759 CCGACTCTGTAATGTTGGCGGTGAGAGAGGATTTGACTACTTTCGCGCGCGC 818
361 CCGGTTCTCCGAGCCGCTCACTTTCGCGAGCCCGAGCAGCCGAGACAGAGCTT 420
819 CCGGTTCTCCGAGCCGCTCACTTTCGCGAGCCCGAGCAGCCGAGACAGAGCTT 878
421 TGGGTCCGGTTTCTAATGCCAAACCTTGACCGGAGGTATGACTTACCTGCCACAGG 480
879 TGGGTCCGGTTTCTAATGCCAAACCTTGACCGGAGGTATGACTTACCTGCCACAGG 938
481 CTGGCTTTCACACCGAGTACGACGAGGATGAGAGGTTGTTGTTAGATTATG 540
939 CTGGCTTTCACACCGAGTACGACGAGGATGAGAGGTTGTTGTTAGATTATG 998
541 TGGAGCACCCCGGCGACGGTGTGACGTTCTTGTCAATTATCACCGAGAAATCGGGGAGC 600
999 TGGAGCACCCCGGCGACGGTGTGACGTTCTTGTCAATTATCACCGAGAAATCGGGGAGC 1058
601 CAGATTTATGTTGTGCTTGTGATTAAGAGACCTGTGCACTTGTCTACAGTAAGT 660
1059 CAGATTTATGTTGTGCTTGTGATTAAGAGACCTGTGCACTTGTCTACAGTAAGT 1118
661 GAAATTTATGGCAGTGGGTGATGAGTGTGAGTTTGTGTGTTAAATTTTTTTTAAAT 720
1119 GAAATTTATGGCAGTGGGTGATGAGTGTGAGTTTGTGTGTTAAATTTTTTTTAAAT 1178
721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATTGTGATTTTTTTTAAAGGTCGTGTC 780
1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATTGTGATTTTTTTTAAAGGTCGTGTC 1238
781 TGAACCTGAGGCTGAGGCCGACGAGAACCGAGCCTGCAAGACTTACCGCGCTCTTAA 840
1239 TGAACCTGAGGCTGAGGCCGACGAGAACCGAGCCTGCAAGACTTACCGCGCTCTTAA 1298
841 AATGGCCCTGTATCTCTGAGACGCCGACATCACTGTGTCTAGAGATGCAATAGTAG 900
1299 AATGGCCCTGTATCTCTGAGACGCCGACATCACTGTGTCTAGAGATGCAATAGTAG 1358
901 TACGATAGCTGTGATCTCGGCTCTTTTAAACACCTCTCTGAGATACACCGGTGTGCC 960
1359 TACGATAGCTGTGATCTCGGCTCTTTTAAACACCTCTCTGAGATACACCGGTGTGCC 1418

Qy 961 GCTGTCCTCATTAACCAAGTTGCGTGAGAGTTGTTGGGGGTGCGCAAGCTGTGAAATG 1020
Db 1419 GCTGTGCCCCATTAAACCAAGTTGCGTGAGAGTTGTTGGGGGTGCGCAAGCTGTGAAATG 1478
Qy 1021 TATCGAGAGCTTGTCTTAAAGAGCTGGGCAACCTTTGAGCTTGAAGCTTAAACCCGAG 1080
Db 1479 TATCGAGAGCTTGTCTTAAAGAGCTGGGCAACCTTTGAGCTTGAAGCTTAAACCCGAG 1538
Qy 1081 GCCATAAGGTGTAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTTGCTGAATGAGT 1140
Db 1539 GCCATAAGGTGTAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTTGCTGAATGAGT 1598
Qy 1141 TGAATGAATTAATTAAGGGGAGATATATGTTTAACTGCATGGCGGTGTAATAGGGGC 1200
Db 1599 TGAATGAATTAATTAAGGGGAGATATATGTTTAACTGCATGGCGGTGTAATAGGGGC 1658
Qy 1201 GGGGCTTAAGGGATATATATGCGCGCTGAGCTAATCTTGGTTACATCTGACCTCATGGA 1260
Db 1659 GGGGCTTAAGGGATATATATGCGCGCTGAGCTAATCTTGGTTACATCTGACCTCATGGA 1718
Qy 1261 GGCCTTGGAGCTTGTGGAAGATTTTCTGCTGTGCTAATCTTGTGAAACAGAGCTCTAA 1320
Db 1719 GGCCTTGGAGCTTGTGGAAGATTTTCTGCTGTGCTAATCTTGTGAAACAGAGCTCTAA 1778
Qy 1321 CAGTACCTCTGTTTGGAGGTTTCTGTGGGGCTCATCCGAGCAAGTTAGTCTGAG 1380
Db 1779 CAGTACCTCTGTTTGGAGGTTTCTGTGGGGCTCATCCGAGCAAGTTAGTCTGAG 1838
Qy 1381 AATTAAAGAGATTAACAAGTGGGAATTTGAAGCTTTGAAATCTGTGTGAGCTGTT 1440
Db 1839 AATTAAAGAGATTAACAAGTGGGAATTTGAAGCTTTGAAATCTGTGTGAGCTGTT 1898
Qy 1441 TGAATCTTGAATCTGGGTCAACAGGGCTTTTCCAGAGAAAGTCAATCAAGCTTTGGA 1500
Db 1899 TGAATCTTGAATCTGGGTCAACAGGGCTTTTCCAGAGAAAGTCAATCAAGCTTTGGA 1958
Qy 1501 TTTTTCACACCGGGGGGCGGTGGGGCTGTGTTGCTTTTGTGCTTTTAAAGATTA 1560
Db 1959 TTTTTCACACCGGGGGGCGGTGGGGCTGTGTTGCTTTTGTGCTTTTAAAGATTA 2018
Qy 1561 ATGAGAGCAAGAAACCCATCTGAGCGGGGGGTACTGCTGAGATTTTGTGCGCATGCAATC 1620
Db 2019 ATGAGAGCAAGAAACCCATCTGAGCGGGGGGTACTGCTGAGATTTTGTGCGCATGCAATC 2078
Qy 1621 GTGAGAGCGGTTGTGAGACACAAGATTCGCTGCTACTGTGTGTTCCGTCGCGCCGAC 1680
Db 2079 GTGAGAGCGGTTGTGAGACACAAGATTCGCTGCTACTGTGTGTTCCGTCGCGCCGAC 2138
Qy 1681 GATAATACCGACGGAGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1740
Db 2139 GATAATACCGACGGAGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2198
Qy 1741 GCAGAGCCCATGGAACCGGAGCGGCTGGAACCTCGGGAAATGAATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCCATGGAACCGGAGCGGCTGGAACCTCGGGAAATGAATGTTGTACAGGTG 2258
Qy 1801 GCTGAACCTGATCCAGAACTGAGACGCAATTTGACAAATTAACAAGATGCGCAGGCGCTA 1860
Db 2259 GCTGAACCTGATCCAGAACTGAGACGCAATTTGACAAATTAACAAGATGCGCAGGCGCTA 2318
Qy 1861 AAGGGGGTAAAGAGGGAGCGGGGGCTTGTGAGCTTCAAGAGAGGCTTAAAGATCTAGCT 1920
Db 2319 AAGGGGGTAAAGAGGGAGCGGGGGCTTGTGAGCTTCAAGAGAGGCTTAAAGATCTAGCT 2378
Qy 1921 TTTAGCTTAATGACACAGACCGCTCTGAGTATTAATCTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACACAGACCGCTCTGAGTATTAATCTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGGCTTAATGAGCTTGAATCTGCTGCGCAGAAATTAATCATAGAGAGCTGACCTTAC 2040
Db 2439 TGGCTTAATGAGCTTGAATCTGCTGCGCAGAAATTAATCATAGAGAGCTGACCTTAC 2498
Qy 2041 TGGCTGACGACGAGGAGTGAATTTTGAAGAGCTTATAGGGTATATGCAAAAGTGGCACTT 2100

Db 2499 TGGCTGACGACGAGGAGTGAATTTTGAAGAGCTTATAGGGTATATGCAAAAGTGGCACTT 2558
Qy 2101 AGGCAGATTTGCAAGTACCAAGATCAGCAACTGTAAATATCAAGAAATTTGTCTACATT 2160
Db 2559 AGGCAGATTTGCAAGTACCAAGATCAGCAACTGTAAATATCAAGAAATTTGTCTACATT 2618
Qy 2161 TCTGGAAACGGGGCCGAGGTGAGATAGATACGAGATAGGGTGGCTTTAGATGTAGC 2220
Db 2619 TCTGGAAACGGGGCCGAGGTGAGATAGATACGAGATAGGGTGGCTTTAGATGTAGC 2678
Qy 2221 ATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAAGGGGGGTATATGAATGTAGG 2280
Db 2679 ATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAAGGGGGGTATATGAATGTAGG 2738
Qy 2281 TTTACTGGCCCCAATTTTACCGGTACCGTTTCTGTGCCAATACCACTTATCTCTACAC 2340
Db 2739 TTTACTGGCCCCAATTTTACCGGTACCGTTTCTGTGCCAATACCACTTATCTCTACAC 2798
Qy 2341 GGTGTAAAGCTTTCTATGGGTTTAAACAATACCTGTGTGGAAGCTTGAACCGATGTAGGGTT 2400
Db 2799 GGTGTAAAGCTTTCTATGGGTTTAAACAATACCTGTGTGGAAGCTTGAACCGATGTAGGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGTGTGCGCCCAAAAGCAGGGCT 2460
Db 2859 CGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGTGTGCGCCCAAAAGCAGGGCT 2918
Qy 2461 TCAATTAAGAAATGCGCTCTTTGAAGGTGTACCTTGGGTATCTGTGTGAGGGTAACTCC 2520
Db 2919 TCAATTAAGAAATGCGCTCTTTGAAGGTGTACCTTGGGTATCTGTGTGAGGGTAACTCC 2978
Qy 2521 AGGGTGGCCCAACAATGTGGCTTCCGACTGTGTGCTTCAATGTCTAGTGAAGGTTGGCT 2580
Db 2979 AGGGTGGCCCAACAATGTGGCTTCCGACTGTGTGCTTCAATGTCTAGTGAAGGTTGGCT 3038
Qy 2581 GTGATTAAGCATTAACATGTATGTGGCACTGGAGACAGGGGCTCTCGATGCTGAC 2640
Db 3039 GTGATTAAGCATTAACATGTATGTGGCACTGGAGACAGGGGCTCTCGATGCTGAC 3098
Qy 2641 TGTCTGGACGGCAACCTGTCACTGTGAAGACCAATTCACCTAGCCAGCCTCTCGCAAG 2700
Db 3099 TGTCTGGACGGCAACCTGTCACTGTGAAGACCAATTCACCTAGCCAGCCTCTCGCAAG 3158
Qy 2701 GCTTGGCCAGTGTGTTGAGCATTAATCAATGCAATTTGAGTCACTAAAGATTTGCTTGAAGCCC 2820
Db 3159 GCTTGGCCAGTGTGTTGAGCATTAATCAATGCAATTTGAGTCACTAAAGATTTGCTTGAAGCCC 3218
Qy 2761 AGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCACTAAAGATTTGCTTGAAGCCC 2880
Db 3219 AGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCACTAAAGATTTGCTTGAAGCCC 3278
Qy 2821 GAGAGCATGTCCAAAGGTGAACCTGAACGGGGGTGTTGACATGACATGAAGATCTGGAG 2880
Db 3279 GAGAGCATGTCCAAAGGTGAACCTGAACGGGGGTGTTGACATGACATGAAGATCTGGAG 3338
Qy 2881 GTGCTGAGGTACAGTGAAGACCTGACCAAGGTGAGACCTTGCAGAGTGTGGCGGTTAAACAT 2940
Db 3339 GTGCTGAGGTACAGTGAAGACCTGACCAAGGTGAGACCTTGCAGAGTGTGGCGGTTAAACAT 3398
Qy 2941 AATTAGAAACAGGCTGTGATGTGAGTGTGAACCGAAGAGTGTAGGCCCATGACTGTGTG 3000
Db 3399 AATTAGAAACAGGCTGTGATGTGAGTGTGAACCGAAGAGTGTAGGCCCATGACTGTGTG 3458
Qy 3001 CTGGGCTGACCGCGCTGAGTTTGGCTCTAGCGATGAAGATCAAGATTGAG 3052
Db 3459 CTGGGCTGACCGCGCTGAGTTTGGCTCTAGCGATGAAGATCAAGATTGAG 3510

RESULT 11
AX451988
LOCUS AX451988 35935 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 1 from Patent WO024393.
ACCESSION AX451988

VERSION	AX451988.1	GI:21711988
KEYWORDS	Human adenovirus type 5	
SOURCE	Human adenovirus type 5	
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.	
REFERENCE	1	
AUTHORS	Arrendasiz Borunda,J. and Aguilar Cordova,E.	
TITLE	Recombinant viral and non-viral vectors containing the human urokinase plasminogen activator gene and its utilization in the treatment of various types of hepatic, renal, pulmonary, pancreatic and cardiac fibrosis and hypertrophic scars	
JOURNAL	Patient: WO 024393-A 1 06-JUN-2002;	
FEATURES	TGT LAB S A DE C V (MX)	
SOURCE	Location/Qualifiers	
	1..35935	
	/organism="Human adenovirus type 5"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:28285"	
ORIGIN		
Query Match	100.0%;	Score 3052; DB 6; Length 35935;
Best Local Similarity	100.0%;	Pred. No. 0;
Matches 3052; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 CGTGTAGTATTTATACCCGGTGAAGTCTCAAGAGCCACTTGAAGTCCAGCGAGT 60	
DB	459 CGTGTAGTATTTATACCCGGTGAAGTCTCAAGAGCCACTTGAAGTCCAGCGAGT 518	
QY	61 AGAGTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAATAAGACATTTATCTGCC 120	
DB	519 AGAGTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAATAAGACATTTATCTGCC 578	
QY	121 ACGGAGGTGTATTAACGGAAGAAATGGCGCAGCTTTTGAACAGCTGATTCGAAGAG 180	
DB	579 ACGGAGGTGTATTAACGGAAGAAATGGCGCAGCTTTTGAACAGCTGATTCGAAGAG 638	
QY	181 TACTGCTGATTAATCTTCCACTCTAGCCATTTTGAACACACTTACCTTACGAACTGT 240	
DB	639 TACTGCTGATTAATCTTCCACTCTAGCCATTTTGAACACACTTACCTTACGAACTGT 698	
QY	241 ATGATTTAGAGTGAACGCGCCCGGAAAGATCCCAACGAGAGGCGGTTTCCGACATTTTTC 300	
DB	699 ATGATTTAGAGTGAACGCGCCCGGAAAGATCCCAACGAGAGGCGGTTTCCGACATTTTTC 758	
QY	301 CCGACTCTGTAATGTGGCGGTGACGAAAGGATTTGACTTCACTTTCGCGCGGCGC 360	
DB	759 CCGACTCTGTAATGTGGCGGTGACGAAAGGATTTGACTTCACTTTCGCGCGGCGC 818	
QY	361 CCGGTTCTCCGAGACCGCTCACCTTTCGCGACGCCGAGCAGCCGAGACGAGAGCT 420	
DB	819 CCGGTTCTCCGAGACCGCTCACCTTTCGCGACGCCGAGCAGCCGAGACGAGAGCT 878	
QY	421 TGGGTCGGGTTTCTATGCAAACTTTGACCGGAGGTGATGATCTTAACCTGCCACGAGG 480	
DB	879 TGGGTCGGGTTTCTATGCAAACTTTGACCGGAGGTGATGATCTTAACCTGCCACGAGG 938	
QY	481 CTGGCTTTCCACCGAGTGAACGAGATGAAGAGGTGAGAGGTTGTGTAGATTATG 540	
DB	939 CTGGCTTTCCACCGAGTGAACGAGATGAAGAGGTGAGAGGTTGTGTAGATTATG 998	
QY	541 TGGAGACCCCGGAGCAGGTTGACAGTCTTGTCAATTATCACCGAGAGATACCGGGAGCC 600	
DB	999 TGGAGACCCCGGAGCAGGTTGACAGTCTTGTCAATTATCACCGAGAGATACCGGGAGCC 1058	
QY	601 CAGATATTATGTTCGTTTGTCTATATGAGACCTGTGGCATGTTGTCTACAGTAAGT 660	
DB	1059 CAGATATTATGTTCGTTTGTCTATATGAGACCTGTGGCATGTTGTCTACAGTAAGT 1118	
QY	661 GAAATATTAGGCGAGTGATGATGAGTGTGGGTTGTGTGATTTTATTTTAT 720	
DB	1119 GAAATATTAGGCGAGTGATGATGAGTGTGGGTTGTGTGATTTTATTTTAT 1178	
QY	721 TTTTACAGTTTGTGTTTAAAGATTTTGTATTGTGATTTTAAAGGTCCTGTCTC 780	

DB	1179 TTTTACAGTTTGTGTTTAAAGATTTTGTATTGTATTTTAAAGGTCCTGTCTC 1238	
QY	781 TGAACCTGAGCTGAGCCCGAGCCAGAACCGGAGCTTGCAAGACTTACCGCGCTCTTA 840	
DB	1239 TGAACCTGAGCTGAGCCCGAGCCAGAACCGGAGCTTGCAAGACTTACCGCGCTCTTA 1298	
QY	841 AATGGCCCTGCTATCTCTGAGAGCCCGACATCACTGTGCTGAGAAATGCAATAGTAG 900	
DB	1299 AATGGCCCTGCTATCTCTGAGAGCCCGACATCACTGTGCTGAGAAATGCAATAGTAG 1358	
QY	901 TACGGATAGCTGTGACTCCGGTCTTTTAAACACCTTCTGAGATACCCCGTGTCTCC 960	
DB	1359 TACGGATAGCTGTGACTCCGGTCTTTTAAACACCTTCTGAGATACCCCGTGTCTCC 1418	
QY	961 GCTGTGCCCATTTAAACAGTTGCCGTGAGAGTTGGGGGTGCGCAGGCTGTGGAATG 1020	
DB	1419 GCTGTGCCCATTTAAACAGTTGCCGTGAGAGTTGGGGGTGCGCAGGCTGTGGAATG 1478	
QY	1021 TATGAGGACTTGCTTAAACGAGCCGAGCAACCTTGGACTGTAGCTGTAAACGCCCCAG 1080	
DB	1479 TATGAGGACTTGCTTAAACGAGCCGAGCAACCTTGGACTGTAGCTGTAAACGCCCCAG 1538	
QY	1081 GCCATTAAGTGTAAACCTGTGATTCGTGTGTGTTAAACGCTTTGTTGCTGAATAGT 1140	
DB	1539 GCCATTAAGTGTAAACCTGTGATTCGTGTGTGTTAAACGCTTTGTTGCTGAATAGT 1598	
QY	1141 TGATGTAACTTTAATAAGGAGTGAATATGTTTAACTTGACATGCGCTGTTAAATGGGCG 1200	
DB	1599 TGATGTAACTTTAATAAGGAGTGAATATGTTTAACTTGACATGCGCTGTTAAATGGGCG 1658	
QY	1201 GGGGCTTAAAGGGATATTAATGCGCGGTGGGCTTAATCTTGGATTACATCTGACCTATGGA 1260	
DB	1659 GGGGCTTAAAGGGATATTAATGCGCGGTGGGCTTAATCTTGGATTACATCTGACCTATGGA 1718	
QY	1261 GGCTTGGAGTGTTTGGAAGATTTTCTGCTGTGCGTAATCTGTGGAACAGAGCTCTAA 1320	
DB	1719 GGCTTGGAGTGTTTGGAAGATTTTCTGCTGTGCGTAATCTGTGGAACAGAGCTCTAA 1778	
QY	1321 CAGTACTCTTGGTTTGGAGGTTCTGTGGGGCTCATCCAGGCAAAAGTTAGTCTGAG 1380	
DB	1779 CAGTACTCTTGGTTTGGAGGTTCTGTGGGGCTCATCCAGGCAAAAGTTAGTCTGAG 1838	
QY	1381 AATTAAAGAGATTAACAAGTGGGAATTTGAAGAGCTTTTGAATCTGTGGTGAAGTCT 1440	
DB	1839 AATTAAAGAGATTAACAAGTGGGAATTTGAAGAGCTTTTGAATCTGTGGTGAAGTCT 1898	
QY	1441 TGATCTTTGAATCTGGGTCAACAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTTGA 1500	
DB	1899 TGATCTTTGAATCTGGGTCAACAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTTGA 1958	
QY	1501 TTTTTCACACCCGGGGCGCGCTGCGGTGCTGTGGCTTTTGTAGTTTATTAAGATTA 1560	
DB	1959 TTTTTCACACCCGGGGCGCGCTGCGGTGCTGTGGCTTTTGTAGTTTATTAAGATTA 2018	
QY	1561 ATGAGCGGAAGAAACCATCATGAGCGGGGGTACCTGCTGGAATTTTGTGGCATATGCT 1620	
DB	2019 ATGAGCGGAAGAAACCATCATGAGCGGGGGTACCTGCTGGAATTTTGTGGCATATGCT 2078	
QY	1621 GTGGAGAGCGGTTGTGAGACAAAGAAATGCTGTGCTTCCGTCCGCGCGGC 1680	
DB	2079 GTGGAGAGCGGTTGTGAGACAAAGAAATGCTGTGCTTCCGTCCGCGCGGC 2138	
QY	1681 GATTAATCCGACCGAGAGACGACGACGACGAGAGAGAAACCGAGGCGCGCGGACGGA 1740	
DB	2139 GATTAATCCGACCGAGAGACGACGACGACGAGAGAGAAACCGAGGCGCGCGGACGGA 2198	
QY	1741 GCAGAGCCCATGGAACCGAGAGCGGCGCTGAGCCCTCGGGAATGATGTTGTACAGGTG 1800	
DB	2199 GCAGAGCCCATGGAACCGAGAGCGGCGCTGAGCCCTCGGGAATGATGTTGTACAGGTG 2258	
QY	1801 GCTGAACGTATCCAGAACTGAGACGCAATTTTGACAAATTAACAGAGATGGGACGGGCTA 1860	

Db 2259 GCTGACTGATCCAGAACTGAGACGCAATTTTGACAAATTACAGAGATGGCGGCTA 2318
Qy 1861 AAGGGGTTAAAGAGGAGCGGGGGCTTTGTAGGCTACAGAGAGCTAGGAATCTAGCT 1920
Db 2219 AAGGGGGTAAAGAGGAGCGGGGGCTTTGTAGGCTACAGAGAGGCTAGGAATCTAGCT 2378
Qy 1921 TTTTGTGTTAATGACCAACACCGCTCTGAGTGATTAATCTTTTCAACAGATCAAGATTAAT 1980
Db 2279 TTTTGTGTTAATGACCAACACCGCTCTGAGTGATTAATCTTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGCGCTATGAGCTTGAATCTGCTGGCGGAGAAAGTATTCATAGAGAGCTGACCACTTAC 2040
Db 2439 TGCGCTATGAGCTTGAATCTGCTGGCGGAGAAAGTATTCATAGAGAGCTGACCACTTAC 2498
Qy 2041 TGCGCTGACCGGAGGATGATTTTGGAGAGGCTATTAGGCTATATGCAAGGTGGCACTT 2100
Db 2499 TGCGCTGACCGGAGGATGATTTTGGAGAGGCTATTAGGCTATATGCAAGGTGGCACTT 2558
Qy 2101 AGGCGCAATTCGAAGTACAAATCAGCAACTTGTAAATATCAGGAATTTGTTGCTACATT 2160
Db 2559 AGGCGCAATTCGAAGTACAAATCAGCAACTTGTAAATATCAGGAATTTGTTGCTACATT 2618
Qy 2161 TCTGGGAAACGGGGCGGAGGTGAGATAGATAAGAGATAGAGGTGGCTTTAGATGTAGC 2220
Db 2619 TCTGGGAAACGGGGCGGAGGTGAGATAGATAAGAGATAGAGGTGGCTTTAGATGTAGC 2678
Qy 2221 ATGATAAATATGTGGCCCGGGGGTGTGGCAATGACCGGGGTGTATTATATGATGTAAG 2280
Db 2679 ATGATAAATATGTGGCCCGGGGGTGTGGCAATGACCGGGGTGTATTATATGATGTAAG 2738
Qy 2281 TTTTCTGGCCCCAATTTTACGGGTACGGTTTTCTGGCCAAATACCACCTTATCTTACAC 2340
Db 2739 TTTTCTGGCCCCAATTTTACGGGTACGGTTTTCTGGCCAAATACCACCTTATCTTACAC 2798
Qy 2341 GGTTAAGCTTCTATGGGTTTAAACAATCCTGTGTGAGAGGCTGGACCGATGTAAGGTT 2400
Db 2799 GGTTAAGCTTCTATGGGTTTAAACAATCCTGTGTGAGAGGCTGGACCGATGTAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTAACTGTCTGAGAAAGGGGTGTGTGTGCGCCCAAAAGCAGGCT 2460
Db 2859 CGGGGCTGTGCTTTTAACTGTCTGAGAAAGGGGTGTGTGTGCGCCCAAAAGCAGGCT 2918
Qy 2461 TCAATTAAGAAATGCTTTTGAAGAGGTACCTTGGGTATCTGTCTGAGAGGTAACTCC 2520
Db 2919 TCAATTAAGAAATGCTTTTGAAGAGGTACCTTGGGTATCTGTCTGAGAGGTAACTCC 2978
Qy 2521 AGGGTGGCCCAATGTGGCTCCGACTGTGGTTGCTTATGCTAGTAAAGAGGCTGCT 2580
Db 2979 AGGGTGGCCCAATGTGGCTCCGACTGTGGTTGCTTATGCTAGTAAAGAGGCTGCT 3038
Qy 2581 GTGATTAAGCAATCATGTGTATGTGGCAACTGCGAGACAGGGGCTCTCAGATGCTGACC 2640
Db 3039 GTGATTAAGCAATCATGTGTATGTGGCAACTGCGAGACAGGGGCTCTCAGATGCTGACC 3098
Qy 2641 TGTCTGGAACGGCAACTGTCACTGTGTAAGACCAATTCAGTACGAGGCACTCTGCGAAG 2700
Db 3099 TGTCTGGAACGGCAACTGTCACTGTGTAAGACCAATTCAGTACGAGGCACTCTGCGAAG 3158
Qy 2701 GCCTGGGCAAGTGTGAGCATTAACAATCCGCGTGTCTTGGCATTTGGGTTAAAGG 2760
Db 3159 GCCTGGGCAAGTGTGAGCATTAACAATCCGCGTGTCTTGGCATTTGGGTTAAAGG 3218
Qy 2761 AGGGGGGTGTTCTTACCTTACCAATGCAATTTAGTACACATAAGATTTGCTGAGCCC 2820
Db 3219 AGGGGGGTGTTCTTACCTTACCAATGCAATTTAGTACACATAAGATTTGCTGAGCCC 3278
Qy 2821 GAGAGCAATGTCAGAGTGAACCTGAAACGGGGTGTGTAATGCAATGAAATCTGGAAG 2880
Db 3279 GAGAGCAATGTCAGAGTGAACCTGAAACGGGGTGTGTAATGCAATGAAATCTGGAAG 3338
Qy 2881 GTGCTGAGGTAGATGAGACCGGCAAGGTGAGACCTGTGAGATGTGGCGGTAAACAT 2940
Db 3339 GTGCTGAGGTAGATGAGACCGGCAAGGTGAGACCTGTGAGATGTGGCGGTAAACAT 3398

Qy 2941 ATTGGAACCAAGCTGTGATGCTGATGTGACCGAGAGAGCTGAGCCCGATCACTTGCTG 3000
Db 3399 ATTGGAACCAAGCTGTGATGCTGATGTGACCGAGAGAGCTGAGCCCGATCACTTGCTG 3458
Qy 3001 CTGGCCCTGCAACCCGCGCTGAGTTTGGCTCTAGCGGATGAAGTACAGATTGAG 3052
Db 3459 CTGGCCCTGCAACCCGCGCTGAGTTTGGCTCTAGCGGATGAAGTACAGATTGAG 3510

RESULT 12
AX683770
LOCUS AX683770 35935 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 1 from Patent W003006662.
VERSION AX683770
KEYWORDS AX683770.1 GI:29370798
SOURCE Human adenovirus type 5
ORGANISM Human adenovirus type 5
REFERENCE 1
AUTHORS Iggo,R.D., Fuerer,C. and Homicsko,K.G.
TITLE Anti-neoplastic viral agents
JOURNALS Patent: WO 0306662-A 1 23-JAN-2003;
BTG International Limited (GB)
FEATURES
source
1. .35935
/organism="Human adenovirus type 5"
/mol_type="unassigned DNA"
/db_xref="taxon:28285"

ORIGIN
Query Match 100.0%; Score 3052; DB 6; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGTGATGTTATTTATACCGGGTGAATTCCTCAAGAGGCCACTCTTGAGTGCACGGCT 60
Db 459 CGGTGATGTTATTTATACCGGGTGAATTCCTCAAGAGGCCACTCTTGAGTGCACGGCT 518
Qy 61 AGAGTTTCTCTCCGAGCGGCTCCGACACCGGAGCTGAATAAGACATTTATCTGCC 120
Db 519 AGAGTTTCTCTCCGAGCGGCTCCGACACCGGAGCTGAATAAGACATTTATCTGCC 578
Qy 121 ACGAGGTGTTATTAACGAAAGATGCGCGCACTTTTGGACCACTGATGGAAGG 180
Db 579 ACGAGGTGTTATTAACGAAAGATGCGCGCACTTTTGGACCACTGATGGAAGG 638
Qy 181 TACTGGCTGATTAATCTTCACTTCTAGCCATTTTGAACCACTTACCTTACGAACTGT 240
Db 639 TACTGGCTGATTAATCTTCACTTCTAGCCATTTTGAACCACTTACCTTACGAACTGT 698
Qy 241 ATGATTTAGACGTACCGGCCCCGAAAGATCCCAAGAGAGCGGTTTCCGAGATTTTTC 300
Db 699 ATGATTTAGACGTACCGGCCCCGAAAGATCCCAAGAGAGCGGTTTCCGAGATTTTTC 758
Qy 301 CCGACTCTGTAATGTGGCGGTGACGAAAGGATTTGACTTCACTTTTCCGCGCGGC 360
Db 759 CCGACTCTGTAATGTGGCGGTGACGAAAGGATTTGACTTCACTTTTCCGCGCGGC 818
Qy 361 CCGGTTCTCCGAGACCGGCTTCACTTTTCCGCGACGCCGAGACCCGAGACCGGAGAGGCT 420
Db 819 CCGGTTCTCCGAGACCGGCTTCACTTTTCCGCGACGCCGAGACCCGAGAGAGGCT 878
Qy 421 TGAGTCCGTTTCTATGCAAACTTGTACCGAGGTGATGATCTTTCCTGCAAGAG 480
Db 879 TGAGTCCGTTTCTATGCAAACTTGTACCGAGGTGATGATCTTTCCTGCAAGAG 938
Qy 481 CTGACTTTTCAACCAAGTACGACGAGATGAAGAGGTGAGAGGTTGTGTTAATTATG 540
Db 939 CTGACTTTTCAACCAAGTACGACGAGATGAAGAGGTGAGAGGTTGTGTTAATTATG 998
Qy 541 TGAGACACCCCGGAGCGGTTGACAGGTCTTGTCAATTATCAACGAGAGAAATACGGGGAGCC 600

Db 999 TGGAGCAACCCGGGACGGTTGCAAGTCTTGTCAATTACACGGAGAAATACGGGGAGCC 1058
Qy 601 CAGATATTATGTGTTCCGTTTGTCTATATAGAGACCTGTGGCACTGTTGTCTACAGTAAGT 660
Db 1059 CAGATATTATGTGTTCCGTTTGTCTATATAGAGACCTGTGGCATGTTGTCTACAGTAAGT 1118
Qy 661 GAAATTTATGGGCAAGTGGGTATAGAGTGTGGGTTGTGTGGTAATTTTTTTTTTAAAT 720
Db 1119 GAAATTTATGGGCAAGTGGGTATAGAGTGTGGGTTGTGTGGTAATTTTTTTTTTAAAT 1178
Qy 721 TTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGGTCCTGTGTC 780
Db 1179 TTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGGTCCTGTGTC 1238
Qy 781 TGAACCTAGACCTGAGCCCGAGCCGAGAACCCGAGCCTTGCAAGACTTACCCTCCTTAA 840
Db 1239 TGAACCTAGACCTGAGCCCGAGCCGAGAACCCGAGCCTTGCAAGACTTACCCTCCTTAA 1298
Qy 841 AATGGCCGCTGTATCCTGAGACGCCCGACATCACTGTGTCTAGAGAAATGCAATATATAG 900
Db 1289 AATGGCCGCTGTATCCTGAGACGCCCGACATCACTGTGTCTAGAGAAATGCAATATAG 1358
Qy 901 TACGGATAGCTGTGACTCCGGTCTTCTAACACACTTCTGAGATACACCCGGTGTGCC 960
Db 1359 TACGGATAGCTGTGACTCCGGTCTTCTAACACACTTCTGAGATACACCCGGTGTGCC 1418
Qy 961 GCTGTGCCCCCAATTAACCAAGTTCCTGTAGAGTGTGTGGGGGTGCCCGAGGCTGTGGAATG 1020
Db 1419 GCTGTGCCCCCAATTAACCAAGTTCCTGTAGAGTGTGTGGGGGTGCCCGAGGCTGTGGAATG 1478
Qy 1021 TATCGAGGACTTGTCTTAACGAGCCTGGGCAACTTTTGGACTTGGACTGTAAACGCCCCAG 1080
Db 1479 TATCGAGGACTTGTCTTAACGAGCCTGGGCAACTTTTGGACTTGGACTGTAAACGCCCCAG 1538
Qy 1081 GCCATTAAGGTGTAAACCTGTGATGTGCTGTGTGTGTTAACCGCTTTTGTGTGATGAGT 1140
Db 1539 GCCATTAAGGTGTAAACCTGTGATGTGCTGTGTGTGTTAACCGCTTTTGTGTGATGAGT 1598
Qy 1141 TGAATGTAGTTTAATTAAGGGGTGAGATATATGTTTAACTTGCATGGCCGTGTTAAATGGGGC 1200
Db 1599 TGAATGTAGTTTAATTAAGGGGTGAGATATATGTTTAACTTGCATGGCCGTGTTAAATGGGGC 1658
Qy 1201 GGGGCTTAAAGGGTATATATATGCGCGCTGGGCTAATCTTGGTTACATCTGACCTCATGGA 1260
Db 1659 GGGGCTTAAAGGGTATATATATGCGCGCTGGGCTAATCTTGGTTACATCTGACCTCATGGA 1718
Qy 1261 GGGCTTGAAGTGTGTAAGAAATTTTCTGTGTGCGTAACCTTGTGAAACAGAGCTTAA 1320
Db 1719 GGGCTTGAAGTGTGTAAGAAATTTTCTGTGTGCGTAACCTTGTGAAACAGAGCTTAA 1778
Qy 1321 CAGTACCTCTTGTGTTTGGAGAGTTTCTGTGGGCTCATCCCAAGCAAGTTAGTCTGAG 1380
Db 1779 CAGTACCTCTTGTGTTTGGAGAGTTTCTGTGGGCTCATCCCAAGCAAGTTAGTCTGAG 1838
Qy 1381 AATTAAAGAGATTACAGAGTGGGAAATTTGAAGAGCTTTGAAATCCTGTGTGAGCTGTT 1440
Db 1839 AATTAAAGAGATTACAGAGTGGGAAATTTGAAGAGCTTTGAAATCCTGTGTGAGCTGTT 1898
Qy 1441 TGAATCTTTGAATCTGGGTCAACCAAGCGCTTTTCCAGAGAAAGTCAATCAAGCTTTGGA 1500
Db 1899 TGAATCTTTGAATCTGGGTCAACCAAGCGCTTTTCCAGAGAAAGTCAATCAAGCTTTGGA 1958
Qy 1501 TTTTTCACACCCGGGGCCGCTGCGGCTGTGTTGCTTTTGGAGTTTAAATTAAGAGTA 1560
Db 1959 TTTTTCACACCCGGGGCCGCTGCGGCTGTGTTGCTTTTGGAGTTTAAATTAAGAGTA 2018
Qy 1561 ATGGAGCAAGAAACCACTGTAGAGGGGGGATACCTGTGATTTTGTGGCATGCACTCT 1620
Db 2019 ATGGAGCAAGAAACCACTGTAGAGGGGGGATACCTGTGATTTTGTGGCATGCACTCT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACACAAGAAATCGCCTGTACTGTTGTCTTCGGTCCGCCGCC 1680

Db 2079 GTGAGAGCGGTTGTGAGACACAAGAAATCGCCTGTACTGTGTTGCTTCGGTCCGCCGCC 2138
Qy 1681 GATTAATCCGACCGAGAGACAGACAGCAGAGAGAAACCAAGGGGGCGGCCGACGGA 1740
Db 2139 GATTAATCCGACCGAGAGAGACAGACAGCAGAGAGAAACCAAGGGGGCGGCCGACGGA 2198
Qy 1741 GCAGAGCCCATGGAACCCGAGAGCCCGGCTGAGACCCCTGGGAAATGAATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCCCGGCTGAGACCCCTGGGAAATGAATGTTGTACAGGTG 2258
Qy 1801 GCTGAATCTATCCAGATCTGAGACGATTTTGCAATTAACAGAGATGGGCAAGGCTTA 1860
Db 2259 GCTGAATCTATCCAGATCTGAGACGATTTTGCAATTAACAGAGATGGGCAAGGCTTA 2318
Qy 1861 AAGGGGGTAAAGAGGAGCGGGGGGCTTGTGAGGCTTACAGAGAGGCTAGGAATCTAGCT 1920
Db 2319 AAGGGGGTAAAGAGGAGCGGGGGGCTTGTGAGGCTTACAGAGAGGCTAGGAATCTAGCT 2378
Qy 1921 TTTAGCTTAATGACACAGACACCGTCTGAGTGTATTACTTTTCAMCAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACACAGACACCGTCTGAGTGTATTACTTTTCAMCAGATCAAGATTAAT 2438
Qy 1981 TGGCTTAATGAGCTTGAATCTGTGGCGCAGAGATATTCCATAGAGACTGACCACTTAC 2040
Db 2439 TGGCTTAATGAGCTTGAATCTGTGGCGCAGAGATATTCCATAGAGACTGACCACTTAC 2498
Qy 2041 TGGCTGACGACAGGGGGATGATTTTGAAGAGGCTATTAGGGATATTGCAAGGTGGCACTT 2100
Db 2499 TGGCTGACGACAGGGGGATGATTTTGAAGAGGCTATTAGGGATATTGCAAGGTGGCACTT 2558
Qy 2101 AGGCAATTTGCAAGTACCAAGATCAGCAAACTTGTAAATATACAGAAATTTGTGTACATT 2160
Db 2559 AGGCAATTTGCAAGTACCAAGATCAGCAAACTTGTAAATATACAGAAATTTGTGTACATT 2618
Qy 2161 TCTGGGAAACGGGGCCGAGGTGTGAGATATGATACGAGAGATAGGGTGCCTTTAAGTGTAGC 2220
Db 2619 TCTGGGAAACGGGGCCGAGGTGTGAGATATGATACGAGAGATAGGGTGCCTTTAAGTGTAGC 2678
Qy 2221 ATGATTAATATGTGGCCGGGGGGTCTTGGCATGGAACGGGGGTGTTATTGAATGTAAAG 2280
Db 2679 ATGATTAATATGTGGCCGGGGGGTCTTGGCATGGAACGGGGGTGTTATTGAATGTAAAG 2738
Qy 2281 TTTTACTGGCCCCAATTTTACCGGTACGGTCTTCTGTGCCAATACCAACTTATCTACAC 2340
Db 2739 TTTTACTGGCCCCAATTTTACCGGTACGGTCTTCTGTGCCAATACCAACTTATCTACAC 2798
Qy 2341 GGTGTAAAGCTTCTATGTGGTTTAAACAATACTGTGTGGAAGCTGTGACCGATTAAGGTT 2400
Db 2799 GGTGTAAAGCTTCTATGTGGTTTAAACAATACTGTGTGGAAGCTGTGACCGATTAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTACTGTGCTGGAAGGGGGGTGTGTGTGCCCCCAAAAGCAGGGCT 2460
Db 2859 CGGGGCTGTGCTTTTACTGTGCTGGAAGGGGGGTGTGTGTGCCCCCAAAAGCAGGGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTTTGAAGGTGTACTTTGGGTATCTGTGTGAGGTTACTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTTTGAAGGTGTACTTTGGGTATCTGTGTGAGGTTACTCC 2978
Qy 2521 AGGGTGGCCCAATAATGTGGCTCCGACTGTGTGTCTTCAATGCTATGGAAGAGCTGTGCT 2580
Db 2979 AGGGTGGCCCAATAATGTGGCTCCGACTGTGTGTCTTCAATGCTATGGAAGAGCTGTGCT 3038
Qy 2581 GTGATTAAGCAATACATGTATGTGGCAACTGCGAGAGACAGGGCTCTCAGATCTGACC 2640
Db 3039 GTGATTAAGCAATACATGTATGTGGCAACTGCGAGAGACAGGGCTCTCAGATCTGACC 3098
Qy 2641 TGTCTGAGACGGCAACTGTCACTGTGTAAGACCAATTCACGTAGCCAGCACTCTCGAAG 2700
Db 3099 TGTCTGAGACGGCAACTGTCACTGTGTAAGACCAATTCACGTAGCCAGCACTCTCGAAG 3158
Qy 2701 GCTGTGCAAGTGTGTTGAGCAATACATCTGACCCGCTGTCTTGTGCAATTTGGGTAAACAGG 2760
Db 3159 GCTGTGCAAGTGTGTTGAGCAATACATCTGACCCGCTGTCTTGTGCAATTTGGGTAAACAGG 3218

```
Oy 2761 AGGGGGGTGTTCTCACTTACCAATGCAATTGAGTCACTACCTAAGATATTGCTTGAGCCC 2820
Db 3319 AGGGGGGGTTCCTACCTTACCAATGCAATTGAGTCACTACCTAAGATATTGCTTGAGCCC 3278
Oy 2821 GAGAGCATGTCCAAAGGTGAACCTGAAAGGGGGGTTTGATGATGACCATGAAATGATCTGGAG 2880
Db 3279 GAGAGCATGTCCAAAGGTGAACCTGAAAGGGGGTGTGATGATGACCATGAAATGATCTGGAG 3338
Oy 2881 GTGCTGAGTACGATGAGACCCGACACGAGTGCAGACCTCTCGAGTGTGGCGGTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGACCCGACACGAGTGCAGACCTCTCGAGTGTGGCGGTAAACAT 3398
Oy 2941 ATTGGAACCAAGCTGTGATGTGATGTGACCCGAGAGCTGAGGCCCGCATCTTGCTG 3000
Db 3399 ATTGGAACCAAGCTGTGATGTGATGTGACCCGAGAGCTGAGGCCCGCATCTTGCTG 3458
Oy 3001 CTGGCGCTGCACCGCGCTGAGTTGGCTCTAGCGCATGAAGATACGATTGAG 3052
Db 3459 CTGGCGCTGCACCGCGCTGAGTTGGCTCTAGCGCATGAAGATACGATTGAG 3510

RESULT 13
ADRCOMPEN 35935 bp DNA linear VRL 08-APR-1996
LOCUS Maecadenovirus h5 gene, complete genome.
DEFINITION M73260 M29978
ACCESSION M73260.1 GI:209842
KEYWORDS protein 5 precursor; protein IIIa; protein V; protein pVI; protein pVII; protein pVIII.
SOURCE Human adenovirus type 5
ORGANISM Human adenovirus type 5
REFERENCE 1 (bases 1 to 35935)
AUTHORS Chroboczek, J., Bieber, F., and Jacrot, B.
TITLE The sequence of the genome of adenovirus type 5 and its comparison with the genome of adenovirus type 2
JOURNAL Virology 186 (1), 280-285 (1992)
MEDLINE 92087470
PUBMED 1727603
COMMENT Original
FEATURES
source location/Qualifiers
1..35935
/organism="Human adenovirus type 5"
/mol_type="genomic DNA"
/db_xref="taxon:28285"
<11565..12297
/feature="52/55 K protein gene"
/codon_start=2
/protein_id="AA096406.1"
/db_xref="GI:209843"
/translation="SFNNHVRTLVAREEVALIGLHMLDFVSALEQNPNSKFLMAQLFL
IGVSRDNEAFRDALNIVEBGRWMLDLINLSIVQERSLADVAIYNYSMS
LGRFYARKIYHTPYPIDKEVIGKGFYRWMLKYLTLSDDIGVNRIRHKAVSRR
RELSDRLEHSLQALACTGSGDREABEYFPAGADLRAPRRLLEAAGAPGLAVAP
AKRANVGVEYIEDDEDEYEPDEGEY"
12318..14075
/codon_start=1
/product="protein IIIa"
/protein_id="AA096407.1"
/db_xref="GI:289094"
/translation="WMQDATDPAYRALIQSPGLNSTDMRQVMRIMSLITANPDA
FRQPPQANRLSALILEAVPARANPTHEKVLIVNALENRAIRPDEAGLVYDALLQRY
ARVYGNVQVTLDRLVGDBREAVAGBERAQOQNGVWVLANAFSLTOPAVPRGOED
YTNVSAALRLMTVTQSEVYQSGPDYFQTSRQGLQTVNLQAFKMLQGLMGVRAPT
GDRATVSLTLPNSRLTLILAPFDGSGVSRDYLGHILTLVREBAIGQAHVDHTQ
EITVSRLQGOEDPGLSEATLNYLLTPRQKITPSLHNSSEERILRYQSVSLNM
RBDGTPVALDMTARNBERGMYASRRPINKMLQYLHRAAANVEIFNALINLHMLP
PQGYVTGFEVPEBNDGFLWDDIDDSVSPQPTLLELQOQEAALARKSFFRPSS
LSLDGAAPRSDASSPPSLIGSLSTRTTTPRLIGEBEYLNGLLPQRKKNLPPIF
PNNGISLVDKMSKWTYAOGRHVDVPCRPRTRRQRHQRGLVMEDDSDADSSVLD
LGSGNPPAHLRPLGRMF"
16286..16474
```

```
CDS
/codon_start=1
/product="protein pVII"
/protein_id="AA096408.1"
/db_xref="GI:209845"
/translation="MRAARLAAIGIVTPPRSRRAAAAAAAIAISAMTQGRGVNVW
RDSVGLRVVRRPRPN"
16544..17650
/codon_start=1
/product="protein V"
/protein_id="AA096409.1"
/db_xref="GI:209846"
/translation="MSKRITKEMLQVIAPBEIYGPKEEBODYPRKLKPKKKKKOD
DDELDEVELLHATAPRRVYQMGKRAKRLRGTTLVFPGRSSTPYRYVDEYVG
DEDLQANERLGEFATGKXKDMYALPDEGNPTSLKFTVTLQVLPALAPSEKKG
LKRESGLAPTVQDMVPRQRLQEDVLEKMTPEPELBEVVRPIKQVAPGVQTVV
QIPTSTSLATITGEMTQTSPVASVADAAQVAAASAKSTEVQTDGPMRGGVA
PRRPGSRKXGAASALLPEYALHPSIAPTEGYGVYRPRRATRRRTTGTTRRRR
RROPVLAPISVRVAREGRTLVLPFARHPSIV"
17774..17920
/codon_start=1
/product="protein 5 precursor"
/protein_id="AA096410.1"
/db_xref="GI:209847"
/translation="MRAHRRRRASHRMKGILPLILPLIAAIGAVEIASVALQ
AGRH"
18003..18755
/codon_start=1
/product="protein pVI"
/protein_id="AA096411.1"
/db_xref="GI:209848"
/translation="MEDINFASLAPRGSRPFMGNMODIGTSNMSGAFSGSIWSGI
KNRSTVKNYGNKAMNSITGOMLADRIKEQNFQOKVVDGASGISGVVDLANQVONK
INSKLDLRPVEEPPEPAVEVSPGEGREKRPDPRETLVQIDEPSEYALQGLP
TTRPIAPMANGVLGOHTPVLIDLPADTQOKPVLPGPTAVVYTRPSRASILRAASGP
LSRPPVAGSMQSTLNSIVGLGVQSLKRRCF"
<25819..26484
/feature="100 K protein"
/codon_start=1
/protein_id="AA096412.1"
/db_xref="GI:209849"
/translation="ESQIIGTFELQGPSPDEKSAAPGLKLPGLMTSAVLRKFPEDY
HAHEIRYEDOSRPNALFTACVITQGHIGLOAIKAROEFLIGRGRGVLDPOSG
BELNPIRPPPOQOPRALASODGTOKEAATAATRGGLIGSGRGGRGGGH
DGRIGEPKRSFRKRGVRNRYTLGRIPLAGAEIGNRPQHGTLNLSGGAATRASP
TOP"
26485..26514
/feature="of a 33 K protein"
/number=1
26713..27083
/feature="of a 33 K protein"
/number=2
27174..27857
/codon_start=1
/product="protein pVIII"
/protein_id="AA096413.1"
/db_xref="GI:454806"
/translation="MSKEIPTPYWSYQPMGLAAGAODYSTRINYSAGPHNISRY
NGIRAHNRNRLLEQALITTPRNINRSPALVYQESPAFTVVLPRDAQAEVMT
NSGAOLAGRRHRRVSPGQITLIRGQIGLNDSEVSSSLGIRPDGTFQIGGAGR
SPFPROAILTLQTSSESPRSGGIGTLQFIIEFVSVYFNFSPGPHYPPQFIINPDA
VKSADSDYD"

ORIGIN
Query Match 100.0%; Score 3052; DB 14; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGGTAGTGTATTATACCCGGTGAAGTCTTCAAGAGCCACTTTGAGTCCGCGGACT 60
Db 459 CGGTAGTGTATTATACCCGGTGAAGTCTTCAAGAGCCACTTTGAGTCCGCGGACT 518
Oy 61 AGAGTTTCTCCTCGAGCGCGCTCGACACCGGAGTGAATAAGACATTTATCTGCC 120
```

Db 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACATATTAATCTCC 578
Qy 121 ACCGAGGTTTATTAACCAAGAAATGGCCGCAAGCTTTTGGACCAAGTGAATCGAAGG 180
Db 579 ACGAGGGGTATTAACCAAGAAATGGCCGCAAGCTTTTGGACCAAGTGAATCGAAGG 638
Qy 181 TACTGGCTGATTAATCTTCCACCTCTAGACCAATTTTGAACACCTACCTTCACGAATCTGT 240
Db 639 TACTGGCTGATTAATCTTCCACCTCTAGACCAATTTTGAACACCTACCTTCACGAATCTGT 698
Qy 241 ATGATTNAGACGTACGCGCCCGGAAGATCCCAACGAGAGCGGTTTTCGAGATTTTTC 300
Db 699 ATGATTNAGACGTACGCGCCCGGAAGATCCCAACGAGAGCGGTTTTCGAGATTTTTC 758
Qy 301 CCGACTCTGTAATGTTGGCGGTGACGAAAGGATTTGACTTACTCTTTTCCGCGGCGC 360
Db 759 CCGACTCTGTAATGTTGGCGGTGACGAAAGGATTTGACTTACTCTTTTCCGCGGCGC 818
Qy 361 CCGGTTCTCCGAGCGCCTCACTTTCCGAGACCCGAGCGCGAGAGAGGCT 420
Db 819 CCGGTTCTCCGAGCGCCTCACTTTCCGAGACCCGAGCGCGAGAGAGGCT 878
Qy 421 TGGGTCGGGTTCTATGCAAACTTGTACCGAGGTATGATCTTACTTCCACGAG 480
Db 879 TGGGTCGGGTTCTATGCAAACTTGTACCGAGGTATGATCTTACTTCCACGAG 938
Qy 481 CTGGCTTCCACCAAGTACGACGAGATGAAAGGGGTGAGAGGTTGTGTAAGTTATG 540
Db 939 CTGGCTTCCACCAAGTACGACGAGATGAAAGGGGTGAGAGGTTGTGTAAGTTATG 998
Qy 541 TGGAGCACCCCGGAGCGGTTGACAGTCTTGTCAATTAACCGAGAAATACGCGGAGC 600
Db 999 TGGAGCACCCCGGAGCGGTTGACAGTCTTGTCAATTAACCGAGAAATACGCGGAGC 1058
Qy 601 CAGATTAATATGTTGCTTGTCTATATGAGACCTGTGGCATGTTGTCTACAGTAAT 660
Db 1059 CAGATTAATATGTTGCTTGTCTATATGAGACCTGTGGCATGTTGTCTACAGTAAT 1118
Qy 661 GAAATTAATGGGCAATGGGTATAGAGTGGGTTGTGTGTAATTTTTTTTAT 720
Db 1119 GAAATTAATGGGCAATGGGTATAGAGTGGGTTGTGTGTAATTTTTTTTAT 1178
Qy 721 TTTTACAGTTTGTGTTAAAGATTTTGTATGTGATTTTAAAGGTCCTGTGTC 780
Db 1179 TTTTACAGTTTGTGTTAAAGATTTTGTATGTGATTTTAAAGGTCCTGTGTC 1238
Qy 781 TGAACCTAGCCTGAGCCGAGCCAGAACCGAGCCTGCAAGACTTACCCTGCTTAA 840
Db 1239 TGAACCTAGCCTGAGCCGAGCCAGAACCGAGCCTGCAAGACTTACCCTGCTTAA 1238
Qy 841 AATGGCCGCTGTATCTGAGACCGCCGACATCACTGTGTCTAGAAATCAATAGTAG 900
Db 1289 AATGGCCGCTGTATCTGAGACCGCCGACATCACTGTGTCTAGAAATCAATAGTAG 1358
Qy 901 TACGATAGCTGTGACTCCGCTCTTCTTAACAACCTCTGAGATACACCGGTGTCTCC 960
Db 1359 TACGATAGCTGTGACTCCGCTCTTCTTAACAACCTCTGAGATACACCGGTGTCTCC 1418
Qy 961 GCTGTGCCCCATTAACCAAGTTCGCTGAGAGTGTGTGGCGTCCGACGCTGTGAATG 1020
Db 1419 GCTGTGCCCCATTAACCAAGTTCGCTGAGAGTGTGTGGCGTCCGACGCTGTGAATG 1478
Qy 1021 TATCGAGGACTTGTCTTAAGAGCCTGGCAACTTTTGAAGCTTGAAGCTTAAACGCCAG 1080
Db 1479 TATCGAGGACTTGTCTTAAGAGCCTGGCAACTTTTGAAGCTTGAAGCTTAAACGCCAG 1538
Qy 1081 GCCATTAAGGTGAAACCTGTGATTCGCTGTGTTAAACGCTTGTGCTGATGAGT 1140
Db 1539 GCCATTAAGGTGAAACCTGTGATTCGCTGTGTTAAACGCTTGTGCTGATGAGT 1598
Qy 1141 TGAATTAAGTTTAATTAAGGGGTGAGATATGTTTAACCTTGCAATGCGCTTAAATGGGCG 1200
Db 1599 TGAATTAAGTTTAATTAAGGGGTGAGATATGTTTAACCTTGCAATGCGCTTAAATGGGCG 1658

Qy 1201 GGGGCTTAAAGGATATTAATGCGCGGTGCTTAATCTTGTTACATCTGACTCATGGA 1260
Db 1659 GGGGCTTAAAGGATATTAATGCGCGGTGCTTAATCTTGTTACATCTGACTCATGGA 1718
Qy 1261 GGGTGGGAGTGTGGAGATTTTCTGCTGTGCGTAACTTGTGAGAACAGACTCTTAA 1320
Db 1719 GGGTGGGAGTGTGGAGATTTTCTGCTGTGCGTAACTTGTGAGAACAGACTCTTAA 1778
Qy 1321 CAGTACTCTTGGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAATTAGTCTGAG 1380
Db 1779 CAGTACTCTTGGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAATTAGTCTGAG 1838
Qy 1381 AATTAAGGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGT 1440
Db 1839 AATTAAGGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGT 1898
Qy 1441 TGATTTCTTGAATCTGGGTCAACGAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACGAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTGA 1958
Qy 1501 TTTTTCACACCGGGGCGCGCTGCGCTGCTGTGCTTTTGTAGTTTATTAAGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGCTGCTGTGCTTTTGTAGTTTATTAAGATTA 2018
Qy 1561 ATGAGGGAAGAAACCATCTGAGCGGGGGGTACCTGTGGAATTTTTCGCGCATGCACT 1620
Db 2019 ATGAGGGAAGAAACCATCTGAGCGGGGGGTACCTGTGGAATTTTTCGCGCATGCACT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGTCTACTGTGTCTTCCGTCCGCGGCG 1680
Db 2079 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGTCTACTGTGTCTTCCGTCCGCGGCG 2138
Qy 1681 GATTAATCCGACGAGAGACGACGACGACGACGAGAGAAACCGAGCGCGCGAGGA 1740
Db 2139 GATTAATCCGACGAGAGACGACGACGACGAGAGAAACCGAGCGCGCGAGGA 2198
Qy 1741 GCAGAGCCATGGAACCCGAGAGCGGCGCTGGAACCTCGGGAATGAATGTTGCAGGTG 1800
Db 2199 GCAGAGCCATGGAACCCGAGAGCGGCGCTGGAACCTCGGGAATGAATGTTGCAGGTG 2258
Qy 1801 GCTGAACGTATCCAGAACTGAGACGCAATTTTGAACATTAACAAGATGGGACAGGCTA 1860
Db 2259 GCTGAACGTATCCAGAACTGAGACGCAATTTTGAACATTAACAAGATGGGACAGGCTA 2318
Qy 1861 AAGGGGTAAAGAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGCTTAAAGAACTAGCT 1920
Db 2319 AAGGGGTAAAGAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGCTTAAAGAACTAGCT 2378
Qy 1921 TTTAGCTTAAATGACACAGACACCGCTGAGGTATTTACTTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAAATGACACAGACACCGCTGAGGTATTTACTTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGGCTAATAGACTTGTATCTGTGGCGCAGAAATTTCCATAGAGCAGCTGACCACTTAC 2040
Db 2439 TGGCTAATAGACTTGTATCTGTGGCGCAGAAATTTCCATAGAGCAGCTGACCACTTAC 2498
Qy 2041 TGGCTGACGACGAGGATGATTTTGAAGAGCTATTAGGGTATATGCAAGGTGGCACTT 2100
Db 2499 TGGCTGACGACGAGGATGATTTTGAAGAGCTATTAGGGTATATGCAAGGTGGCACTT 2558
Qy 2101 AGGCGCAATTGCAAGTCAAGATCAGCAAACTTTTAATATCAGAAATGTTGTCTACTT 2160
Db 2559 AGGCGCAATTGCAAGTCAAGATCAGCAAACTTTTAATATCAGAAATGTTGTCTACTT 2618
Qy 2161 TCTGGGAAACGGGCGGAGGTGAGATATGATACGAGATAGAGGTGCGCTTTAGATGAGC 2220
Db 2619 TCTGGGAAACGGGCGGAGGTGAGATATGATATGAGATAGAGGTGCGCTTTAGATGAGC 2678
Qy 2221 ATGATTAATATGTGCGCGGGGCTGCTTGGCATGGAACGGGGGTGTTATTAAGATGTAAG 2280
Db 2679 ATGATTAATATGTGCGCGGGGCTGCTTGGCATGGAACGGGGGTGTTATTAAGATGTAAG 2738

QY 2281 TTACTGGCCCCAATTTTAGCGGTACGGTTTCTCTGGCCAATACCACTTATCTTAAC 2340
| | | | |
Db 2739 TTACTGGCCCCAATTTTAGCGGTACGGTTTCTCTGGCCAATACCACTTATCTTAAC 2798
| | | | |
QY 2341 GGTGAAGCTTCTATAGGTTTAAACAATACCTGTGTGAAGCCGTGAACGATGTAAGGTT 2400
| | | | |
Db 2799 GGTGAAGCTTCTATAGGTTTAAACAATACCTGTGTGAAGCCGTGAACGATGTAAGGTT 2858
| | | | |
QY 2401 CGGGCTGTGCTTTTACTGCTGTGAAGGGGGTGTGTGTGCGCCCAAAAGAGGGCT 2460
| | | | |
Db 2859 CGGGCTGTGCTTTTACTGCTGTGAAGGGGGTGTGTGTGCGCCCAAAAGAGGGCT 2918
| | | | |
QY 2461 TCAATTAGAAATGCTCTTTTGAAGGTGTAACCTTGGGTATCTGTCTGAAGGTAACTCC 2520
| | | | |
Db 2919 TCAATTAGAAATGCTCTTTTGAAGGTGTAACCTTGGGTATCTGTCTGAAGGTAACTCC 2978
| | | | |
QY 2521 AGGGTGCACCAATGTGGCCCTCCGACTGTGGTTCTTCACTGATGAAAAGCGTGCT 2580
| | | | |
Db 2979 AGGGTGCACCAATGTGGCCCTCCGACTGTGGTTCTTCACTGATGAAAAGCGTGCT 3038
| | | | |
QY 2581 GTGATTAAGCAATACATGTGTATGTGGCACTGCGAGAGACAGGGCCTCTCAGATGCTGACC 2640
| | | | |
Db 3039 GTGATTAAGCAATACATGTGTATGTGGCACTGCGAGAGACAGGGCCTCTCAGATGCTGACC 3098
| | | | |
QY 2641 TGCTCGGACGGCACTGTACCTGTGTGAAGACCACTTCACTGACCAAGCCACTCTCGCAAG 2700
| | | | |
Db 3099 TGCTCGGACGGCACTGTACCTGTGTGAAGACCACTTCACTGACCAAGCCACTCTCGCAAG 3158
| | | | |
QY 2701 GCTCGGACGAGTGTGTGAACATACATCTGACCCGCTGTTCTTGTGATTTGGGTAAACGG 2760
| | | | |
Db 3159 GCTCGGACGAGTGTGTGAACATACATCTGACCCGCTGTTCTTGTGATTTGGGTAAACGG 3218
| | | | |
QY 2761 AGGGGGGTGTTCTTCACTTACCAATGCAATTGAGTCACTAAGATATGCTTGAAGCC 2820
| | | | |
Db 3219 AGGGGGGTGTTCTTCACTTACCAATGCAATTGAGTCACTAAGATATGCTTGAAGCC 3278
| | | | |
QY 2821 GAGAGCAATGTCCAGAGTGAACCTGAACGGGGTGTGTGACATGACCATTAAGATCTGGAAG 2880
| | | | |
Db 3279 GAGAGCAATGTCCAGAGTGAACCTGAACGGGGTGTGTGACATGACCATTAAGATCTGGAAG 3338
| | | | |
QY 2881 GTGCTGAGTACGATGAGACCCGACACAGTGTGACAGCCCTGCAAGTGTGGGTAAACAT 2940
| | | | |
Db 3339 GTGCTGAGTACGATGAGACCCGACACAGTGTGACAGCCCTGCAAGTGTGGGTAAACAT 3398
| | | | |
QY 2941 ATTAGAAACCAAGCTGTGTATCTGTGATGTGAACCGAGAGCTGAGGCCGATCACTGTG 3000
| | | | |
Db 3399 ATTAGAAACCAAGCTGTGTATCTGTGATGTGAACCGAGAGCTGAGGCCGATCACTGTG 3458
| | | | |
QY 3001 CTGGCCCTGACCCCGCTGATTTGGCTCTAGCCATGAAATACGATTTGAG 3052
| | | | |
Db 3459 CTGGCCCTGACCCCGCTGATTTGGCTCTAGCCATGAAATACGATTTGAG 3510
| | | | |
RESULT 14
LOCUS AR403723 35978 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6627190.
VERSION AR403723
KEYWORDS AR403723.1 GI:40151372
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35978)
AUTHORS Mold, W.S.M., Toch, K., Doronin, K., Tollefson, A.B. and Kuppenswamy, M.
TITLE Recombinant adenovirus vectors that are replication-competent in
tert-expressing cells
JOURNAL Patent: US 6627190-A 1 30-SEP-2003;
FEATURES Location/Qualifiers
SOURCE 1. 35978
/organism="unknown"
/mol_type="genomic DNA"

Query Match 100.0%; Score 3052; DB 6; Length 35978;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTGAAGTATTTATATCCCGGTAGTTCCCTCAAGAGGCCACTCTGATGTCGACGGAGT 60
| | | | |
Db 459 CGTGAAGTATTTATATCCCGGTAGTTCCCTCAAGAGGCCACTCTGATGTCGACGGAGT 518
| | | | |
QY 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCCGGAGCTGAATGACATATTAATCTGCC 120
| | | | |
Db 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCCGGAGCTGAATGACATATTAATCTGCC 578
| | | | |
QY 121 ACGAGGTGTATTAACGAGAAATGCGCCGACGCTTTTGACCAAGCTGATCGAAGAG 180
| | | | |
Db 579 ACGAGGTGTATTAACGAGAAATGCGCCGACGCTTTTGACCAAGCTGATCGAAGAG 638
| | | | |
QY 181 TACTGGCTGATTAATCTTCACTCTGACCTTTTGAACCACTTACCTTACGAACTGT 240
| | | | |
Db 639 TACTGGCTGATTAATCTTCACTCTGACCTTTTGAACCACTTACCTTACGAACTGT 698
| | | | |
QY 241 ATGATTTAGACGTGACGGCCCGCAAGATCCCAACGAGAGCGGTTTCGAGATTTTTC 300
| | | | |
Db 699 ATGATTTAGACGTGACGGCCCGCAAGATCCCAACGAGAGCGGTTTCGAGATTTTTC 758
| | | | |
QY 301 CCGACTCTGTAATGTGGCGGTGCAAGAGGATTAATCTTACTCATTTTCCGCGCGCC 360
| | | | |
Db 759 CCGACTCTGTAATGTGGCGGTGCAAGAGGATTAATCTTACTCATTTTCCGCGCGCC 818
| | | | |
QY 361 CCGGTTCTCGGAGCCGCTCACCTTCCCGGACCGCCGACACCGGAGAGAGGCT 420
| | | | |
Db 819 CCGGTTCTCGGAGCCGCTCACCTTCCCGGACCGCCGACACCGGAGAGAGGCT 878
| | | | |
QY 421 TGGGTCCGTTTCTATGCAAACTTGTACCGAGGTGATGATCTTACTTCCGACGAGG 480
| | | | |
Db 879 TGGGTCCGTTTCTATGCAAACTTGTACCGAGGTGATGATCTTACTTCCGACGAGG 938
| | | | |
QY 481 CTGGCTTCCACCGACGTGACGACGAGATGAAGAGGTGAGAGGTTGTGTAGATTATG 540
| | | | |
Db 939 CTGGCTTCCACCGACGTGACGACGAGATGAAGAGGTGAGAGGTTGTGTAGATTATG 998
| | | | |
QY 541 TGGAGACCCCGGGACGGTTGACAGTCTTGTCAATTACCGAGAGAAATCGGGGGACC 600
| | | | |
Db 999 TGGAGACCCCGGGACGGTTGACAGTCTTGTCAATTACCGAGAGAAATCGGGGGACC 1058
| | | | |
QY 601 CAGATATTATGTGTTGCTTGTATATGAGACCTGTGATGTTGTCTTACATGTAAGT 660
| | | | |
Db 1059 CAGATATTATGTGTTGCTTGTATATGAGACCTGTGATGTTGTCTTACATGTAAGT 1118
| | | | |
QY 661 GAAATTTATGGGACGTGGGTGATAGAGTGTGGTGTGTGTATTTTTTTTTTAT 720
| | | | |
Db 1119 GAAATTTATGGGACGTGGGTGATAGAGTGTGGTGTGTGTATTTTTTTTTTAT 1178
| | | | |
QY 721 TTTTACGTTTGTGTTTAAAGAAATTTGATGTGATTTTTTTTAAAGGTCCGTGTC 780
| | | | |
Db 1179 TTTTACGTTTGTGTTTAAAGAAATTTGATGTGATTTTTTTTAAAGGTCCGTGTC 1238
| | | | |
QY 781 TGAACCTGAGCCTGAGCCGACGAGCAACCGAGACTGTGCAAGACTACCCGCTCTTAA 840
| | | | |
Db 1239 TGAACCTGAGCCTGAGCCGACGAGCAACCGAGACTGTGCAAGACTACCCGCTCTTAA 1298
| | | | |
QY 841 AATGGCGCTGTCTATCTGAGACGCCGACATCACTGTGTCTTGAAGATGAATAGTAG 900
| | | | |
Db 1299 AATGGCGCTGTCTATCTGAGACGCCGACATCACTGTGTCTTGAAGATGAATAGTAG 1358
| | | | |
QY 901 TACGATAGCTGTGACTCCGGTCTTCTTACACACTCTGAGATACACCGGAGTGTCC 960
| | | | |
Db 1359 TACGATAGCTGTGACTCCGGTCTTCTTACACACTCTGAGATACACCGGAGTGTCC 1418
| | | | |
QY 961 GCTGTGCCCAATTAAACCAAGTGTGAGAGTGTGTGGCGTGTGCAAGCTGTGAAATG 1020
| | | | |
Db 1419 GCTGTGCCCAATTAAACCAAGTGTGAGAGTGTGTGGCGTGTGCAAGCTGTGAAATG 1478
| | | | |

QY 1021 TATGAGGAACTTGCTTAACGAGCCGCGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG 1080
|
|
|
Db 1479 TATGAGGAACTTGCTTAACGAGCCGCGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG 1538
|
|
|
QY 1081 GCCATAAGGTGTAAACCTGTGATTCGCTGTGTGTAAACGCCCTTTGTTTGTGTGAATGAGT 1140
|
|
|
Db 1539 GCCATAAGGTGTAAACCTGTGATTCGCTGTGTGTAAACGCCCTTTGTTTGTGTGAATGAGT 1598
|
|
|
QY 1141 TGATGTAACTTAATTAAGGTGTGAATTAATTTTAACCTTGACATGGCCGTGTTAAATGTGGGC 1200
|
|
|
Db 1599 TGATGTAACTTAATTAAGGTGTGAATTAATTTTAACCTTGACATGGCCGTGTTAAATGTGGGC 1658
|
|
|
QY 1201 GGGGCTTAAGGCTATATATATGCGCCGTGAGCTATCTTGGTTACATCTGACCTCATGGA 1260
|
|
|
Db 1659 GGGGCTTAAGGCTATATATATGCGCCGTGAGCTATCTTGGTTACATCTGACCTCATGGA 1718
|
|
|
QY 1261 GGGCTTGGAGTGTGTGGAAGATTTTTCTGCTGTGCGTAACCTTGCTGGAACAGAGCTCTAA 1320
|
|
|
Db 1719 GGGCTTGGAGTGTGTGGAAGATTTTTCTGCTGTGCGTAACCTTGCTGGAACAGAGCTCTAA 1778
|
|
|
QY 1321 CAGTACCTCTGCTTTTGGAGAGTTTCTGTGGGGCTCATCCGAGCAAGTTAGTCTGAG 1380
|
|
|
Db 1779 CAGTACCTCTGCTTTTGGAGAGTTTCTGTGGGGCTCATCCGAGCAAGTTAGTCTGAG 1838
|
|
|
QY 1381 AATTAAGAGAGATTACAAGTGGAAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1440
|
|
|
Db 1839 AATTAAGAGAGATTACAAGTGGAAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1898
|
|
|
QY 1441 TGATTTCTTTGAATCTGGGTCAACAGCGCTTTTTCAGAGAAAGTCAATCAAGCTTTTGA 1500
|
|
|
Db 1899 TGATTTCTTTGAATCTGGGTCAACAGCGCTTTTTCAGAGAAAGTCAATCAAGCTTTTGA 1958
|
|
|
QY 1501 TTTTTCACACCGGGGGCGCTGCGGCTGCTGCTTTTGTGAGTTTAAAGATTA 1560
|
|
|
Db 1959 TTTTTCACACCGGGGGCGCTGCGGCTGCTGCTTTTGTGAGTTTAAAGATTA 2018
|
|
|
QY 1561 ATGAGAGCAAGAAACCCATCTGAGCGGGGGGTACCTGTGATTTTCTGAGCATGCT 1620
|
|
|
Db 2019 ATGAGAGCAAGAAACCCATCTGAGCGGGGGGTACCTGTGATTTTCTGAGCATGCT 2078
|
|
|
QY 1621 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGTCTACTGTGTCTTCCGTCGCCCGGC 1680
|
|
|
Db 2079 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGTCTACTGTGTCTTCCGTCGCCCGGC 2138
|
|
|
QY 1681 GATTAATCCGACGAGAGACGACGACGACGAGAGAGAAAGCGGGCGCGCGACAGA 1740
|
|
|
Db 2139 GATTAATCCGACGAGAGACGACGACGACGAGAGAGAAAGCGGGCGCGCGACAGA 2198
|
|
|
QY 1741 GCAGAGCCATGGAACCCGAGAGCGCGCTGTGACCTTCGAGAAATGAAATGTTGTACAGGTG 1800
|
|
|
Db 2199 GCAGAGCCATGGAACCCGAGAGCGCGCTGTGACCTTCGAGAAATGAAATGTTGTACAGGTG 2258
|
|
|
QY 1801 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAACAATTACAGAGATGGCAGGGGCTA 1860
|
|
|
Db 2259 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAACAATTACAGAGATGGCAGGGGCTA 2318
|
|
|
QY 1861 AAGGGGGTAAAGAGAGAGCGGGGGCTTGTAGGCTACAGAGAGGCTAAGGATCTAGCT 1920
|
|
|
Db 2319 AAGGGGGTAAAGAGAGAGCGGGGGCTTGTAGGCTACAGAGAGGCTAAGGATCTAGCT 2378
|
|
|
QY 1921 TTTAGCTTAATGACACAGACCCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
|
|
|
Db 2379 TTTAGCTTAATGACACAGACCCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
|
|
|
QY 1981 TGGCTTAATGAGCTTGTATCTGCTGGCGCAAGATTTTCATAGAGCAGCTGACACTTAC 2040
|
|
|
Db 2439 TGGCTTAATGAGCTTGTATCTGCTGGCGCAAGATTTTCATAGAGCAGCTGACACTTAC 2498
|
|
|
QY 2041 TGGCTGAGCCAGGGGATGATTTTGAAGAGGCTATTGAGGCTATATGCAAAAGGTGCACTT 2100
|
|
|
Db 2499 TGGCTGAGCCAGGGGATGATTTTGAAGAGGCTATTGAGGCTATATGCAAAAGGTGCACTT 2558
|
|
|
QY 2101 AGGCAAGATTGCAAGTACAGCAAACTGTAAATATCAGGAATTTGTTGTACACTT 2160
|
|
|

Db 2559 AGGCAAGATTGCAAGTACCAAGATCAGCAAACTGTAAATATCAGGAATTTGTTGTACACTT 2618
|
|
|
QY 2161 TCTGGGAACCGGGCCGAGGTGTGAGATATGATACGAGAGATAGGGTGGCTTTAGATGTAGC 2220
|
|
|
Db 2619 TCTGGGAACCGGGCCGAGGTGTGAGATATGATACGAGAGATAGGGTGGCTTTAGATGTAGC 2678
|
|
|
QY 2221 ATGATTAATATGTGGCCGGGGGGTGTGGCATGGAACGGGGGTGTTATTAATGAATGAAG 2280
|
|
|
Db 2679 ATGATTAATATGTGGCCGGGGGGTGTGGCATGGAACGGGGGTGTTATTAATGAATGAAG 2738
|
|
|
QY 2281 TTTACTGGCCCAATTTTAAACCGGTATTCCTGTGACCAATACCAACTTATCTTACAC 2340
|
|
|
Db 2739 TTTACTGGCCCAATTTTAAACCGGTATTCCTGTGACCAATACCAACTTATCTTACAC 2798
|
|
|
QY 2341 GGTGTAAAGCTTTCTATGGGTTTAAACAATCTGTGTGTGAAGCTGTGACCGATGTAAAGGTT 2400
|
|
|
Db 2799 GGTGTAAAGCTTTCTATGGGTTTAAACAATCTGTGTGTGAAGCTGTGACCGATGTAAAGGTT 2858
|
|
|
QY 2401 CCGGGCTGTGCTTTTACTGTGCTGGAAGGGGGTGGTGTGTGCGCCCAAAAGCAGGGCT 2460
|
|
|
Db 2859 CCGGGCTGTGCTTTTACTGTGCTGGAAGGGGGTGGTGTGTGCGCCCAAAAGCAGGGCT 2918
|
|
|
QY 2461 TCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGGTATCTGTCTGAGGGTAACTCC 2520
|
|
|
Db 2919 TCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGGTATCTGTCTGAGGGTAACTCC 2978
|
|
|
QY 2521 AGGGTGGCCCAACAATGTGGCTCCGACTGTGTGTGCTTCACTGTGTGAAAAGGTGGCT 2580
|
|
|
Db 2979 AGGGTGGCCCAACAATGTGGCTCCGACTGTGTGTGCTTCACTGTGTGAAAAGGTGGCT 3038
|
|
|
QY 2581 GTGATTAAGCAATTAATGATATGTGGCAATGTGCAAGAGCAGAGGCTCTCAGATCTGACC 2640
|
|
|
Db 3039 GTGATTAAGCAATTAATGATATGTGGCAATGTGCAAGAGCAGAGGCTCTCAGATCTGACC 3098
|
|
|
QY 2641 TGCTGGACGGCAACTGTGCACTGTGTGAAGACCAATTCACGTGACCACTCTCGCAAG 2700
|
|
|
Db 3099 TGCTGGACGGCAACTGTGCACTGTGTGAAGACCAATTCACGTGACCACTCTCGCAAG 3158
|
|
|
QY 2701 GCTGTGCAATGTGTGTGAGCAATATCTGACCCGCTGTCTTGTGCAATTTGGGTAAACAG 2760
|
|
|
Db 3159 GCTGTGCAATGTGTGTGAGCAATATCTGACCCGCTGTCTTGTGCAATTTGGGTAAACAG 3218
|
|
|
QY 2761 AGGGGGGTGTTCCTCACTTCAATGCAATTTGAGTCACTAAGATATTGCTTGAGGCC 2820
|
|
|
Db 3219 AGGGGGGTGTTCCTCACTTCAATGCAATTTGAGTCACTAAGATATTGCTTGAGGCC 3278
|
|
|
QY 2821 GAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGACATGACATGAAGATCTGGAAG 2880
|
|
|
Db 3279 GAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGACATGACATGAAGATCTGGAAG 3338
|
|
|
QY 2881 GTGCTGAGTATCAATGATGACCCGACCAAGGTGACAGACCTTGGCGAGTGTGGCGGTAAATCAT 2940
|
|
|
Db 3339 GTGCTGAGTATCAATGATGACCCGACCAAGGTGACAGACCTTGGCGAGTGTGGCGGTAAATCAT 3398
|
|
|
QY 2941 ATTAGAACAGACCTGTGATGTGATGTGACCGAGAGAGCTGAGAGCCGATCACTTGGTGTG 3000
|
|
|
Db 3399 ATTAGAACAGACCTGTGATGTGATGTGACCGAGAGAGCTGAGAGCCGATCACTTGGTGTG 3458
|
|
|
QY 3001 CTGGCTGCAACCCGCGCTGAGTTTGGCTTACGAGTGAAGATACAGATTGAG 3052
|
|
|
Db 3459 CTGGCTGCAACCCGCGCTGAGTTTGGCTTACGAGTGAAGATACAGATTGAG 3510
|
|
|

RESULT 15
AR310582
LOCUS AR310582 7090 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 18 from patent US 6558948.
ACCESSION AR310582
VERSION AR310582.1 GI:31703596
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 7090)
AUTHORS Kochanek,S. and Schiedner,G.
TITLE Permanent amniocytic cell line, its production and use for the
JOURNAL production of gene transfer vectors
FEATURES Patent: US 6558948-A 18 06-MAY-2003;
source Location/Qualifiers
1..7090
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 98.5%; Score 3006.8; DB 6; Length 7090;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3008; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

43 TCTTGAGTGCAGGAGTAGAGTTTCTCTCCGAGCGCTCCGACACCGGAGCTGAAAA 102
2749 TATGAGATGCCAGGAGTAGAGTTTCTCTCCGAGCGCTCCGACACCGGAGCTGAAAA 2808
103 TGAGACATATTATCTGCCAGGAGGTATTATACCGAAGAAATGGCCGACATCTTTGG 162
2809 TGAGACATATTATCTGCCAGGAGGTATTATACCGAAGAAATGGCCGACATCTTTGG 2868
163 ACCAGCTGATCGAAGAGTACTGGCTGATATCTTCCACTCTCTAGCCATTTTGAACAC 222
2869 ACCAGCTGATCGAAGAGTACTGGCTGATATCTTCCACTCTCTAGCCATTTTGAACAC 2928
223 CTACCCCTTACAGACCTGATATGATTTTGAAGCGGCGCCGAAAGATCCAAACGAGAG 282
2929 CTACCCCTTACAGACCTGATATGATTTTGAAGCGGCGCCGAAAGATCCAAACGAGAG 2988
283 CGGTTTGCAGATTTTCCGACCTCTGTATGTTGGCGGTGCAGAAAGGATTTGACTTAC 342
2989 CGGTTTGCAGATTTTCCGACCTCTGTATGTTGGCGGTGCAGAAAGGATTTGACTTAC 3048
343 TCACTTTTCCGCGCGCGCGCTCTCGGAGCGGCTCACTTTCCGCGAGCCCGAGC 402
3049 TCACTTTTCCGCGCGCGCGCTCTCGGAGCGGCTCACTTTCCGCGAGCCCGAGC 3108
403 AGCCGAGACAGAGACCTTGGGTCGCGTTTCTATGACCAACCTTGTACCGAGGTGATCG 462
3109 AGCCGAGACAGAGACCTTGGGTCGCGTTTCTATGACCAACCTTGTACCGAGGTGATCG 3168
463 ATCTTACTGACAGAGCTGGCTTTCCACCAGTGAAGAGAGATGAAGAGGTGAG 522
3169 ATCTTACTGACAGAGCTGGCTTTCCACCAGTGAAGAGAGATGAAGAGGTGAG 3228
523 AGTTTGTGTAGATTATGTGAGACACCCCGGACCGTTTGACAGGTCTTTGATATACCC 582
3229 AGTTTGTGTAGATTATGTGAGACACCCCGGACCGTTTGACAGGTCTTTGATATACCC 3288
583 GAGAGATATACGGGGGACCCAGATATTATGTGCTTGGCTTATGAGACCTGTGCA 642
3289 GAGAGATATACGGGGGACCCAGATATTATGTGCTTGGCTTATGAGACCTGTGCA 3348
643 TGTGTGTCTACAGTAAAGTAAATTAAGGAGTGGGTGATGAGTGGTGGTTGGT 702
3349 TGTGTGTCTACAGTAAAGTAAATTAAGGAGTGGGTGATGAGTGGTGGTTGGT 3408
703 GGTAAATTTTTTTTAAATTTTAAAGTTTGTGGTTTAAAGAAATTTTGTATGTGATTTT 762
3409 GGTAAATTTTTTTTAAATTTTAAAGTTTGTGGTTTAAAGAAATTTTGTATGTGATTTT 3468
763 TTTAAAGTCTGTGTCTGAACCTGAGCCTGAGCCGAGCAGAAACCGAGCCTGCAAG 822
3469 TTTAAAGTCTGTGTCTGAACCTGAGCCTGAGCCGAGCAGAAACCGAGCCTGCAAG 3528
823 ACCTACCCGCGCTTAAATGGCGCTGTATCTTGAGACGCCCGACATCACTGTGTTC 882
3529 ACCTACCCGCGCTTAAATGGCGCTGTATCTTGAGACGCCCGACATCACTGTGTTC 3588
883 TAGGAATGCAATAGTAGTAGAGTAGCTCGGCTCTTCTAACAACAACCTCTCTGA 942

3589 TAGGAATGCAATAGTAGTAGAGTAGCTCGGCTCTTCTAACAACAACCTCTCTGA 3648
943 GATACACCCGGTGGTCCCGCTGTGACCCCATTTAAACAGATTGCCGTGAGATTGGTGGCG 1002
3649 GATACACCCGGTGGTCCCGCTGTGACCCCATTTAAACAGATTGCCGTGAGATTGGTGGCG 3708
1003 TCGCAGGCTGTGGAATGTATCGAGACTTGTCTTAAACGAGCTGGGCAACCTTTGACCTT 1062
3709 TCGCAGGCTGTGGAATGTATCGAGACTTGTCTTAAACGAGCTGGGCAACCTTTGACCTT 3768
1063 GAGCTGTAACGCCGCCAGGCTATTAAGGTGAACCTGTGATGCGTGTGGTTAAAGGCC 1122
3769 GAGCTGTAACGCCGCCAGGCTATTAAGGTGAACCTGTGATGCGTGTGGTTAAAGGCC 3828
1123 TTTGTGTCTGAATGAATGATTAATTAATTAAGGAGTGAATTAATGTTAACTTGA 1182
3829 TTTGTGTCTGAATGAATGATTAATTAATTAAGGAGTGAATTAATGTTAACTTGA 3888
1183 TGGCGTTTAAATGGGCGGCGCTTAAAGGATATTAATGCGCGCTGATCTTGGT 1242
3889 TGGCGTTTAAATGGGCGGCGCTTAAAGGATATTAATGCGCGCTGATCTTGGT 3948
1243 TAGACTGACCTCAATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGGCTTACTT 1302
3949 TAGACTGACCTCAATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGGCTTACTT 4008
1303 GCTGGAACAGAGCTCTTAACAGTACTCTTGGTTTGAAGGTTTCTGTGGGCTATCCCA 1362
4009 GCTGGAACAGAGCTCTTAACAGTACTCTTGGTTTGAAGGTTTCTGTGGGCTATCCCA 4068
1363 GGCAAAGTATGCTGCAAGATTAAAGAGATTACAGTGGGAATTTGAAGCTTTTGA 1422
4069 GGCAAAGTATGCTGCAAGATTAAAGAGATTACAGTGGGAATTTGAAGCTTTTGA 4128
1423 ATCTGTGTGAGAGCTGTTTGAATCTTGAATCTGGGTCAACAGGCGCTTTTCAAGGAA 1482
4129 ATCTGTGTGAGAGCTGTTTGAATCTTGAATCTGGGTCAACAGGCGCTTTTCAAGGAA 4188
1483 GGTGATCAAGACTTGTGATTTTCCACACCGGCGGCTGCGCTGTGTGCTTTT 1542
4189 GGTGATCAAGACTTGTGATTTTCCACACCGGCGGCTGCGCTGTGTGCTTTT 4248
1543 GAGTTTATTAAGATTAATGAGCGAAGAAACCATCTGAGCGGCGGTACCTGTGGA 1602
4249 GAGTTTATTAAGATTAATGAGCGAAGAAACCATCTGAGCGGCGGTACCTGTGGA 4308
1603 TTTTCTGGCATGATCTGTGAGAGGCTTGTGAGACACAAGAAATGCGCTGACTGTT 1662
4309 TTTTCTGGCATGATCTGTGAGAGGCTTGTGAGAGCAACAAGAAATGCGCTGACTGTT 4368
1663 GTCTTCCGTCGCGCCGCGATTAATCCGACGAGAGACAGACGACGACGAGAGAAC 1722
4369 GTCTTCCGTCGCGCCGCGATTAATCCGACGAGAGACAGACGACGAGAGAAC 4428
1723 CAGCGCGCGCGGACGAGACAGACCCATGGAACCCGAGACCGGCTGGAACCTCGGGA 1782
4429 CAGCGCGCGCGGACGAGACAGACCCATGGAACCCGAGACCGGCTGGAACCTCGGGA 4488
1783 ATGAATGTGTGAACGAGGCGCTGAACCTGATCCAGAACGAGCATTTTGAACAATTACA 1842
4489 ATGAATGTGTGAACGAGGCGCTGAACCTGATCCAGAACGAGCATTTTGAACAATTACA 4548
1843 GAGGATGGGCAAGGCTTAAAGGGGTTAAAGGAGAGCGGGGCTTGTAGGCTTACAGAG 1902
4549 GAGGATGGGCAAGGCTTAAAGGGGTTAAAGGAGAGCGGGGCTTGTAGGCTTACAGAG 4608
1903 GAGGCTTGAATCTAGCTTTTATGCTTAAATGACAGACACCGTCTGTAGTGTATTAATTT 1962
4609 GAGGCTTGAATCTAGCTTTTATGCTTAAATGACAGACACCGTCTGTAGTGTATTAATTT 4668
1963 CAACAGATCAAGGATTAATGAGCTTAAATGAGCTTATCTGTGGGCGAGAGATTTCCATA 2022

Search completed: October 28, 2005, 06:30:19
Job time : 12695 secs

Db	4669	CAACAGATCAAGATTAATTGGCTTAATGAGCTTGATCTGTGGCGCAGAGATATTCATA	4728
Qy	2023	GAGCAGCTGACCACTTACTGTGCTGTGACAGGGGATGATTTTGGAGAGGCTAATTAGGTA	2082
Db	4729	GAGCAGCTGACCACTTACTGTGCTGTGACAGGGGATGATTTTGGAGAGGCTAATTAGGTA	4788
Qy	2083	TATGCAAAAGGTGGCACTTAGGCGCAGATGCAAGTACAAAGATCAGCAACTGTAAATATC	2142
Db	4789	TATGCAAAAGGTGGCACTTAGGCGCAGATGCAAGTACAAAGATCAGCAACTGTAAATATC	4848
Qy	2143	AGGAATTGTTCTACATTCTGGGAAACGGGCGCAGAGTGAAGATGATACGAGAGATAGG	2202
Db	4849	AGGAATTGTTCTACATTCTGGGAAACGGGCGCAGAGTGAAGATGATACGAGAGATAGG	4908
Qy	2203	GTGGCCTTTAATGATGATGATTAATATGTGCGCGGGGGTCTTGAGATGACCGGGTG	2262
Db	4909	GTGGCCTTTAATGATGATGATTAATATGTGCGCGGGGGTCTTGAGATGACCGGGTG	4968
Qy	2263	GTTATTTAATGATGATGATTTACTGCGCCCAATTTTACGGGTACGGTTTCTGGCCAAAT	2322
Db	4969	GTTATTTAATGATGATGATTTACTGCGCCCAATTTTACGGGTACGGTTTCTGGCCAAAT	5028
Qy	2323	ACCAACCTTATCTACACGGGTGAAGCTTCTATGGGTTTAACAATACCTGTGTGAAGCC	2382
Db	5029	ACCAACCTTATCTACACGGGTGAAGCTTCTATGGGTTTAACAATACCTGTGTGAAGCC	5088
Qy	2383	TGGAACCGATGTAAAGGGGTTCGGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGT	2442
Db	5089	TGGAACCGATGTAAAGGGGTTCGGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGT	5148
Qy	2443	CGCCCCAAMAGCAGGGCTTCAATTAGAAATGCCCTTTGAAAGGTGTACCTTGGGTATC	2502
Db	5149	CGCCCCAAMAGCAGGGCTTCAATTAGAAATGCCCTTTGAAAGGTGTACCTTGGGTATC	5208
Qy	2503	CTGTCTGAAGGGTAACTCCAGGGTGGCCCAATATGTGCGCTCCGACTGTGTGCTTCAATG	2562
Db	5209	CTGTCTGAAGGGTAACTCCAGGGTGGCCCAATATGTGCGCTCCGACTGTGTGCTTCAATG	5268
Qy	2563	CTAGTGAAGAAAGCGTGGCTGTGATTAAGCATTAACATGTGATGGCACTGGAGGACAGG	2622
Db	5269	CTAGTGAAGAAAGCGTGGCTGTGATTAAGCATTAACATGTGATGGCACTGGAGGACAGG	5328
Qy	2623	GCTCTCTCAGATGCTGACCTGTGCGACGGCAACTGTCACTGCTGAMAGCACTTCACTGA	2682
Db	5329	GCTCTCTCAGATGCTGACCTGTGCGACGGCAACTGTCACTGCTGAMAGCACTTCACTGA	5388
Qy	2683	GCCAGCCACTCTCCGCAAGGCTGTGCGCAAGTGTGAGCATTAACATGACCCGCTGTCC	2742
Db	5389	GCCAGCCACTCTCCGCAAGGCTGTGCGCAAGTGTGAGCATTAACATGACCCGCTGTCC	5448
Qy	2743	TTGCATTTGGGTAAACAGGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCACT	2802
Db	5449	TTGCATTTGGGTAAACAGGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCACT	5508
Qy	2803	AAGATATTGCTTGAAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTGACATG	2862
Db	5509	AAGATATTGCTTGAAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTGACATG	5568
Qy	2863	ACCATGAAGATCTGGAAGGTGTGAGGTACGATGAGACCCGCAACGAGTGCAGACCTTGC	2922
Db	5569	ACCATGAAGATCTGGAAGGTGTGAGGTACGATGAGACCCGCAACGAGTGCAGACCTTGC	5628
Qy	2923	GAGTGTGGCGGTAAACATATTAGGAACAGGCTGTGATGCTGATGTGACGAGGAGCTG	2982
Db	5629	GAGTGTGGCGGTAAACATATTAGGAACAGGCTGTGATGCTGATGTGACGAGGAGCTG	5688
Qy	2983	AGGCCCGATCACTTGTGCTGTGCTGCAACCGCGCTGAAGTTTGGCTTACGATGAAGAT	3042
Db	5689	AGGCCCGATCACTTGTGCTGTGCTGCAACCGCGCTGAAGTTTGGCTTACGATGAAGAT	5748
Qy	3043	ACAGATTGAG 3052	
Db	5749	ACAGATTGAG 5758	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 28, 2005, 00:45:38 ; Search time 1480 Seconds
(without alignments)
12207.467 Million cell updates/sec

Title: US-10-790-562-33

Perfect score: 3052

Sequence: 1 cggctagtcgtcttatacc.....cgatgaagatcacagatcgag 3052

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2004as:*
12: Geneseq2004bs:*
13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	3052	100.0	32802 13 ADR41671	Adr41671 S98-100 (
2	3052	100.0	33699 4 AAC85020	Aac85020 Adenoviru
3	3052	100.0	34448 4 AAC85021	Aac85021 Adenoviru
4	3052	100.0	35934 8 AB282331	Ab282331 Human ade
5	3052	100.0	35935 2 AAV07258	Aav07258 Adenoviru
6	3052	100.0	35935 4 AAC85026	Aac85026 Complete
7	3052	100.0	35935 6 ABS69882	Ab669882 Human ade
8	3052	100.0	35935 6 ABS69883	Ab669883 Human ade
9	3052	100.0	35935 8 ACA61116	ACA61116 Adenoviru
10	3052	100.0	35935 8 ACA61117	ACA61117 Adenoviru
11	3052	100.0	35935 10 ACA60761	ACA60761 Human ade
12	3052	100.0	35935 13 ADR41672	Adr41672 Wild type
13	3052	100.0	35978 6 AAD27971	Aad27971 Recombina
14	3052	98.5	7090 5 AAH20746	Aah20746 Plasmid S
15	2994	98.1	3408 9 ACC70006	Acc70006 Nucleocid
16	2963	97.1	37339 5 AAS15612	Aas15612 Mouse ost
17	2959.4	97.0	11152 2 AAV32373	Aav32373 Complete
18	2959.4	97.0	11152 3 AAA59047	Aaa59047 Nucleocid
19	2959.4	97.0	11152 6 ABA94256	Ab94256 Nucleocid
20	2959.4	97.0	11152 10 ADB75153	Adb75153 Plasmid p

21	2959.4	97.0	11152 10 ADF48798	Adf48798 El expres
22	2959.4	97.0	14455 2 AAV32374	Aav32374 Complete
23	2959.4	97.0	14455 3 AAA59050	Aaa59050 Nucleocid
24	2959.4	97.0	14455 6 ABA94259	Ab94259 Nucleocid
25	2959.4	97.0	14455 10 ADB75156	Adb75156 Plasmid p
26	2959.4	97.0	14455 10 ADF48801	Adf48801 El/fibre
27	2959	97.0	7607 3 AAA59076	Aaa59076 Nucleocid
28	2959	97.0	7607 6 ABA94278	Ab94278 Nucleocid
29	2959	97.0	7607 9 AAL56864	Aal56864 DNA seque
30	2959	97.0	7607 10 ADB75124	Adb75124 Chromosom
31	2959	97.0	7607 10 ADF48758	Adf48758 Plasmid p
32	2948	96.6	35937 6 ABS69881	Ab669881 Human ade
33	2948	96.6	35937 9 ACC70007	Acc70007 Nucleocid
34	2947.4	96.6	35759 10 ADF60698	Adf60698 Ade genom
35	2947.4	96.6	35759 13 ADS00148	Ads00148 Human ade
36	2869.4	94.0	4853 10 ADR65745	Adr65745 Human ade
37	2822	92.5	33592 4 AAC85018	Aac85018 Adenoviru
38	2822	92.5	33988 4 AAC85023	Aac85023 Adenoviru
39	2822	92.5	34341 4 AAC85019	Aac85019 Adenoviru
40	2822	92.5	34737 4 AAC85024	Aac85024 Adenoviru
41	2822	92.5	35724 4 AAC85022	Aac85022 Adenoviru
42	2822	92.5	35871 6 AAD27972	Aad27972 Recombina
43	2822	92.5	36114 4 AAC85025	Aac85025 Adenoviru
44	2161	70.8	34303 2 AAV07261	Aav07261 Adenoviru
45	2043	66.9	31976 13 ADR41670	Adr41670 Oncolytic

ALIGNMENTS

RESULT 1
ID ADR41671 standard; DNA; 32802 BP.
XX
XX ADR41671;
XX
XX 04-NOV-2004 (first entry)
XX
XX S98-100 (32802bp) adenovirus DNA used as positive control.
XX
XX
XX Lytic agent; ds; chaparone; heat shock protein; stimulus;
XX tumour shrinkage; oncolysis; HSP; HSP-GRA; cancer reactive antigen;
XX nasopharyngeal carcinoma; chondrosarcoma; colon cancer; breast; prostate;
XX ovarian; stomach carcinoma; rectum; malignant hepatoma; melanoma; p53;
XX tumour suppressor gene; variant; genetically modified Ad5; S98-002;
XX E1b region; E3; E1b-55KD; gene; ascites.
XX
XX Human adenovirus type 5.
XX Synthetic.
XX
XX
XX Key Location/Qualifiers
XX misc_feature 2501..3328
XX FT /*tag= a
XX FT /note= "Partial E1b region"
XX
XX WO2004066947-A2.
XX
XX 12-AUG-2004.
XX
XX PD
XX
XX 28-JAN-2004; 2004WO-US002330.
XX
XX PF
XX
XX 28-JAN-2003; 2003US-0443095P.
XX
XX PR
XX
XX (SHAN-) SHANGHAI SUNWAY BIOTECH CO LTD.
XX
XX Hu F, Wu B;
XX
XX WPI; 2004-580848/56.
XX
XX DR
XX
XX Abtacting tumor cells in a subject having at least one tumor site by
XX contacting the tumor cells in at least one tumor with a lytic agent in
XX vivo and applying a sufficient in vivo stimulus to the treated tumor
XX forming a stimulated tumor.
XX
XX PT

XX Example 1, SEQ ID NO 3, 129bp, English.

CC The present invention relates to the compositions and methods for
CC ablating tumour cells in a subject having one or more tumour sites. The
CC method includes introduction of a lytic agent into a tumour (which forms
CC a treated tumour) and application of stimulus to the treated tumour. The
CC stimulus (physical, chemical or biological) induces the level of
CC chaperone proteins (heat shock proteins) in the tumour cells. The
CC combination of the lytic agent and tumour cell stimulus leads to tumour
CC shrinkage. The invention relates to the synchronisation between oncolysis
CC and elevated expression of a heat shock protein (HSP), which results in
CC sufficient release of HSP-CRA (cancer reactive antigen). The sufficient
CC levels of HSP-CRA exhibit a signal immunogenic enough to the immune
CC system in order to elicit an immune response against the cancer. The
CC method of the invention is useful in ablating tumour cells for treating
CC nasopharyngeal carcinoma, chondrosarcoma, colon cancer, breast cancer,
CC prostate cancer, ovarian cancer, stomach carcinoma, rectum cancer,
CC malignant hepatoma, melanoma, ascites etc. Mutations of the p53 gene
CC exist in more than half of cancer cases. The treated or non-treated
CC cancers which consist of a defective p53 tumour suppressor gene or an
CC activated oncogene are good candidates for this method of therapy. The
CC oncolytic viruses of this invention comprise genetically modified Ad5
CC variants. This oncolytic adenovirus selectively replicates in cancer
CC cells with a p53 mutation and lyses cancer cells with high specificity.
CC The genome of a wild type Ad5 is composed of 35,935 bps. Genetically
CC modified variant Ad5 (598-001) has an extra stop codon at position 2025
CC (E1b region) and possesses deletions in E1b region (in between 2,501 and
CC 3,328) and in E3 (in between 27865 and position 30,995) region. In normal
CC cells E1b-55KD binds and inactivates the protein encoded by the p53 gene
CC and initiates viral replication. The 598-001 variant is not able to
CC replicate in normal cells, but replicates rapidly in cancer cells in
CC which the p53 protein is dysfunctional. The function of E3 is related to
CC the ability of an adenovirus to escape from the surveillance of the
CC immune system. The complete deletion of the E3 region in 598-001 enables
CC the immune system easier recognition and elimination of this virus. 598
CC -002 is another genetically modified variant Ad5. It has deletions in the
CC region encoding E1b-55KD (in between 2,501 and 3,328) and of the entire
CC E3 region (in between 27865 and position 30,995). The variant sequences
CC of Ad5 are unable to integrate into the human genome, but selectively
CC replicate in cancer cells. So, 598-001 and 598-002 are safe for use in
CC humans and animals. The presented sequence is the 598-100 (32802bp)
CC adenovirus DNA which is used as positive control. Note: This sequence is
CC shown as SEQ ID No 3 in the sequence listing but not clearly mentioned in
CC example 1 of the specification.

XX Sequence 32802 BP; 7543 A; 9233 C; 9139 G; 6887 T; 0 U; 0 Other;

Query Match 100.0%; Score 3052; DB 13; Length 32802;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTAGTGTATTTATACCGCGTGAATTCCTCAAGAGCCACTCTTGAGTCCAGCGAGT 60
DB 459 CGTGTAGTGTATTTATACCGCGTGAATTCCTCAAGAGCCACTCTTGAGTCCAGCGAGT 518
QY 61 AGAGTTTCTCCTCCGAGCGGCTCGACACCGGAGCTGAATAATGAGATATTTATCGCC 120
DB 519 AGAGTTTCTCCTCCGAGCGGCTCGACACCGGAGCTGAATAATGAGATATTTATCGCC 578
QY 121 ACGGAGGTGTATTATACCGAAGAAATGCGCGCAGTCTTTTGACACGAGCTGATCGAAGAG 180
DB 579 ACGGAGGTGTATTATACCGAAGAAATGCGCGCAGTCTTTTGACACGAGCTGATCGAAGAG 638
QY 181 TACTGGCTGATTAATCTTCACTCTAGCCATTTTGAACAACCTTACCTTACGAACTGT 240
DB 639 TACTGGCTGATTAATCTTCACTCTAGCCATTTTGAACAACCTTACCTTACGAACTGT 698
QY 241 ATGATTTAGAGTGAACGCGCCCGGAAAGATCCCAACGAGGAGCGGTTTCGAGATTTTTC 300
DB 699 ATGATTTAGAGTGAACGCGCCCGGAAAGATCCCAACGAGGAGCGGTTTCGAGATTTTTC 758
QY 301 CCGACTCTGTATGTGGCGGTGACGAAAGGATGACTTACTCACTTTCCGCGCGGC 360

DB 759 CCGACTCTGTATGTGGCGGTGACGAAAGGATGACTTACTCACTTTCCGCGCGGC 818
QY 361 CCGGTTCTCCGAGCCGCTCACTTTTCCGCGACGCCCGAGACCCGAGACAGAGAGCTT 420
DB 819 CCGGTTCTCCGAGCCGCTCACTTTTCCGCGACGCCCGAGACCCGAGACAGAGAGCTT 878
QY 421 TGGTCCGGTTTCTATGACCAAACTTGTAACCGAGAGTATGATCTTACCTGCCACGAG 480
DB 879 TGGTCCGGTTTCTATGACCAAACTTGTAACCGAGAGTATGATCTTACCTGCCACGAG 938
QY 481 CTGGCTTTCCACCCAGTACGACGAGAGATGAAGAGGTGAGAGATTGTGTAAATTATG 540
DB 939 CTGGCTTTCCACCCAGTACGACGAGAGATGAAGAGGTGAGAGATTGTGTAAATTATG 998
QY 541 TGGAGCACCCCGGACAGGTTGACAGTCTGTCTATTAACCGAGAGATACGGGGAGCC 600
DB 999 TGGAGCACCCCGGACAGGTTGACAGTCTGTCTATTAACCGAGAGATACGGGGAGCC 1058
QY 601 CAGATATTATGTGTGCTTGTATATGAGACCTGTGGCATGTGTCTACAGTAACT 660
DB 1059 CAGATATTATGTGTGCTTGTCTATATGAGACCTGTGGCATGTGTCTACAGTAACT 1118
QY 661 GAAATTTATGGGCAGTGGGATGATGAGTGTGGTGTGTGTGTAAATTTTTTTTAAAT 720
DB 1119 GAAATTTATGGGCAGTGGGATGATGAGTGTGGTGTGTGTGTAAATTTTTTTTAAAT 1178
QY 721 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTTTAAAGATCCTGTGTC 780
DB 1179 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTTTAAAGATCCTGTGTC 1238
QY 781 TGAACCTGAGGCTGAGCCGAGCCGAGAACCGAGACTGCAAGACCTACCCGCGCTCTAA 840
DB 1239 TGAACCTGAGGCTGAGCCGAGCCGAGAACCGAGACTGCAAGACCTACCCGCGCTCTAA 1298
QY 841 AATGCGCCTGCTATCCTGAGACGCGCCGACATCACTGTGTCTAGAGAAATGCAATAGTAG 900
DB 1299 AATGCGCCTGCTATCCTGAGACGCGCCGACATCACTGTGTCTAGAGAAATGCAATAGTAG 1358
QY 901 TACGGAATAGCTGTACCTCGGCTCTTTTAAACACACCTTCTGAGATACCCGGGTGTC 960
DB 1359 TACGGAATAGCTGTACCTCGGCTCTTTTAAACACACCTTCTGAGATACCCGGGTGTC 1418
QY 961 GCTGTGCCCAATTAACAGATGCGGAGAGTGTGGGGGTGCGCAGGCTGTGGAATG 1020
DB 1419 GCTGTGCCCAATTAACAGATGCGGAGAGTGTGGGGGTGCGCAGGCTGTGTGAATG 1478
QY 1021 TATGAGAGACTTGTCTTAACGAGCTGGGCAACCTTTGGAATTTAGCTGTAAACGCCCCAG 1080
DB 1479 TATGAGAGACTTGTCTTAACGAGCTGGGCAACCTTTGGAATTTAGCTGTAAACGCCCCAG 1538
QY 1081 GCCATTAAGGTGTAAACCTGTGATTTGCTGTGTGTGTAAACGCTTTGTTGCTGAATAGT 1140
DB 1539 GCCATTAAGGTGTAAACCTGTGATTTGCTGTGTGTGTAAACGCTTTGTTGCTGAATAGT 1598
QY 1141 TGATGTAAAGTTTAAATAAGGAGTGAATGTTTAACTTGATGCGCGTTTAAATGGGGC 1200
DB 1599 TGATGTAAAGTTTAAATAAGGAGTGAATGTTTAACTTGATGCGCGTTTAAATGGGGC 1658
QY 1201 GGGGCTTAAAGGTATTAATGCGCGGTGCTAATCTTGTGTTAATCTGACCTCATGGA 1260
DB 1659 GGGGCTTAAAGGTATTAATGCGCGGTGCTAATCTTGTGTTAATCTGACCTCATGGA 1718
QY 1261 GGCCTGGAGAGTGTGGAAGATTTTCTGCTGTGCGTAACTGCTGGAACGAGACTCTAA 1320
DB 1719 GGCCTGGAGAGTGTGGAAGATTTTCTGCTGTGCGTAACTGCTGGAACGAGACTCTAA 1778
QY 1321 CAGTACTCTTGGTTTGAAGGTTTCTGTGGGGGTCAATCCAGGCAAGTTAGTCTGAG 1380
DB 1779 CAGTACTCTTGGTTTGAAGGTTTCTGTGGGGGTCAATCCAGGCAAGTTAGTCTGAG 1838
QY 1381 AATTAAAGAGATTAAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGAGTGT 1440

XX	The invention relates to a recombinant vector (V1) which is replication-competent in a neoplastic cell and which overexpresses an adenovirus death protein (ADP). The vector can be used in a method for promoting death of a neoplastic cell that comprises contacting the neoplastic cell with at least one V1; and a composition comprising V1 and a second recombinant virus which is: (a) replication defective and which expresses an anti-cancer gene product, where V1 complements replication of the second recombinant virus; or (b) replication-competent in a neoplastic cell. V1, together with one or more replication-defective adenovirus which expresses an anti-cancer gene product, are useful in cancer therapy. Overexpression of ADP by V1 results in faster lysis of cells and spread of the virus throughout a cell monolayer than viruses expressing wild-type levels of ADP. The present sequence represents the complete nucleotide sequence of an adenovirus subgroup C anti-cancer vector G21 containing E3 deletion and overexpressing ADP														
XX	Sequence	33699	BP;	7771	A;	9497	C;	9310	G;	7121	T;	0	U;	0	Other;
XX	Query Match			100.0%;	Score	3052;	DB	4;	Length	33699;					
XX	Best Local Similarity			100.0%;	Pred.	No.	0;								
XX	Matches	3052;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;					
QY	1	CGGTAGCTGATTTATATACCCGGTAGTTCCTCAAGAGCCACTCTTGAAGTGGCACCAGCT	60												
DB	459	CGTGTAGTGAATTTATATACCCGGTAGTTCCTCAAGAGCCACTCTTGAAGTGGCACCAGCT	518												
QY	61	AGAGTTTCTCTCCGAGCCGCTCCGACACGGAGACTGAAAATGACATATTATCTGCC	120												
DB	519	AGAGTTTCTCTCCGAGCCGCTCCGACACGGAGACTGAAAATGACATATTATCTGCC	578												
QY	121	ACGGAGGTGTTATTACCGAAGAAATGSCCGCCAGTCTTTGGACCAAGTATCGAAGAG	180												
DB	579	ACGGAGGTGTTATTACCGAAGAAATGSCCGCCAGTCTTTGGACCAAGTATCGAAGAG	638												
QY	181	TACGTGGCTGAATATCTTCCACTCTCTAGCAATTTGAAACACTAACCTTACCGAACTGT	240												
DB	639	TACGTGGCTGAATATCTTCCACTCTCTAGCAATTTGAAACACTAACCTTACCGAACTGT	698												
QY	241	ATGATTTAGACGTGACGCGCCCGCAGATCCCAAGAGAGCGTTTCGACAGATTTTTC	300												
DB	699	ATGATTTAGACGTGACGCGCCCGCAGATCCCAAGAGAGCGTTTCGACAGATTTTTC	758												
QY	301	CCGACTCTGTATGTTGGCGGTGACAGAAAGGATGACTTACTCACTTTCCGCGCGGC	360												
DB	759	CCGACTCTGTATGTTGGCGGTGACAGAAAGGATGACTTACTCACTTTCCGCGCGGC	818												
QY	361	CCGGATTCCGGAGCGGCTCAACCTTTCCCGGACGCCGAGACGCCGAGACGAGAGCT	420												
DB	819	CCGGATTCCGGAGCGGCTCAACCTTTCCCGGACGCCGAGACGCCGAGACGAGAGCT	878												
QY	421	TGGGTCCGGTTCTATGCGCAACCTTGTACCGAGGTGATCGATCTTACCTGCGACGAG	480												
DB	879	TGGGTCCGGTTCTATGCGCAACCTTGTACCGAGGTGATCGATCTTACCTGCGACGAG	938												
QY	481	CTGGCTTTCCACCAGTGACGACGAGATGAAAGAGGTGAGAGATTGTGTTAAGATTAG	540												
DB	939	CTGGCTTTCCACCAGTGACGACGAGATGAAAGAGGTGAGAGATTGTGTTAAGATTAG	998												
QY	541	TGAGACACCCGGGACGAGTTGACAGGCTTGTGCTATTATCACCGAGAGATACGGGGAC	600												
DB	999	TGAGACACCCGGGACGAGTTGACAGGCTTGTGCTATTATCACCGAGAGATACGGGGAC	1058												
QY	601	CAGATATTATGTGTCGCTTTGCTATATGAGACCTGTGACATGTTGTCTACAGTAAGT	660												
DB	1059	CAGATATTATGTGTCGCTTTGCTATATGAGACCTGTGACATGTTGTCTACAGTAAGT	1118												
QY	661	GAAATATTATGGGACGTGGGTGATAGAGTGGGTTGGTGAGTAAATTTTTTTTAAAT	720												
DB	1119	GAAATATTATGGGACGTGGGTGATAGAGTGGGTTGGTGAGTAAATTTTTTTTAAAT	1178												
QY	721	TTTTCACGTTTGTGGTTTAAAGAAATTTGTATGTGATTTTAAAAAGTCTGTGTC	780												

Db 519 AGAGTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGMAAATGAGACATATTAATCTGCC 578
Qy 121 ACGGAGGTTATTAACGAGAAATGGCGCAGCTTTTGACACAGTGAATCGAAGG 180
Db 579 ACGGAGGTTATTAACGAGAAATGGCGCAGCTTTTGAGACAGTGAATCGAAGG 638
Qy 181 TACTGGCTGAATATCTTCCACTCTTACGCAATTTGAAACAACCTTACCGAAGCTGT 240
Db 639 TACTGGCTGAATATCTTCCACTCTTACGCAATTTGAAACAACCTTACCGAAGCTGT 698
Qy 241 ATGATTTAGAGTGAACGGCCCCCGAAAGATCCGACAGAGAGCGGTTTCGAGATTTTC 300
Db 699 ATGATTTAGAGTGAACGGCCCCCGAAAGATCCGACAGAGAGCGGTTTCGAGATTTTC 758
Qy 301 CCGACTCTGATATGTTGGCGGTCAGAAAGGATTTGACTTCACTTTCGCGCGCGC 360
Db 759 CCGACTCTGATATGTTGGCGGTCAGAAAGGATTTGACTTCACTTTCGCGCGCGC 818
Qy 361 CCGGTTCTCCGAGACGGCTCACTTTCGCGCAGCCGAGACGCGAGAGAGAGCT 420
Db 819 CCGGTTCTCCGAGACGGCTCACTTTCGCGCAGCCGAGAGCGCGAGAGAGCT 878
Qy 421 TGGGTCGGGTTCTATGCGCAAACTTTGTAACGGAGTGAATGATCTTACTCGCCAGAG 480
Db 879 TGGGTCGGGTTCTATGCGCAAACTTTGTAACGGAGTGAATGATCTTACTCGCCAGAG 938
Qy 481 CTGGCTTCCACCGCAGTACGACGAGATGAAGAGGATGAGGATTTGTTAGATTATG 540
Db 939 CTGGCTTCCACCGCAGTACGACGAGATGAAGAGGATGAGGATTTGTTAGATTATG 998
Qy 541 TGGAGCACCCGCGGACGCTTGACAGTCTTGTCAATTAACCGAGAGAAACGCGGGAGC 600
Db 999 TGGAGCACCCGCGGACGCTTGACAGTCTTGTCAATTAACCGAGAGAAACGCGGGAGC 1058
Qy 601 CAGATATTAATGTTGCTTGTCTATATAGAGACTTGTCGATGTTTGTCTACAGTAAGT 660
Db 1059 CAGATATTAATGTTGCTTGTCTATATAGAGACTTGTCGATGTTTGTCTACAGTAAGT 1118
Qy 661 GAAATTTATGGGCAATGGGTGATATAGATGTTGGTTGTGTGTAATTTTTTTTAT 720
Db 1119 GAAATTTATGGGCAATGGGTGATATAGATGTTGGTTGTGTGTAATTTTTTTTAT 1178
Qy 721 TTTTACAGTTTGTGTTAAAGAAATTTGATTTGATTTTAAAGGCTCTGTGC 780
Db 1179 TTTTACAGTTTGTGTTAAAGAAATTTGATTTGATTTTAAAGGCTCTGTGTGC 1238
Qy 781 TGAACCTAGGCTGAGCCGAGCCAGAAACCGAGCTTGAAAGACTTACCCGCTCTAA 840
Db 1239 TGAACCTAGGCTGAGCCGAGCCAGAAACCGAGCTTGAAAGACTTACCCGCTCTAA 1298
Qy 841 AATGGCGCTGCTATCCTGAGACGCGCGACATCACTGTGTCTAGAAATGAATAGTAG 900
Db 1299 AATGGCGCTGCTATCCTGAGACGCGCGACATCACTGTGTCTAGAAATGAATAGTAG 1358
Qy 901 TACGATAGCTGTGACTCCGCTCTTCTTAACACACTCTCTGAGATACACCGGTGTGCC 960
Db 1359 TACGATAGCTGTGACTCCGCTCTTCTTAACACACTCTCTGAGATACACCGGTGTGCC 1418
Qy 961 GCTGTGCCCATTAACCAAGTTGCCGTGAGAGTTGTGTGGCGCTGCAGGCTGTGAATG 1020
Db 1419 GCTGTGCCCATTAACCAAGTTGCCGTGAGAGTTGTGTGGCGCTGCAGGCTGTGAATG 1478
Qy 1021 TATGAGAGACTTGTCTTAACGAGCCTGGGCAACCTTTGACCTTGAACCTTAAACGCCAG 1080
Db 1479 TATGAGAGACTTGTCTTAACGAGCCTGGGCAACCTTTGACCTTGAACCTTAAACGCCAG 1538
Qy 1081 GCAATAAGGTGTAACCTGTGATTCGTGTGTGTTAAAGCCTTGTGTTGCTGAATGAGT 1140
Db 1539 GCAATAAGGTGTAACCTGTGATTCGTGTGTGTTAAAGCCTTGTGTTGCTGAATGAGT 1598
Qy 1141 TGATGTAAGTTAATAAAGGTGAGATATGTTTAACTTGCAATGCGCTGTTAAATGGGCG 1200
Db 1599 TGATGTAAGTTAATAAAGGTGAGATATGTTTAACTTGCAATGCGCTGTTAAATGGGCG 1658

Qy 1201 GGGGCTTAAAGGTAATTAATGCGCGTGGGCTAATCTTGTTACATCTGACTCATGGA 1260
Db 1659 GGGGCTTAAAGGTAATTAATGCGCGCTGGGCTAATCTTGTTACATCTGACTCATGGA 1718
Qy 1261 GGGTGGAGTGTGTAAGATTTTCTGTGTGCTGAATCTTCTGTGAACAGAGCTCTAA 1320
Db 1719 GGGTGGAGTGTGTAAGATTTTCTGTGTGCTGAATCTTCTGTGAACAGAGCTCTAA 1778
Qy 1321 CAGTAACCTTTGGTTTGGAGTTTCTGTGGGCTCAATCCAGGCAAAATGATGTGAG 1380
Db 1779 CAGTAACCTTTGGTTTGGAGTTTCTGTGGGCTCAATCCAGGCAAAATGATGTGAG 1838
Qy 1381 AATTAAGAGATTAACAAGTGGGAATTTGAAGAGCTTTTGAATCTGTGTGAGTGT 1440
Db 1839 AATTAAGAGATTAACAAGTGGGAATTTGAAGAGCTTTTGAATCTGTGTGAGTGT 1898
Qy 1441 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCAAGAGAAAGTCAATCAAGCTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCAAGAGAAAGTCAATCAAGCTTGA 1958
Qy 1501 TTTTTCACACCGGGGCGCGCTGCGCTGTGTGCTTTTGTAGTTTAAAGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGCTGTGTGCTTTTGTAGTTTAAAGATTA 2018
Qy 1561 ATGAGCGAAGAAACCCATCTGAGCGGGGGTAACTGTGGAATTTTCTGCGCATGCACT 1620
Db 2019 ATGAGCGAAGAAACCCATCTGAGCGGGGGTAACTGTGGAATTTTCTGCGCATGCACT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACAACAAGATCGCTGTCTACTGTGTCTTCCGTCGCGCGG 1680
Db 2079 GTGAGAGCGGTTGTGAGACAACAAGATCGCTGTCTACTGTGTCTTCCGTCGCGCGG 2138
Qy 1681 GATTAATCCGACGAGAGACGACGACGACGAGAGAAAGCCAGGCGCGCGACAGGA 1740
Db 2139 GATTAATCCGACGAGAGACGACGACGACGAGAGAAAGCCAGGCGCGCGACAGGA 2198
Qy 1741 GCAGAGCCATGGAACCGGAGAGCGGCTGTGACCTCTGGGAATGAATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCATGGAACCGGAGAGCGGCTGTGACCTCTGGGAATGAATGTTGTACAGGTG 2258
Qy 1801 GCTGAACGTATCCAGAACTGAGACGCAATTTTGAACAATTAACAAGATGGCAGGGCTA 1860
Db 2259 GCTGAACGTATCCAGAACTGAGACGCAATTTTGAACAATTAACAAGATGGCAGGGCTA 2318
Qy 1861 AAGGGGTAAAGAGAGAGCGGGGCTTGTGAGGCTACAGAGAGGCTTAAGAACTTACT 1920
Db 2319 AAGGGGTAAAGAGAGAGCGGGGCTTGTGAGGCTACAGAGAGGCTTAAGAACTTACT 2378
Qy 1921 TTTAGCTTAAATGACACAGACCGTCTGAGTGTATTACTTTTCAACAGATCAAGGATTA 1980
Db 2379 TTTAGCTTAAATGACACAGACCGTCTGAGTGTATTACTTTTCAACAGATCAAGGATTA 2438
Qy 1981 TGCCTAATGACTTGAATCTGTGGCGCAAGATTTCCATAGAGCAGCTGACCACTTAC 2040
Db 2439 TGCCTAATGACTTGAATCTGTGGCGCAAGATTTCCATAGAGCAGCTGACCACTTAC 2498
Qy 2041 TGGCTGAGCGGAGATGATTTTGAAGAGCTATTAAGGATTAATGCAAGGTGGCACTT 2100
Db 2499 TGGCTGAGCGGAGATGATTTTGAAGAGCTATTAAGGATTAATGCAAGGTGGCACTT 2558
Qy 2101 AGGCGAGTTTGCAAGTCAAGATCAGCAACTTGTAAATATCAGAAATGTTGTCTACAT 2160
Db 2559 AGGCGAGTTTGCAAGTCAAGATCAGCAACTTGTAAATATCAGAAATGTTGTCTACAT 2618
Qy 2161 TCTGGAAACGGGGCGAGGTGAGATTAACGAGGATAGAGGTGCGCTTTAGATGAGC 2220
Db 2619 TCTGGAAACGGGGCGAGGTGAGATTAACGAGGATAGAGGTGCGCTTTAGATGAGC 2678
Qy 2221 ATGATTAATATGTGGCGGGGCTGTGCAATGACCGGGCTGTATTAATGAATGTAAG 2280
Db 2679 ATGATTAATATGTGGCGGGGCTGTGCAATGACCGGGCTGTATTAATGAATGTAAG 2738

QY 2281 TTTACTGSCCCCAATTTTAGGGTACGGTTTTCTCGCCAAATACCACTTATCTTACAC 2340
DB 2739 TTTACTGSCCCCAATTTTAGGGTACGGTTTTCTCGCCAAATACCACTTATCTTACAC 2798
QY 2341 GGTGTAAAGCTTCTATAGGTTTAAACAATACCTGTGTGAAGCCGTGATGAAGGTT 2400
DB 2799 GGTGTAAAGCTTCTATAGGTTTAAACAATACCTGTGTGAAGCCGTGATGAAGGTT 2858
QY 2401 CGGGGCTGTGCTTTTACTGCTGTGAAGGGGGTGTGTGTGCGCCCAAAAGAGGCT 2460
DB 2859 CGGGGCTGTGCTTTTACTGCTGTGAAGGGGGTGTGTGTGCGCCCAAAAGAGGCT 2918
QY 2461 TCAATTAGAAATGCTCTTTGAAAGGTATCCTTGGGTATCCTGTCTGAGGTTACTCC 2520
DB 2919 TCAATTAGAAATGCTCTTTGAAAGGTATCCTTGGGTATCCTGTCTGAGGTTACTCC 2978
QY 2521 AGGGTGCAGCAATATGTAGCCCTCCGACTGTGGTTGCTTCATGTAGTAAAGCGTGCCT 2580
DB 2979 AGGGTGCAGCAATATGTAGCCCTCCGACTGTGGTTGCTTCATGTAGTAAAGCGTGCCT 3038
QY 2581 GTGATTAAAGCATTAACATGTATGTGGCAACTGCGAGAGACAGGGCTCTCAGATGCTGACC 2640
DB 3039 GTGATTAAAGCATTAACATGTATGTGGCAACTGCGAGAGACAGGGCTCTCAGATGCTGACC 3098
QY 2641 TGCTCGGACGGCACTGTACCTGTGTGAAGCAATTCAGTACCAAGCACTTCTGCAAG 2700
DB 3099 TGCTCGGACGGCACTGTACCTGTGTGAAGCAATTCAGTACCAAGCACTTCTGCAAG 3158
QY 2701 GCTGTGCGCAAGTTTGAACATTAACATTAACATTAACATTAACATTAACATTAACATTA 2760
DB 3159 GCTGTGCGCAAGTTTGAACATTAACATTAACATTAACATTAACATTAACATTAACATTA 3218
QY 2761 AGGGGGGTGTCTCTAATCTTAAATGCAATTTGAGTCACTTAAAGATTTGCTTGAAGCCC 2820
DB 3219 AGGGGGGTGTCTCTAATCTTAAATGCAATTTGAGTCACTTAAAGATTTGCTTGAAGCCC 3278
QY 2821 GAGAGCATGTCCAGTGAACCTGAACGGGGTGTGTGATGATGATGATGATGATGATGATGAT 2880
DB 3279 GAGAGCATGTCCAGTGAACCTGAACGGGGTGTGTGATGATGATGATGATGATGATGATGAT 3338
QY 2881 GTGCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
DB 3339 GTGCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3398
QY 2941 ATTAGGAACCAAGCTGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
DB 3399 ATTAGGAACCAAGCTGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 3458
QY 3001 CTGAGCTGACACCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3052
DB 3459 CTGAGCTGACACCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3510

RESULT 4
ID AB282331 standard; DNA; 35934 BP.
XX AB282331;
XX AC
XX 14-MAY-2003 (first entry)
DE Human adenovirus type 5 genome.
XX
XX Human adenovirus type 5 genome.
XX Adenovirus; PIX; protein IX; gene delivery efficiency; haemostatic;
XX cytostatic; anti-HIV; virucide; gene therapy; genome; de.
XX Human adenovirus type 5.
XX PN W0200296939-A2.
XX 05-DEC-2002.
XX 29-MAY-2002; 2002MO-EP005942.
XX PF

XX 30-MAY-2001; 2001US-0293974P.
PR (TRGE) TRANSGENE SA.
XX
XX Rosa Calatrava M;
PI WPI; 2003-183888/18.
DR
XX Novel modified adenovirus protein IX and its presence in virus or virus-
PT like particle, useful for improving gene delivery efficiency in target
PT cell of virus or virus-like particle.
XX
XX Disclosure; Fig 6; 126pp; English.
XX
XX The invention relates to a novel adenovirus protein IX (PIX) modified by
CC mutation of one or more amino acids of PIX as compared to corresponding
CC wild-type PIX and/or to comprise a binding moiety. The presence of
CC modified PIX in a virus or virus-like particle (VLP) results in improved
CC gene delivery efficiency in the target cell of a virus or VLP as compared
CC to the gene delivery efficiency of a virus or VLP containing wild-type
CC PIX. The protein of the invention has haemostatic, cytostatic, anti-HIV,
CC and virucide activity. The sequence may have a use in gene therapy. The
CC present sequence represents the human adenovirus type 5 genome
XX
SQ Sequence 35934 BP; 8367 A; 10072 C; 9761 G; 7734 T; 0 U; 0 Other;
Query Match 100.0%; Score 3052; DB 8; Length 35934;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTGTAGTATTTTAAACCGGTGAGTTCTTCAAGAGCCACTTGTAGTCCAGCAAGT 60
DB 459 CGTGTAGTATTTTAAACCGGTGAGTTCTTCAAGAGCCACTTGTAGTCCAGCAAGT 518
QY 61 AGAGTTTCTCCCTCCGAGCGGCTCCGACACCGGAGCTGAAATAGACATTTATCTGCC 120
DB 519 AGAGTTTCTCCCTCCGAGCGGCTCCGACACCGGAGCTGAAATAGACATTTATCTGCC 578
QY 121 ACGGAGGTGTTATTAACGAAGAAATGAGCCGCACTTTTGAACACACTGATCGAAGAG 180
DB 579 ACGGAGGTGTTATTAACGAAGAAATGAGCCGCACTTTTGAACACACTGATCGAAGAG 638
QY 181 TACTGCTGATATCTTCACTCTTACCACTTTTGAACCACTTACCTTCAAGAACTGT 240
DB 639 TACTGCTGATATCTTCACTCTTACCACTTTTGAACCACTTACCTTCAAGAACTGT 698
QY 241 ATGATTTAGACGTGACGGCCCGGAGATCCCAACGAGAGGCGGTTTCGAGATTTTC 300
DB 699 ATGATTTAGACGTGACGGCCCGGAGATCCCAACGAGAGGCGGTTTCGAGATTTTC 758
QY 301 CCGACTCTGATATGTTGGCGGTGACGAGAGGATTTGACTTACTTTCGCGCGGC 360
DB 759 CCGACTCTGATATGTTGGCGGTGACGAGAGGATTTGACTTACTTTCGCGCGGC 818
QY 361 CCGGTTTCCGAGAGCGGCTTCACTTTCGCGAGCGGAGAGCCGAGAGAGAGCT 420
DB 819 CCGGTTTCCGAGAGCGGCTTCACTTTCGCGAGCGGAGAGCCGAGAGAGAGCT 878
QY 421 TGGGTCCGTTTCTATGACCAAACTTTGACCGAGAGGATCGTAACTTCCGACAGAG 480
DB 879 TGGGTCCGTTTCTATGACCAAACTTTGACCGAGAGGATCGTAACTTCCGACAGAG 938
QY 481 CTGAGCTTCAACCAAGTACGAGAGGATGAAGAGGTGAGAGTTGTGTAGATTATG 540
DB 939 CTGAGCTTCAACCAAGTACGAGAGGATGAAGAGGTGAGAGTTGTGTAGATTATG 998
QY 541 TGAAGCACCCCGGACAGGTTGACAGGTTCTTGTCTATTATCACCGAGGAATACGGGGAGC 600
DB 999 TGAAGCACCCCGGACAGGTTGACAGGTTCTTGTCTATTATCACCGAGGAATACGGGGAGC 1058
QY 601 CAGATATTATGTGTGCTTGTGATATGAGGACCTTGGCATGTTGTCTACAGTAAGT 660

Db 1059 CAGATATTATGTGTCGCTTGTGATATATAGAGAACCTGTGCGATGTTTGTCTACAGTAAGT 1118
Qy 661 GAAATTTATGCGGCGATGAGTATAGAGTGTGGGTTTGTGTGGTAATTTTTTTTTTAT 720
Db 1119 GAAATTTATGCGGCGATGAGTATAGAGTGTGGGTTTGTGTGGTAATTTTTTTTTTAT 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATTGTATTTTTTTTTTAAAGGTCGTGTGC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATTGTATTTTTTTTTTAAAGGTCGTGTGC 1238
Qy 781 TGAACCTGAGCTTGAGCCGACCGAGCAAAACCGAGCTTGCAAGACCTACCCGCTCTTAA 840
Db 1239 TGAACCTGAGCTTGAGCCGACCGAGCAAAACCGAGCTTGCAAGACCTACCCGCTCTTAA 1298
Qy 841 AATGCGCCCTGCTATCCCTGAGAACGCGCCGACATCACTGTGTCTAGAGAAATGCAATAGTAG 900
Db 1299 AATGCGCTGCTATCCCTGAGAACGCGCCGACATCACTGTGTCTAGAGAAATGCAATAGTAG 1358
Qy 901 TACGGATAGCTGTGACTCCGGTCCCTTCTTACACACCTCTGAGATACACCCGGTGTGCC 960
Db 1359 TACGGATAGCTGTGACTCCGGTCCCTTCTTACACACCTCTGAGATACACCCGGTGTGCC 1418
Qy 961 GCTGTGCCCATTTAAACCAAGTTCCTGTGAGAGTGTGGGCGTGCACAGCTGTGAAATG 1020
Db 1419 GCTGTGCCCATTTAAACCAAGTTCCTGTGAGAGTGTGGGCGTGCACAGCTGTGAAATG 1478
Qy 1021 TATGAGAGACTTGTCTTAAACGAGCCCTGGGCAACCTTTGGACTTGAAGCTTAAACCCCCAG 1080
Db 1479 TATGAGAGACTTGTCTTAAACGAGCCCTGGGCAACCTTTGGACTTGAAGCTTAAACCCCCAG 1538
Qy 1081 GCCATTAAGGTGTAAACCTGTATTGCGTGTGTGTTAAACGCTTGTGTTTGTCTGATGAGT 1140
Db 1539 GCCATTAAGGTGTAAACCTGTATTGCGTGTGTGTTAAACGCTTGTGTTTGTCTGATGAGT 1598
Qy 1141 TGAATGTAAGTTTAAAGGTGAGATATATGTTTAACTTGCAATGCGCTGTTAAATGGGCG 1200
Db 1599 TGAATGTAAGTTTAAAGGTGAGATATATGTTTAACTTGCAATGCGCTGTTAAATGGGCG 1658
Qy 1201 GGGGCTTAAAGGGATATATAGCGCGCGTGGGCTAACTTGGTTTCAATGACCTGACATGGA 1260
Db 1659 GGGGCTTAAAGGGATATATAGCGCGCGTGGGCTAACTTGGTTTCAATGACCTGACATGGA 1718
Qy 1261 GGGCTTGAAGTGTGGAAGATTTTTCTGTGTGCGTAACTTGCTGGAACAGAGCTCTTAA 1320
Db 1719 GGGCTTGAAGTGTGGAAGATTTTTCTGTGTGCGTAACTTGCTGGAACAGAGCTCTTAA 1778
Qy 1321 CAGTAACTCTTGGTTTGTGAGAGTTCTGTGGGCGTCAATCCAGGCAAAATTAGTGTGAG 1380
Db 1779 CAGTAACTCTTGGTTTGTGAGAGTTCTGTGGGCGTCAATCCAGGCAAAATTAGTGTGAG 1838
Qy 1381 AATTAAAGGAGATTACAAAGTGGGAATTTGAAGAGCTTTGAAATCTGTGGTGAAGCTGT 1440
Db 1839 AATTAAAGGAGATTACAAAGTGGGAATTTGAAGAGCTTTGAAATCTGTGGTGAAGCTGT 1898
Qy 1441 TGAATCTTGTGAATCTGGGTCAACAGGCGCTTTTCCAAAGAGAAGTCAATCAAGACTTTGA 1500
Db 1899 TGAATCTTGTGAATCTGGGTCAACAGGCGCTTTTCCAAAGAGAAGTCAATCAAGACTTTGA 1958
Qy 1501 TTTTTCACACCGGGGCGCGCTGCGGCTGTGTGTGCTTTTGAAGTTTAAAGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGGCTGTGTGTGCTTTTGAAGTTTAAAGATTA 2018
Qy 1561 ATGAGCGGAAGAAACCACTGAGCGGGGGGTAACCTGTGGAATTTTCTGGGCAATGCAATCT 1620
Db 2019 ATGAGCGGAAGAAACCACTGAGCGGGGGGTAACCTGTGGAATTTTCTGGGCAATGCAATCT 2078
Qy 1621 GTGAGAGAGCGGTTGTGAGACAAAGAAATGCGCTGTACTGTGTGCTTCCGTCGCGCCGCG 1680
Db 2079 GTGAGAGAGCGGTTGTGAGACAAAGAAATGCGCTGTACTGTGTGCTTCCGTCGCGCGCG 2138
Qy 1681 GATATATACGACGAGAGACAGCAGCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 2139 GATATATACGACGAGAGACAGCAGCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2198

Qy 1741 GCAGAGCCCATGGAACCCGAGAGCCGCGCTGACCCCTCGGGAAATGAATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCCGCGCTGACCCCTCGGGAAATGAATGTTGTACAGGTG 2258
Qy 1801 GCTGAACCTGTATCCAGAACCTGAGACGCAATTTTGAACAAATTAACAGAGATGGGCAAGGCTA 1860
Db 2259 GCTGAACCTGTATCCAGAACCTGAGACGCAATTTTGAACAAATTAACAGAGATGGGCAAGGCTA 2318
Qy 1861 AAGGGGGTAAAGAGGAGCGGGGGGCTTTGTAGGCTTACAGAGAGGCTAAGGAATCTAGCT 1920
Db 2319 AAGGGGGTAAAGAGGAGCGGGGGGCTTTGTAGGCTTACAGAGAGGCTAAGGAATCTAGCT 2378
Qy 1921 TTTAGCTTAAATGACACAGACCCGCTGAGAGTATTAATCTTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAAATGACACAGACCCGCTGAGAGTATTAATCTTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGCCTTAATGAGCTTGAATCTGTGCGCAGAGATTTCAATAGACAGCTGACCACTTAC 2040
Db 2439 TGCCTTAATGAGCTTGAATCTGTGCGCAGAGATTTCAATAGACAGCTGACCACTTAC 2498
Qy 2041 TGGCTGACGCCAGGGGATGATTTTGAAGAGCTTATTAGGGTATTATGCAAGGTGGCACTT 2100
Db 2499 TGGCTGACGCCAGGGGATGATTTTGAAGAGCTTATTAGGGTATTATGCAAGGTGGCACTT 2558
Qy 2101 AGGCCAGATTGCAAGTACAAAGATCAGCAAACTTGTAAATATCAGGAATTTGTTGCTACATT 2160
Db 2559 AGGCCAGATTGCAAGTACAAAGATCAGCAAACTTGTAAATATCAGGAATTTGTTGCTACATT 2618
Qy 2161 TCTGGGAACGGGGCCGAGGTGAGAGATATGATACGAGAGATAGGGTGGCTTTTATGATGATG 2220
Db 2619 TCTGGGAACGGGGCCGAGGTGAGAGATATGATACGAGAGATAGGGTGGCTTTTATGATGATG 2678
Qy 2221 ATGATTAATATGAGCCGGGGGCTTGGCAATGGAACGGGGGTGTTATTAAGAAATGTAAG 2280
Db 2679 ATGATTAATATGAGCCGGGGGCTTGGCAATGGAACGGGGGTGTTATTAAGAAATGTAAG 2738
Qy 2281 TTTTACGGCCCAATTTTAAACGCTGATCGGTTTCTGTGCAATACCAACTTATCTTACAC 2340
Db 2739 TTTTACGGCCCAATTTTAAACGCTGATCGGTTTCTGTGCAATACCAACTTATCTTACAC 2798
Qy 2341 GGTGTAAAGCTTTATATGAGGTTTAAACAAATACCTGTGTGGAAGCTGGACCGATGAAGGTT 2400
Db 2799 GGTGTAAAGCTTTATATGAGGTTTAAACAAATACCTGTGTGGAAGCTGGACCGATGAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTAACTGTGCTGGAAGGGGTGTGTGTGSCCCCAAAAGAGGGCT 2460
Db 2859 CGGGGCTGTGCTTTTAACTGTGCTGGAAGGGGTGTGTGTGSCCCCAAAAGAGGGCT 2918
Qy 2461 TCAATTTAAAGAAATGCTCTTTTGAAGAGTGTACCTTGGGTAATCTGTCTGAGGGTAACTCC 2520
Db 2919 TCAATTTAAAGAAATGCTCTTTTGAAGAGTGTACCTTGGGTAATCTGTCTGAGGGTAACTCC 2978
Qy 2521 AAGGTGCGCACAATGTGGCTCCGACTGTGTGTGCTTCAATGTAGTGAAGAGGTGGCT 2580
Db 2979 AAGGTGCGCACAATGTGGCTCCGACTGTGTGTGCTTCAATGTAGTGAAGAGAGGTGGCT 3038
Qy 2581 GTGATTTAAGCAATACATGTATGTGGAACCTGCGAGAGACAGGGGCTCTCAGATCTGACC 2640
Db 3039 GTGATTTAAGCAATACATGTATGTGGAACCTGCGAGAGACAGGGGCTCTCAGATCTGACC 3098
Qy 2641 TGTCTGAGACGGCAACTGTCACTGTGAAGACAAATTCAGTACAGACCACTCTGCAAG 2700
Db 3099 TGTCTGAGACGGCAACTGTCACTGTGAAGACAAATTCAGTACAGACCACTCTGCAAG 3158
Qy 2701 GCTGTGCAAGTGTGTAAGCAATACATGACCGGCTGTTCCTTGTGCAATTTGGGTAAACAG 2760
Db 3159 GCTGTGCAAGTGTGTAAGCAATACATGACCGGCTGTTCCTTGTGCAATTTGGGTAAACAG 3218
Qy 2761 AAGGGGGGTGTTCTTAATCTTACAAATGCAATTTTGTAGTCACTAAGATTAATGCTTGAAGCC 2820
Db 3219 AAGGGGGGTGTTCTTAATCTTACAAATGCAATTTTGTAGTCACTAAGATTAATGCTTGAAGCC 3278

Qy 2821 GAGGAGCATGTCAGGTGAACCTGAACGGGGTGTGTCATGACCATGAAGATCTGGAG 2880
Db 3279 GAGGAGCATGTCAGGTGAACCTGAACGGGGTGTGTCATGACCATGAAGATCTGGAG 3338
Qy 2881 GTGCTGAGTACGATGAGACCCGACAGAGTGCAGACCTGCGATGCGGTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGACCCGACAGAGTGCAGACCTGCGATGCGGTAAACAT 3398
Qy 2941 ATTGAGAACCAAGCTGTGATCTGATGTGATCCAGAGAGTGAAGCCCGATCACTTGATG 3000
Db 3399 ATTGAGAACCAAGCTGTGATCTGATGTGATCCAGAGAGTGAAGCCCGATCACTTGATG 3458
Qy 3001 CTGGCCCTGACCCGCGCTGAGTTGGCTCTGACGATGAAGATAGATTGAG 3052
Db 3459 CTGGCCCTGACCCGCGCTGAGTTGGCTCTGACGATGAAGATAGATTGAG 3510
RESULT 5
AAV07258
ID AAV07258 standard; DNA, 35935 BP.
AC AAV07258;
XX 17-OCT-2003 (revised)
DT 26-SEP-1998 (first entry)
XX Adenovirus 5 genome.
DE Adenovirus 5 genome.
XX Adenovirus 5; Ad5; vector; gene therapy; de.
OS Human adenovirus type 5.
XX MO9817783-A1.
PN 30-APR-1998.
PD 23-OCT-1997; 97MO-US019541.
PF 23-OCT-1996; 96US-00735609.
PR 23-OCT-1996; 96US-00735609.
XX (UNMI) UNIV MICHIGAN.
XX Chamberlain JS, Amalfitano A, Hauser MA, Kumar-Singh R;
PI Hartigan-O'Connor DJ;
XX WPI, 1998-261485/23.
XX New adenoviral recombinant plasmid(s) - comprise sequences provided for
PT expression of large foreign DNA fragments, used for, e.g. gene therapy of
PT genetic disease(s).
XX Disclosure; Page 69-86; 139pp; English.
XX This nucleotide sequence comprises the adenovirus 5 (Ad5) genome. The
XX invention provides improved adenoviral vectors and packaging cell lines.
XX One type of improved vector comprises deletions within the E2b region of
XX the adenoviral genome (see also AAV07261). These E2b-deleted virus are
XX used in conjunction with novel cell lines that constitutively express E2b
XX gene products. The invention also provides vectors deleted for all viral
XX coding regions. These "gutted" vectors permit the transfer of large genes
XX (e.g. up to 35 kb) to cells, as demonstrated by the transfer of the
XX dystrophin gene to the muscle of mice. The E2b-deleted and gutted vectors
XX provide improved adenoviral vectors useful for a wide variety of gene
XX therapy applications. (Updated on 17-OCT-2003 to standardise OS field)
SQ Sequence 35935 BP; 8367 A; 10074 C; 9760 G; 7734 T; 0 U; 0 Other;
Query Match 100.0%; Score 3052; DB 2; Length 35935;
Best Local Similarity 100.0%; Freq. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTGTAGTATTATACCGGTGAGTTCTCAAGAGGCCACTCTTGAGTGCAGCAGT 60
|||||

Db 459 CGTGTAGTATTATACCGGTGAGTTCTCAAGAGGCCACTCTTGAGTGCAGCAGT 518
Qy 61 AGATTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAATAATGACATATTCTGCC 120
Db 519 AGATTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAATAATGACATATTCTGCC 578
Qy 121 ACGAGAGTATTATACCGAAAGAAATGCGCCCACTCTTTGGACACAGTGTGCAAGAG 180
Db 579 ACGAGAGTATTATACCGAAAGAAATGCGCCCACTCTTTGGACACAGTGTGCAAGAG 638
Qy 181 TACTGCTGATTAATCTTCCACTCTCTAGCAATTTGAACCACTTACCTTCAGAGATG 240
Db 639 TACTGCTGATTAATCTTCCACTCTCTAGCAATTTGAACCACTTACCTTCAGAGATG 698
Qy 241 ATGATTTAGACGTGACCGCCCGGAGAGTCCACGAGAGCGGTTTCGAGATTTTTC 300
Db 699 ATGATTTAGACGTGACCGCCCGGAGAGTCCACGAGAGCGGTTTCGAGATTTTTC 758
Qy 301 CCGACTCTGTAATGTTGGCGGTGAGAGGATTTGACTTACTCATCTTTCCGCGCGC 360
Db 759 CCGACTCTGTAATGTTGGCGGTGAGAGGATTTGACTTACTCATCTTTCCGCGCGC 818
Qy 361 CCGGTTCTCGGAGCGGCTCACCTTTCCGCGAGCCGAGCGGAGGAGAGGAGCT 420
Db 819 CCGGTTCTCGGAGCGGCTCACCTTTCCGCGAGCCGAGCGGAGGAGAGGAGCT 878
Qy 421 TGCGTCCGTTTCTATGCAAACTTGTACCGAGGTGATGATCTTACCTGACGAGG 480
Db 879 TGCGTCCGTTTCTATGCAAACTTGTACCGAGGTGATGATCTTACCTGACGAGG 938
Qy 481 CTGCTTTCCACCGACGACGAGAGATGAAGAGGTGAGAGTTGTGTAGATTATG 540
Db 939 CTGCTTTCCACCGACGACGAGAGATGAAGAGGTGAGAGTTGTGTAGATTATG 998
Qy 541 TGAGACACCCCGGAGCGGTTGACAGCTTGTCAATATCAACCGAGGAAATACGGGGAGC 600
Db 999 TGAGACACCCCGGAGCGGTTGACAGCTTGTCAATATCAACCGAGGAAATACGGGGAGC 1058
Qy 601 CAGATATTATGTTGCTTGTGCTATATGAGACCTGTGACATGTTGTACAGTAAGT 660
Db 1059 CAGATATTATGTTGCTTGTGCTATATGAGACCTGTGACATGTTGTGTACAGTAAGT 1118
Qy 661 GAAATTTATGCGAGAGGTGATGAGATGAGTGGTTTGTGTGTATATTTTAT 720
Db 1119 GAAATTTATGCGAGAGGTGATGAGATGAGTGGTTTGTGTGTATATTTTAT 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGATTTTAAAGAGTCTGTGTC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGATTTTAAAGAGTCTGTGTC 1238
Qy 781 TGAACCTGAGCTGAGCCGAGCCAGAACCGAGCTGCAAGACTTACCGCGTCTTAA 840
Db 1239 TGAACCTGAGCTGAGCCGAGCCAGAACCGAGCTGCAAGACTTACCGCGTCTTAA 1298
Qy 841 AATGCGGCTCTATCTCTGAGAGCCCGACATCACTGTGTCTAGAGAAATGCAATAGTAG 900
Db 1299 AATGCGGCTCTATCTCTGAGAGCCCGACATCACTGTGTCTAGAGAAATGCAATAGTAG 1358
Qy 901 TACGATAGCTGAGCTCGGCTCTTCTTACACACCTCTGAGATACCCGGGTGCC 960
Db 1359 TACGATAGCTGAGCTCGGCTCTTCTTACACACCTCTGAGATACCCGGGTGCC 1418
Qy 961 GCTGTGCCCATTTAAACCAAGTTCCGTGAGAGTTGTGGCGTGCAGGCTGTGATG 1020
Db 1419 GCTGTGCCCATTTAAACCAAGTTCCGTGAGAGTTGTGGCGTGCAGGCTGTGATG 1478
Qy 1021 TATCGAGAGTTCCTTAAACGAGCTGAGCACTTTGAGATTTGAGCTGTAAAGCCCCAG 1080
Db 1479 TATCGAGAGTTCCTTAAACGAGCTGAGCACTTTGAGATTTGAGCTGTAAAGCCCCAG 1538
Qy 1081 GCCATAGAGTGTAAACCTGTGATTTGCGTGTGTGTTAACCTTTGTTCTGAATAGT 1140
Db 1539 GCCATAGAGTGTAAACCTGTGATTTGCGTGTGTGTTAACCTTTGTTCTGAATAGT 1598

QY 1141 TGATGTAACTTTAATAAGGTGAGATTAATGTTTAACCTTGATGGCTGTTAAATGGGCG 1200
DB 1599 TGAATGAAGTTTAATAAAGGTGAGATTAATGTTTAACCTTGATGGCTGTTAAATGGGCG 1658
QY 1201 GGGGCTTAAAGGGATTAATAATGCGCGTGGGCTAATCTTGTTACATCTGACCTCATGGA 1260
DB 1659 GGGGCTTAAAGGGATTAATAATGCGCGTGGGCTAATCTTGTTACATCTGACCTCATGGA 1718
QY 1261 GCGTTGGAGTGTGGAAAGATTTTTCTGCTGTGCGTAACCTTGCTGGAACAGAGCTCTAA 1320
DB 1719 GCGTTGGAGTGTGGAAAGATTTTTCTGCTGTGCGTAACCTTGCTGGAACAGAGCTCTAA 1778
QY 1321 CAGTAACCTCTTGTTGGAGGTTCTGTGGGCTCAATCCAGGCAAGTAAGTCTCAG 1380
DB 1779 CAGTAACCTCTTGTTGGAGGTTCTGTGGGCTCAATCCAGGCAAGTAAGTCTCAG 1838
QY 1381 AATTAAAGAGATTAACAAGTGGAAATTTGAAGACTTTTGAATCTGTGGTGAAGTGT 1440
DB 1839 AATTAAAGAGATTAACAAGTGGAAATTTGAAGACTTTTGAATCTGTGGTGAAGTGT 1898
QY 1441 TGATCTTTGAATCTGGGTCAACAGCGCTTTTCCAAAGAGGTCAATCAAGACTTTGGA 1500
DB 1899 TGATCTTTGAATCTGGGTCAACAGCGCTTTTCCAAAGAGGTCAATCAAGACTTTGGA 1958
QY 1501 TTTTTCACACCGGGGGCGCTGGGCTGTGCTTTTGAAGTTTAAAGATTA 1560
DB 1959 TTTTTCACACCGGGGGCGCTGGGCTGTGCTTTTGAAGTTTAAAGATTA 2018
QY 1561 ATGAGAGGAAGAAACCATCTGAGCGGGGGTACCTGAGATTTTCTGAGCATGCACT 1620
DB 2019 ATGAGAGGAAGAAACCATCTGAGCGGGGGTACCTGAGATTTTCTGAGCATGCACT 2078
QY 1621 GTGAGAGCGGTTGTGAGACAAAGAAATCGCTGCTACTGTGTTCTTCGTCGCGCGGC 1680
DB 2079 GTGAGAGCGGTTGTGAGACAAAGAAATCGCTGCTACTGTGTTCTTCGTCGCGCGGC 2138
QY 1681 GATTAATCCGACGGAGAGACAGACAGACAGAGAGAGAGCGCGGGCGCGAGGA 1740
DB 2139 GATTAATCCGACGGAGAGAGACAGACAGACAGAGAGAGAGCGCGGGCGCGAGGA 2198
QY 1741 GCAGAGCCCATGGAACCGAGAGCGGCTTGGAACCTCGGAAATGAATGTTGACAGGTG 1800
DB 2199 GCAGAGCCCATGGAACCGAGAGCGGCTTGGAACCTCGGAAATGAATGTTGACAGGTG 2258
QY 1801 GCTGAACGTATCCAGAACTGAGACGCAATTTGACAAATTAACAAGATGCGCAGGCTTA 1860
DB 2259 GCTGAACGTATCCAGAACTGAGACGCAATTTGACAAATTAACAAGATGCGCAGGCTTA 2318
QY 1861 AAGGGGGTAAAGAGAGAGCGGGGGCTTGAGGCTACAGAGAGGCTAAGGAATCTAGCT 1920
DB 2319 AAGGGGGTAAAGAGAGAGCGGGGGCTTGAGGCTACAGAGAGGCTAAGGAATCTAGCT 2378
QY 1921 TTTAGCTTAATGACACAGACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
DB 2379 TTTAGCTTAATGACACAGACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
QY 1981 TGGCTTAATGAGCTTGTCTGTGGCGCAAGATTTCAATAGACAGCTGACCACTTAC 2040
DB 2439 TGGCTTAATGAGCTTGTCTGTGGCGCAAGATTTCAATAGACAGCTGACCACTTAC 2498
QY 2041 TGGCTGACGACGAGGGGATGATTTTGAAGGCTATTAGGGATTAAGCAAGGTGGCACTT 2100
DB 2499 TGGCTGACGACGAGGGGATGATTTTGAAGGCTATTAGGGATTAAGCAAGGTGGCACTT 2558
QY 2101 AGGCACAGATTGCAAGTACAAAGATCAGCAAACTTGAATATCAGGAATTTGTTGTACACTT 2160
DB 2559 AGGCACAGATTGCAAGTACAAAGATCAGCAAACTTGAATATCAGGAATTTGTTGTACACTT 2618
QY 2161 TCTGGGAAACGGGGCGAGAGTGAAGTATACGAGATAGGGGTGGCTTTAGATGATGAC 2220
DB 2619 TCTGGGAAACGGGGCGAGAGTGAAGTATACGAGATAGGGGTGGCTTTAGATGATGAC 2678

QY 2221 ATGATTAATATGTGGCGGGGGTCTTGACATGAGACGGGGGTGTTATTAATGATGTAAG 2280
DB 2679 ATGATTAATATGTGGCGGGGGTCTTGACATGAGACGGGGGTGTTATTAATGATGTAAG 2738
QY 2281 TTTACTGCCCCCAATTTTAAACGGATCGGTTTCTTGCCAAATACAACTTATCTTACAC 2340
DB 2739 TTTACTGCCCCCAATTTTAAACGGATCGGTTTCTTGCCAAATACAACTTATCTTACAC 2798
QY 2341 GGTGTAAAGCTTCTATGGGTTTAAACAATCCTGTGTGGAACCTTGACCAATGTAAGGTT 2400
DB 2799 GGTGTAAAGCTTCTATGGGTTTAAACAATCCTGTGTGGAACCTTGACCAATGTAAGGTT 2858
QY 2401 CGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGGTGTGTGCGCCCAAAAGAGAGGCT 2460
DB 2859 CGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGGTGTGTGCGCCCAAAAGAGAGGCT 2918
QY 2461 TCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGAGTATCTGTCTGAGGTTACTCC 2520
DB 2919 TCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGAGTATCTGTCTGAGGTTACTCC 2978
QY 2521 AGGGTGGCCCAATGTGGCTCTCGACTGTGTGTTGCTTCAATGCTAGTGAAGAGCTGGCT 2580
DB 2979 AGGGTGGCCCAATGTGGCTCTCGACTGTGTGTTGCTTCAATGCTAGTGAAGAGCTGGCT 3038
QY 2581 GTGATTAAGCATTAACATGATGTATGAGCACTGCGAGACAGGGGCTCTCAGATGCTGACC 2640
DB 3039 GTGATTAAGCATTAACATGATGTATGAGCACTGCGAGACAGGGGCTCTCAGATGCTGACC 3098
QY 2641 TGCTGGAGCGCAACTGTGTCACTGTGTAAGACCAATTCACGTAGCCCACTCTGCAAG 2700
DB 3099 TGCTGGAGCGCAACTGTGTCACTGTGTAAGACCAATTCACGTAGCCCACTCTGCAAG 3158
QY 2701 GCGTGGCAAGTGTGTCATTAATCATGACCCGCTGTTCTTGCAATTTGGGTTAAACAG 2760
DB 3159 GCGTGGCAAGTGTGTCATTAATCATGACCCGCTGTTCTTGCAATTTGGGTTAAACAG 3218
QY 2761 AGGGGGGTGTTTCTCACTTACCAATGCAATTTGATGACACTAAGATTTGCTTGAGCCC 2820
DB 3219 AGGGGGGTGTTTCTCACTTACCAATGCAATTTGATGACACTAAGATTTGCTTGAGCCC 3278
QY 2821 GAGAGCATGTCCAAAGGTGAACCTGGAACGGGGTGTGTAATGATGACATGAAAGATCTGMAAG 2880
DB 3279 GAGAGCATGTCCAAAGGTGAACCTGGAACGGGGTGTGTAATGATGACATGAAAGATCTGMAAG 3338
QY 2881 GTGCTAGATGTACATGATGACCCGACCAAGTGTGACACCTGCGAGTGTGGGGTAAACAT 2940
DB 3339 GTGCTAGATGTACATGATGACCCGACCAAGTGTGACACCTGCGAGTGTGGGGTAAACAT 3398
QY 2941 ATTAGAAACAGACCTGTGATGTGATGTGACCGAGAGCTGAGGCCGATCACTTGGTG 3000
DB 3399 ATTAGAAACAGACCTGTGATGTGATGTGACCGAGAGCTGAGGCCGATCACTTGGTG 3458
QY 3001 CTGGCTTGACACCGGCTGTGATTTGCTCTTACGATGAAGATACAGATTGAG 3052
DB 3459 CTGGCTTGACACCGGCTGTGATTTGCTCTTACGATGAAGATACAGATTGAG 3510

RESULT 6
AACB5026
ID AACB5026 standard; DNA, 35935 BP.
XX
AC AACB5026;
XX
DT 08-MAY-2001 (first entry)
XX
Complete nucleotide sequence of the genome of Ad5.
XX
DE Adenovirus death protein; ADP; neoplastic; cell death; cancer therapy;
KW anti-cancer; gene therapy; cyostatic; Ad5, de.
XX
OS Maestadenovirus.
XX
PN W0200104282-A2.

XX	18-JAN-2001.
PD	
XX	
PF	12-JUL-2000; 2000WO-US018971.
XX	
PR	12-JUL-1999; 99US-00351778.
XX	
PA	(UNSL-) UNIV SAINT LOUIS.
XX	
P1	Wold WSM, Toch K, Doronin K, Tollefson AE,
DR	WPI, 2001-103079/11.
XX	
PT	Recombinant vector which is replication-competent in a neoplastic cell
PT	and overexpresses an adenovirus death protein, useful in cancer therapy
PT	when used together with replication-defective adenovirus which expresses
PT	an anti-cancer gene.
XX	
PS	Disclosure; Fig 21; 196pp; English.
XX	
CC	The invention relates to a recombinant vector (V1) which is replication-
CC	competent in a neoplastic cell and which overexpresses an adenovirus
CC	death protein (ADP). The vector can be used in a method for promoting
CC	death of a neoplastic cell that comprises contacting the neoplastic cell
CC	with at least one V1; and a composition comprising V1 and a second.
CC	recombination virus which is: (a) replication defective and which
CC	expresses an anti-cancer gene product, where V1 complements replication
CC	of the second recombination virus; or (b) replication-competent in a
CC	neoplastic cell. V1, together with one or more replication-defective
CC	adenovirus which expresses an anti-cancer gene product, are useful in
CC	cancer therapy. Overexpression of ADP by V1 results in faster lysis of
CC	cells and spread of the virus throughout a cell monolayer than viruses
CC	expressing wild-type levels of ADP. The present sequence represents the
CC	complete nucleotide sequence of the genome of human adenovirus Ad5,
CC	useful for cancer gene therapy
CC	
XX	
SQ	Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;
	Query Match 100.0%; Score 3052; DB 4; Length 35935;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CGGTAGTGTATTTATACCGCGTGATTCTTCAGAGGCCACTCTTYGAGTGCACGAGT 60
DB	459 CGTAGTAGTATTTATACC CGGTGAGTCTTCAGAGGCCACTCTYGAGTGCACGAGT 518
OY	61 AGAGTTTTCTCTCCGAGCCGCTCCGAGACGGGACGTAAAAATGACATAATTATCTGCC 120
DB	519 AGAGTTTTCTCTCCGAGCCGCTCCGAGACGGGACGTAAAAATGACATAATTATCTGCC 578
OY	121 ACAGAGGTGTATTATACCGAAGAATAGCGCGCAGCTTTTGGACAAGCTGATCGAAGAG 180
DB	579 ACAGAGGTGTATTATACCGAAGAATAGCGCGCAGCTTTTGGACAAGCTGATCGAAGAG 638
OY	181 TACTGCGTATTAATCTTCCACCTCTCACTCATTTTGAACCAACTTACCTTCACGAACTGT 240
DB	639 TACTGCGTATTAATCTTCCACCTCTCACTCATTTTGAACCAACTTACCTTCACGAACTGT 698
OY	241 ATGATTTAGACGTACCGCCCCCGCAAGATCCCAACGAGAGGCGGTTTGCAGATTTTTC 300
DB	699 ATGATTTAGACGTACCGCCCCCGCAAGATCCCAACGAGAGGCGGTTTGCAGATTTTTC 758
OY	301 CCGACTCTGTATGTATGGCGGTGACGAAAGGATGTAAGTACTCACTTTTCCGCGCGGCGC 360
DB	759 CCGACTCTGTATGTATGGCGGTGACGAAAGGATGTAAGTACTCACTTTTCCGCGCGGCGC 818
OY	361 CCGGTTCTCCGAGCGCGCTCACCTTTTCCCGGACGCCGAGACGCCGAGACGAGAGCCT 420
DB	819 CCGGTTCTCCGAGCGCGCTCACCTTTTCCCGGACGCCGAGACGCCGAGAGCCT 878
OY	421 TTGGATCCGGTTTCTATGCGCAAACCTTTGACCGGAGGTATGATTTTACCTGCGACGAG 480
DB	879 TTGGATCCGGTTTCTATGCGCAAACCTTTGACCGGAGGTATGATTTTACCTGCGACGAG 938

QY	481	CTGGCTTTCCACCCAGTGAACAAGATGAAGAGGGGAGAGATTTGTGTAATATG	540
Db	939	CTGGCTTTCCACCCAGTGAACAAGATGAAGAGGGGAGAGATTTGTGTAATATG	998
QY	541	TGAGACACCCCGGCAACGGTTGACAGTTCTTGCTATATCACCGAGAAATACGGGGAC	600
Db	999	TGAGACACCCCGGCAACGGTTGACAGTTCTTGCTATATCACCGAGAAATACGGGGAC	1058
QY	601	CAGATATATATGTTCGCTTTGCTATATAGAGACCTGTGGATATTTGTCTACAGTAAGT	660
Db	1059	CAGATATATATGTTCGCTTTGCTATATAGAGACCTGTGGATATTTGTCTACAGTAAGT	1118
QY	661	GAATAATTATGGGACAGTGGGATATAGAGTGTGGGTTGGTGCTAAATTTTTTTTTTAAT	720
Db	1119	GAATAATTATGGGACAGTGGGATATAGAGTGTGGGTTGGTGCTAAATTTTTTTTTTAAT	1178
QY	721	TTTTACAGTTTGTGTGTTTAAAGATTTTGTATTTGATTTTTTTTAAAGGCTCTGTCT	780
Db	1179	TTTTACAGTTTGTGTGTTTAAAGATTTTGTATTTGATTTTTTTTAAAGGCTCTGTCT	1238
QY	781	TGAACCTGAGCCTGAGCCCGACGACGAACCGGAGCCTGACGAACCTACCCGCGCTCTAA	840
Db	1239	TGAACCTGAGCCTGAGCCCGACGACGAACCGGAGCCTGACGAACCTACCCGCGCTCTAA	1298
QY	841	AATGGCGCTGCTATCTTGAGACGCGGACATCACTGTGTCTAGAGATTCAAATAGTAG	900
Db	1299	AATGGCGCTGCTATCTTGAGACGCGGACATCACTGTGTCTAGAGATTCAAATAGTAG	1358
QY	901	TACGGATATGCTGTATACCTCCGTCCTTTCTAACACACCTCTGAGATACACCCGGTGTCTCC	960
Db	1359	TACGGATATGCTGTATACCTCCGTCCTTTCTAACACACCTCTGAGATACACCCGGTGTCTCC	1418
QY	961	GCTGTGCCCATTTAAACAGTTGCGGTGAGAGTTGGTGGGCGTGCACAGCTGTGGAATG	1020
Db	1419	GCTGTGCCCATTTAAACAGTTGCGGTGAGAGTTGGTGGGCGTGCACAGCTGTGGAATG	1478
QY	1021	TATGAGAGACTTGCTTAAACGACCTGTGGCAACTTTTGGACTTGAAGCTGTAAACGCCCCAG	1080
Db	1479	TATGAGAGACTTGCTTAAACGACCTGTGGCAACTTTTGGACTTGAAGCTGTAAACGCCCCAG	1538
QY	1081	GCCATTAAGGTGTAAACCTGTGATTCGCTGTGTGTAAACGCTTTGTTGCTGAATAGT	1140
Db	1539	GCCATTAAGGTGTAAACCTGTGATTCGCTGTGTGTAAACGCTTTGTTGCTGAATAGT	1598
QY	1141	TGATGTAAAGTTTATTAAGGCTGAGATATGTTTAACTTGCATGCGCTGTATTAATGGGCG	1200
Db	1599	TGATGTAAAGTTTATTAAGGCTGAGATATGTTTAACTTGCATGCGCTGTATTAATGGGCG	1658
QY	1201	GGGCTTAAAGGGTATATATATGCGCGCTGGCTATCTTGTTATCATCTGACTCATAGA	1260
Db	1659	GGGCTTAAAGGGTATATATATGCGCGCTGGCTATCTTGTTATCATCTGACTCATAGA	1718
QY	1261	GGCTTGGGAGTGTGGAAGATTTTTCTGCTGTCGTAACCTGTGTGGAACAGAGCTCTAA	1320
Db	1719	GGCTTGGGAGTGTGGAAGATTTTTCTGCTGTCGTAACCTGTGTGGAACAGAGCTCTAA	1778
QY	1321	CAGTACCTTGTGTTTGAAGTTTCTGTGGGCTCATCCAGGCAAAAGTTAGCTTGACG	1380
Db	1779	CAGTACCTTGTGTTTGAAGTTTCTGTGGGCTCATCCAGGCAAAAGTTAGCTTGACG	1838
QY	1381	AATTAAAGAGATTAACAAGTGGAAATTTGAAAGCTTTTAAATCCCTGTGTAGCTGT	1440
Db	1839	AATTAAAGAGATTAACAAGTGGAAATTTGAAAGCTTTTAAATCCCTGTGTAGCTGT	1898
QY	1441	TGATTTCTTGAATCTGGGTCACACAGGCGCTTTTCCAAAGAAAGGTCATCAAGCTTTGGA	1500
Db	1899	TGATTTCTTGAATCTGGGTCACACAGGCGCTTTTCCAAAGAAAGGTCATCAAGCTTTGGA	1958
QY	1501	TTTTTTCCACACCGGGGCGCGCTGTGGCTGTCTGTGCTTTTTTGAAGTTTATTAAGATTA	1560
Db	1959	TTTTTTCCACACCGGGGCGCGCTGTGGCTGTCTGTGCTTTTTTGAAGTTTATTAAGATTA	2018

QY	1561	ATGGAGCGAAGAAACC	CAATCTGAGCGGGGGT	CACTGCTGATTTTCTGGCCATGCACT	1620
Db	2019	ATGAGAGGAAGAAACC	ATCTGACCGGGGGGT	CACTGCTGATTTTCTGGCCATGCACT	2078
QY	1621	GTGAGAGCGGTTGTG	AGACAACAAGATCCGCT	CTGTGTCTTCCGTCGGCCGGC	1680
Db	2079	GTGAGAGCGGTTGTG	AGACAACAAGATCCGCT	CTGTGTCTTCCGTCGGCCGGC	2138
QY	1681	GATAATACCGACG	AGAGGACGACGACGACGAGGAGGAAAGCCG	CGCGCGCGCGACGGA	1740
Db	2139	GATAATACCGACG	AGAGGAGGACGACGACGACGAGGAGGAAAGCCG	CGCGCGCGCGACGGA	2198
QY	1741	GCAGAGCCCATGGA	ACCCGAGAGCCCGCTTGACCTTCGGGATGAA	TGTTGTACAGGTG	1800
Db	2199	GCAGAGCCCATGGA	ACCCGAGAGCCCGCTTGACCTTCGGGATGAA	TGTTGTACAGGTG	2258
QY	1801	GCTAATCTGTATCC	AGAACTGAGACGCAATTTTGCAATTAACAGAGAT	TGGGCAAGGGCTA	1860
Db	2259	GCTAATCTGTATCC	AGAACTGAGACGCAATTTTGCAATTAACAGAGAT	TGGGCAAGGGCTA	2318
QY	1861	AAGGGGGTAAAGAG	GGGAGCGGGGGCTTGTGAGGCTACAGAGAGGCT	AGAGACTACACT	1920
Db	2319	AAGGGGGTAAAGAG	GGGAGCGGGGGCTTGTGAGGCTACAGAGAGGCT	AGAGACTACACT	2378
QY	1921	TTTAGCTTAATGAC	CAACACCGTCTCGAGTGTATTA	CTTTTCAACAGATCAAGATTAAT	1980
Db	2379	TTTAGCTTAATGAC	CAACACCGTCTCGAGTGTATTA	CTTTTCAACAGATCAAGATTAAT	2438
QY	1981	TGCCTTAATGAGCT	TGATCTGTGCGGAGAAAGTATCCATAGAGAGCT	AGACCACTTAC	2040
Db	2439	TGCCTTAATGAGCT	TGATCTGTGCGGAGAAAGTATCCATAGAGAGCT	AGACCACTTAC	2498
QY	2041	TGGCTGCAGCAGG	GGGATGATTTTGTAGAGGCTATTAGAGATAT	TGCAAGGTGGCACTT	2100
Db	2499	TGGCTGCAGCAGG	GGGATGATTTTGTAGAGGCTATTAGAGATAT	TGCAAGGTGGCACTT	2558
QY	2101	AGGCCAAGTTGCA	AGTACAGATCAGCAACTTGTAATATCAGAA	TATGTGCTCAAT	2160
Db	2559	AGGCCAAGTTGCA	AGTACAGATCAGCAACTTGTAATATCAGAA	TATGTGCTCAAT	2618
QY	2161	TCTCGGAAACGGG	CGCGAGTGGATATACGAGAGTACGGGCGCTT	TAGATGTAGC	2220
Db	2619	TCTCGGAAACGGG	CGCGAGTGGATATACGAGAGTACGGGCGCTT	TAGATGTAGC	2678
QY	2221	ATGATAAATATGT	GGGCGGGGCTCTTGACATGACCGGGGTGTAT	TATTAATGAATGAAG	2280
Db	2679	ATGATAAATATGT	GGGCGGGGCTCTTGACATGACCGGGGTGTAT	TATTAATGAATGAAG	2738
QY	2281	TTTACGCGCCCA	ATTTTACGGGTACGGTTTTCTCGCCAAATAC	CAACTTATCTTAC	2340
Db	2739	TTTACGCGCCCA	ATTTTACGGGTACGGTTTTCTCGCCAAATAC	CAACTTATCTTAC	2798
QY	2341	GGTGTAACTCTA	TGGGTTTAAACAATCTGTGTGAAAGCTGTGAC	CCGATGTAAAGGTT	2400
Db	2799	GGTGTAACTCTA	TGGGTTTAAACAATCTGTGTGAAAGCTGTGAC	CCGATGTAAAGGTT	2858
QY	2401	CGGGGCTGTGCTT	TATCTGCTGAGAAAGGGGGTGTGCGCCCAAA	AGCAGGACT	2460
Db	2859	CGGGGCTGTGCTT	TATCTGCTGAGAAAGGGGGTGTGCGCCCAAA	AGCAGGACT	2918
QY	2461	TCAATTAAGAAAT	TGCTCTTTGAAAGGTGTACTTGGGTATCTGT	CTGAGGGTAACTCC	2520
Db	2919	TCAATTAAGAAAT	TGCTCTTTGAAAGGTGTACTTGGGTATCTGT	CTGAGGGTAACTCC	2978
QY	2521	AGGGTGGCCCA	ATGTGGCTCCGACTGTGTGCTTCA	TGCTAATGTAAAGGTGGCT	2580
Db	2979	AGGGTGGCCCA	ATGTGGCTCCGACTGTGTGCTTCA	TGCTAATGTAAAGGTGGCT	3038
QY	2581	GTGATTAAGCA	TAACATGATATGTGTGCAATCTGCAGAGCA	AGGGGCTCTCAATGCTGACC	2640
Db	3039	GTGATTAAGCA	TAACATGATATGTGTGCAATCTGCAGAGCA	AGGGGCTCTCAATGCTGACC	3098
QY	2641	TGCTTCGACGG	CACTGTCACTGCTGTGAAGCAATTCAGCT	AGCAGCACTTCGCAAG	2700

D6	3099	TTGCTGGACGGCACTGTCACCTGCTGAAGACATTCAAGTACCAAGCACTTCGCAAG	315
QY	2701	GCCTGGCCAGAGTTTGAAGCATTAACATACTGACCCCGCTGTTCCCTTGCAATTTGGTAACAG	276
D6	3159	GCCTGGCCAGAGTTTGAAGCATTAACATACTGACCCCGCTGTTCCCTTGCAATTTGGTAACAG	321
QY	2761	AGGGGGGAGTTTCTTACTTACCTTAACATGCAATTTGAGTCACACTAAGATATTGCTTGAGCCC	282
D6	3219	AGGGGGGAGTTTCTTACTTACCTTAACATGCAATTTGAGTCACACTAAGATATTGCTTGAGCCC	327
QY	2821	GAGAGCATGTCCCAAGGTGAACCTGAAACGGGGGTTTGAACATGACCACTGAAGATCTGGAAG	288
D6	3279	GAGAGCATGTCCCAAGGTGAACCTGAAACGGGGGTTTGAACATGACCACTGAAGATCTGGAAG	333
QY	2881	GTGCTGAAGTATGCAATGAGACCCGACACAGATGTCAGACCCCTGCGAGTGTGGCGGTAAACAT	294
D6	3339	GTGCTGAAGTATGCAATGAGACCCGACACAGATGTCAGACCCCTGCGAGTGTGGCGGTAAACAT	339
QY	2941	ATTAGAAACACAGCCTGTGATGTGTGATGTGATGACCGAGAGCTGAGCCCGATCATCTTGGTG	300
D6	3399	ATTAGAAACACAGCCTGTGATGTGTGATGTGATGACCGAGAGCTGAGCCCGATCATCTTGGTG	345
QY	3001	CTGGGCTTGACACCCCGGCTGAGTTTGGCTTACCGCATGGAAGATATACGATTGAG	3052
D6	3459	CTGGGCTTGACACCCCGGCTGAGTTTGGCTTACCGCATGGAAGATATACGATTGAG	3510
RESULT 7			
AB569882	ID	AB569882 standard; DNA; 35935 BP.	
XX	AC	AB569882;	
XX	DT	21-NOV-2002 (first entry)	
DE	XX	Human adenovirus type 5 genome sequence #1.	
XX	XX	Vector; adenovirus; adeno-associated; adenosine deaminase gene; receptor;	
KM	KM	adenosine deaminase deficiency; severe combined immune deficiency; PHN;	
KM	KM	beta-chain; haemoglobin gene; beta-thalassemia; sickle cell disease;	
KM	KM	low density lipoprotein gene; familial hypercholesterolaemia;	
KM	KM	hypoxanthine-guanine phosphoribosyltransferase; Leisch-Nyhan syndrome;	
KM	KM	phenylalanine hydroxylase gene; gene therapy; phenylketonuria;	
KM	KM	dystrophic gene; muscular dystrophy; cystic fibrosis; immunostimulant;	
KM	KM	human cystic fibrosis transmembrane conductance regulator gene;	
KM	KM	antianemic; antilipemic; nootropic; cytoskeletal; dermatological;	
KM	KM	human adenovirus genome; de.	
XX	OS	Human adenovirus type 5.	
XX	PN	US2002102731-A1.	
PD	XX	01-AUG-2002.	
XX	PF	12-FEB-2001; 2001US-00782378.	
XX	PR	02-OCT-2000; 2000US-0237747P.	
XX	PA	(UNNY) UNIV NEW YORK STATE RES FOUND.	
XX	PI	Hearing P, Bahou WF, Sandalon Z, Gnatenko DV;	
XX	DR	WPI; 2002-690619/74.	
XX	PT	Producing vector, by introducing vector having nucleotide sequence,	
XX	PT	adenovirus inverted terminal repeats and packaging sequence, and adeno-	
XX	XX	associated virus terminal repeat, into cell, and culturing cell.	
PS	XX	Example 2; Page 40-56; 191pp; English.	
CC	CC	The present invention relates to a new method of producing a vector. The	
CC	CC	method involves introducing recombinant vector having nucleotide sequence	

(NS) having 5' and 3' end, left and right inverted terminal repeats of
CC adenovirus flanking NS, adenovirus packaging sequence linked to inverted
CC terminal repeat, and adeno-associated virus terminal repeat linked to 3'
CC end of NS, intact cell expressing adenovirus early gene lacking from vector
CC / and culturing cell to produce another vector. The method is useful for
CC generating vectors, especially mad vectors. The method is useful in
CC transferring nucleotide sequences of interest into a cell, for gene
CC transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo.
CC The nucleotide sequences are useful for treating diseases associated with
CC 1c, 1e, adenosine deaminase gene associated with adenosine deaminase
CC deficiency with severe combined immune deficiency, beta-chain of
CC hemoglobin gene associated with beta-thalassemia and sickle cell
CC disease, receptor for low density lipoprotein gene associated with
CC familial hypercholesterolemia, hypoxanthine-guanine
CC phosphoribosyltransferase associated with Lesch-Nyhan syndrome,
CC phenylalanine hydroxylase (PAH) gene associated with phenylketonuria,
CC dystrophin gene associated with muscular dystrophy, and human cystic
CC fibrosis transmembrane conductance regulator gene associated with cystic
CC fibrosis. The present nucleic acid sequence represents a human adenovirus
CC genome sequence that was used in the methods of the invention

XX Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;

Query Match 100.0%; Score 3052; DB 6; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTAGTATTTATTAACCCGGTAGTTCCTCAAGAGCCACTCTTAGTGCCAGCAGT 60
DB 459 CGTGTAGTATTTATTAACCCGGTAGTTCCTCAAGAGCCACTCTTAGTGCCAGCAGT 518
QY 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGACCTGAATAATGACATTTATCTGCC 120
DB 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGACCTGAATAATGACATTTATCTGCC 578
QY 121 ACGGAGGTATTAATACGGAAGAAATGCGCGCAGTCTTTTGACAGCTGATCGAAGG 180
DB 579 ACGGAGGTATTAATACGGAAGAAATGCGCGCAGTCTTTTGACAGCTGATCGAAGG 638
QY 181 TACTGCGTAAATCTTTCACCTCTCACTTGAACCACTTACCTTCAACGACTGT 240
DB 639 TACTGCGTAAATCTTTCACCTCTCACTTGAACCACTTACCTTCAACGACTGT 698
QY 241 ATGATTTAGACGTACGCGCCCGAAGATCCCAAGAGAGCGGTTCCGACATTTTC 300
DB 699 ATGATTTAGACGTACGCGCCCGAAGATCCCAAGAGAGCGGTTCCGACATTTTC 758
QY 301 CCGACTCTGTAAATGTGGCGGTGAGAGAGGATTTGACTTACTCTTCCGCGGCGC 360
DB 759 CCGACTCTGTAAATGTGGCGGTGAGAGAGGATTTGACTTACTCTTCCGCGGCGC 818
QY 361 CCGGTTCTCCGAGCCGCTTCACTTCCGCGACCCGAGACCGGAGAGAGACTCT 420
DB 819 CCGGTTCTCCGAGCCGCTTCACTTCCGCGAGCCCGAGAGAGAGACTCT 878
QY 421 TGGGTCCGGTTTCTATATCCAACTTTGACCGAGGTGATGATCTTACTGCCAGAG 480
DB 879 TGGGTCCGGTTTCTATATCCAACTTTGACCGAGGTGATGATCTTACTGCCAGAG 938
QY 481 CTGGCTTTCACCCAGTGAAGAGAGATTTGAGAGGATTTGTGTAGATTAATG 540
DB 939 CTGGCTTTCACCCAGTGAAGAGAGATTTGAGAGGATTTGTGTAGATTAATG 998
QY 541 TGGAGACCCCGGACAGGTGACAGTCTTGTCACTATCAACCGAGAGATTAACGGGAGC 600
DB 999 TGGAGACCCCGGACAGGTGACAGTCTTGTCACTATCAACCGAGAGATTAACGGGAGC 1058
QY 601 CAGATATTAATGTGCTTGTGCTATATGAGGACCTGTGCGATGTTGTCTACAGTAAGT 660
DB 1059 CAGATATTAATGTGCTTGTGCTATATGAGGACCTGTGCGATGTTGTCTACAGTAAGT 1118
QY 661 GAAATATATGGGACGTGGTGAATGAGTGTGGTTGTGTGTAATTTTTTTAAT 720
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 1119 GAAATATATGGGACGTGGTGAATGAGTGTGGTTGTGTGTAATTTTTTTAAT 1178
QY 721 TTTTACAGTTTGTGTTTAAGAATTTGTATTTGATTTTTTTTAAAGCTCTGTGC 780
DB 1179 TTTTACAGTTTGTGTTTAAGAATTTGTATTTGATTTTTTTTAAAGCTCTGTGC 1238
QY 781 TGAACCTGACCTGAGCCCGAGCCAGAAACCGGACCTGCAAGACTTCCGCGCTCTAA 840
DB 1239 TGAACCTGACCTGAGCCCGAGCCAGAAACCGGACCTGCAAGACTTCCGCGCTCTAA 1298
QY 841 AATGGCCCTGCTATCTCTGAGACGCCCGACATCACTGTGCTTGAAGATGCAATAGAG 900
DB 1299 AATGGCCCTGCTATCTCTGAGACGCCCGACATCACTGTGCTTGAAGATGCAATAGAG 1358
QY 901 TACGATAGCTGTGACTCCGGTCTTCTTAAACACACTCTGAGATACCCCGGTGTCC 960
DB 1359 TACGATAGCTGTGACTCCGGTCTTCTTAAACACACTCTGAGATACCCCGGTGTCC 1418
QY 961 GCTGTGCCCATTTAAACCACTGTCGAGAGATTGGTGGCGCTGCCAGGCTGTGAATG 1020
DB 1419 GCTGTGCCCATTTAAACCACTGTCGAGAGATTGGTGGCGCTGCCAGGCTGTGAATG 1478
QY 1021 TATCGAGACTTGCTTAAACGACCTGGGCAACCTTTGAGACTTGAAGCTTAAAGCCCGAG 1080
DB 1479 TATCGAGACTTGCTTAAACGACCTGGGCAACCTTTGAGACTTGAAGCTTAAAGCCCGAG 1538
QY 1081 GCCATTAAGTGTAAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTTGTGTAATGAGT 1140
DB 1539 GCCATTAAGTGTAAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTTGTGTAATGAGT 1598
QY 1141 TGATGTAAATTAATTAAGGCTGAGATTAATGTTTAACCTGATGCGGTGTTAAATGGGCGC 1200
DB 1599 TGATGTAAATTAATTAAGGCTGAGATTAATGTTTAACCTGATGCGGTGTTAAATGGGCGC 1658
QY 1201 GGGGCTTAAAGGGATTAATTAATGCGCGTGGGCTTAATCTTGGTTACATCTGACCTCATGGA 1260
DB 1659 GGGGCTTAAAGGGATTAATTAATGCGCGTGGGCTTAATCTTGGTTACATCTGACCTCATGGA 1718
QY 1261 GGCCTGGAGGTGTTTGGAGATTTTCTGCTGTGCGTAACCTGTGAGACAGAGCTTAA 1320
DB 1719 GGCCTGGAGGTGTTTGGAGATTTTCTGCTGTGCGTAACCTGTGAGACAGAGCTTAA 1778
QY 1321 CAGTACTCTTGTGTTTGGAGGTTCTGTGGGCTCATCCAGGCAAAAGTTAGTCTGAG 1380
DB 1779 CAGTACTCTTGTGTTTGGAGGTTCTGTGGGCTCATCCAGGCAAAAGTTAGTCTGAG 1838
QY 1381 AATTAAGAGATTAACAAGGGGAAATTTGAAGCTTTGAAATCCGTGGTGAAGCTTT 1440
DB 1839 AATTAAGAGATTAACAAGGGGAAATTTGAAGCTTTGAAATCCGTGGTGAAGCTTT 1898
QY 1441 TGAATCTTTGAAATCTGGGTACACAGGCGCTTTTCAAGAGAGGTCAACAGCTTTGA 1500
DB 1899 TGAATCTTTGAAATCTGGGTACACAGGCGCTTTTCAAGAGAGGTCAACAGCTTTGA 1958
QY 1501 TTTTTCACACCGGGGCGCGCTGCGTCTGTGCTTTTGAAGTTTAAAGATTA 1560
DB 1959 TTTTTCACACCGGGGCGCGCTGCGTCTGTGCTTTTGAAGTTTAAAGATTA 2018
QY 1561 ATGAGGGAAGAAACCATCTGAGCCGGGGGTACTGCTGAGATTTTGTGCAATGACATCT 1620
DB 2019 ATGAGGGAAGAAACCATCTGAGCCGGGGGTACTGCTGAGATTTTGTGCAATGACATCT 2078
QY 1621 GTGAGAGCGGTTGTGAGACACAAGATTCGCTGACTTGTGTCTTCCGTCCGCCCGGC 1680
DB 2079 GTGAGAGCGGTTGTGAGACACAAGATTCGCTGACTTGTGTGTCTTCCGTCCGCCCGGC 2138
QY 1681 GATTAATCCGACCGAGAGACAGACAGACAGACAGAGAGAAACCAAGGCGGCGGCGAGGA 1740
DB 2139 GATTAATCCGACCGAGAGACAGACAGACAGACAGAGAGAAACCAAGGCGGCGGCGAGGA 2198
QY 1741 GCAGAGCCATGGAACCCGAGACCGGCTGAGACCTCTGGGAATGAATGTTGTACAGGTG 1800
DB 2199 GCAGAGCCATGGAACCCGAGACCGGCTGAGACCTCTGGGAATGAATGTTGTACAGGTG 2258

1801 GCTGAATCTGATCCAGAACTGAGACGCAATTTTGAACAATTACAGAGGATGGGACAGGGGCTA 1860
2259 GCTAACTGATCCAGAACTGAGACGCAATTTTGAACAATTACAGAGGATGGGACAGGGGCTA 2318
1861 AAGGGGGTAAAGAGGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGAGATCTAGCT 1920
2319 AAGGGGGTAAAGAGGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGAGATCTAGCT 2378
1921 TTTAGCTTAATGACCAACACCGCTCTGAGTGTATTAATCTTTCAACAGATCAAGATTAAT 1980
2379 TTTAGCTTAATGACCAACACCGCTCTGAGTGTATTAATCTTTCAACAGATCAAGATTAAT 2438
1981 TGCGCTAATGAGCTTGAATCTGCTGGCGCAGAAAGTATTCATAGAGCAGCTGACCACTTAC 2040
2439 TGCGCTAATGAGCTTGAATCTGCTGGCGCAGAAAGTATTCATAGAGCAGCTGACCACTTAC 2498
2041 TGCGCTGACCGAGGGGATGATTTTGAAGAGCTAATTAGGGTATATGCAAAAGGTGGCACTT 2100
2499 TGCGCTGACCGAGGGGATGATTTTGAAGAGCTAATTAGGGTATATGCAAAAGGTGGCACTT 2558
2101 AGGCCAGTTGCAAGTACAAAGTACGCAACTTGTAAATATCAGGAATTTGTTGCTACATT 2160
2559 AGGCCAGTTGCAAGTACAAAGTACGCAACTTGTAAATATCAGGAATTTGTTGCTACATT 2618
2161 TCTGGGAACGGGGGCGAGAGTGAATAGATACGAGAGTAAAGGGTGGCCTTTAGATGTAGC 2220
2619 TCTGGGAACGGGGGCGAGAGTGAATAGATACGAGAGTAAAGGGTGGCCTTTAGATGTAGC 2678
2221 ATGATAAATATGTGGCCGGGGGTGCTTGGCAATGAGACGGGGGTGTTATTTATGAAATGTAAAG 2280
2679 ATGATAAATATGTGGCCGGGGGTGCTTGGCAATGAGACGGGGGTGTTATTTATGAAATGTAAAG 2738
2281 TTTACTGGCCCCCAATTTTAAAGCGGTACGGTTTTCCCTGGCAATACCAACTTATCTTACAC 2340
2739 TTTACTGGCCCCCAATTTTAAAGCGGTACGGTTTTCCCTGGCAATACCAACTTATCTTACAC 2798
2341 GGTGTAAGCTTCTATGAGGTTTAAACAATCCTGTGGAAGCCTGGACGATGTAAAGGTT 2400
2799 GGTGTAAGCTTCTATGAGGTTTAAACAATCCTGTGTGGAAGCCTGGACGATGTAAAGGTT 2858
2401 CGGGGCTGTGCTTTTACTGTGCTGGAAGGGGGGTGTGTGTGCGCCCAAAAAGCAGGGCT 2460
2859 CGGGGCTGTGCTTTTACTGTGCTGGAAGGGGGGTGTGTGTGCGCCCAAAAAGCAGGGCT 2918
2461 TCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGGGTATCTGTCTGAGGGTAACTCC 2978
2919 TCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGGGTATCTGTCTGAGGGTAACTCC 2978
2521 AAGGGTGGCCCAATGTGAGCTCCGACTGTGGTTCTCATGCTAGTAAAGAGCGTGGCT 2580
2979 AAGGGTGGCCCAATGTGAGCTCCGACTGTGGTTCTCATGCTAGTAAAGAGCGTGGCT 3038
2581 GTGATTAAGCAATGATGATGTGTGGAACCTGCGAGGACAGGGGCTCTCAGATGTGACC 2640
3039 GTGATTAAGCAATGATGATGTGTGGAACCTGCGAGGACAGGGGCTCTCAGATGTGACC 3098
2641 TGCTTGGACCGGCAATGCTGCTGTGAAGACATTCACGTAGCCAGCACTCTTGGCAG 2700
3099 TGCTTGGACCGGCAATGCTGCTGTGAAGACATTCACGTAGCCAGCACTCTTGGCAG 3158
2701 GCGTGGCAAGTGTGAGCAATTAACATACGCGCTGTTCCCTGCAATTTGGGTAAACAG 2760
3159 GCGTGGCAAGTGTGAGCAATTAACATACGCGCTGTTCCCTGCAATTTGGGTAAACAG 3218
2761 AAGGGGGTGTCTTCACTTAACCAATGCAATTTGATCACTAAGATATTTGCTTGGAGCC 2820
3219 AAGGGGGTGTCTTCACTTAACCAATGCAATTTGATCACTAAGATATTTGCTTGGAGCC 3278
2821 GAGAGCATGTCCAAAGTGAACCTGAAACGGGGGTGTTGACATGACATGAAGATCTGGAAG 2880
3279 GAGAGCATGTCCAAAGTGAACCTGAAACGGGGGTGTTGACATGACATGAAGATCTGGAAG 3338

2881 GTGCTGAGTACGATGAGACCCCGACAGGTGCAAGACCTCTGCGAGTGTGGCGTAAACAT 2940
3339 GTGCTGAGTACGATGAGACCCCGACAGGTGCAAGACCTCTGCGAGTGTGGCGTAAACAT 3398
2941 ATTAGAACAACGCTGTGATGCTGTGATGTGATGACGAGAGCTGAGGCCCGATCACTTGGTG 3000
3399 ATTAGAACAACGCTGTGATGCTGTGATGTGATGACGAGAGCTGAGGCCCGATCACTTGGTG 3458
3001 CTGGCCCTGCAACCCCGCGTGAATTTGGCTCTAGCGATGAAGATACAGATTGAG 3052
3459 CTGGCCCTGCAACCCCGCGTGAATTTGGCTCTAGCGATGAAGATACAGATTGAG 3510

RESULT 8
ABS69883
ID ABS69883 standard; DNA, 35935 BP.
XX
XX ABS69883;
XX
XX 21-NOV-2002 (first entry)
XX
XX Human adenovirus type 5 genome sequence #2.
DE
XX Vector; adenovirus; adeno-associated; adenosine deaminase gene; receptor;
KW adenosine deaminase deficiency; severe combined immune deficiency; PAB;
KW beta-chain; haemoglobin gene; beta-thalassemia; sickle cell disease;
KW low density lipoprotein gene; familial hypercholesterolemia;
KW hypoxanthine-guanine phosphoribosyltransferase; Lesch-Nyhan syndrome;
KW phenylalanine hydroxylase gene; gene therapy; phenylketonuria;
KW dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant;
KW human cystic fibrosis transmembrane conductance regulator gene;
KW antianaemic; antilipemic; nootropic; cytostatic; dermatological;
KW human adenovirus genome; de.
XX
XX Human adenovirus type 5.
OS
XX US2002102731-A1.
PN
XX 01-AUG-2002.
PD
XX 12-FEB-2001, 2001US-00782378.
PF
XX 02-OCT-2000; 2000US-0237747P.
PR
XX (UNIV) UNIV NEW YORK STATE RES FOUND.
PA
XX Hearing P, Bahou WF, Sandalon Z, Gnatenko DV;
PI
XX WPI; 2002-690619/74.
DR
XX
XX Producing vector, by introducing vector having nucleotide sequence,
PT adenovirus inverted terminal repeats and packaging sequence, and adeno-
PT associated virus terminal repeat, into cell, and culturing cell.
PT
XX
XX Disclosure; Page 56-72; 191pp; English.
PS
XX
XX The present invention relates to a new method of producing a vector. The
CC method involves introducing recombinant vector having nucleotide sequence
CC (NS) having 5' and 3' end, left and right inverted terminal repeats of
CC adenovirus flanking NS, adenovirus packaging sequence linked to inverted
CC terminal repeat, and adeno-associated virus terminal repeat linked to 3'
CC end of NS, into cell expressing adenovirus early gene lacking from vector
CC and culturing cell to produce another vector. The method is useful for
CC generating vectors, especially md vectors. The method is useful in
CC transferring nucleotide sequences of interest into a cell, for gene
CC transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo.
CC The nucleotide sequences are useful for treating diseases associated with
CC it, i.e. adenosine deaminase gene associated with adenosine deaminase
CC deficiency with severe combined immune deficiency, beta-chain of
CC haemoglobin gene associated with beta-thalassemia and sickle cell
CC disease, receptor for low density lipoprotein gene associated with
CC familial hypercholesterolemia, hypoxanthine-guanine
CC phosphoribosyltransferase associated with Lesch-Nyhan syndrome,

CC phenylalanine hydroxylase (PAH) gene associated with phenylketonuria,
CC dystrophin gene associated with muscular dystrophy, and human cystic
CC fibrosis transmembrane conductance regulator gene associated with cystic
CC fibrosis. The present nucleic acid sequence represents a human adenovirus
CC genome sequence that was used in the methods of the invention
XX
SQ Sequence 35935 BF; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;

Query Match 100.0%; Score 3052; DB 6; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGTGTAGATGATTTATATACCGGATGAGTCTCTCAAGAGGCACTTGTAGTGCACGCGAGT 60
459 CGTGTAGATGATTTATATACCGGATGAGTCTCTCAAGAGGCACTTGTAGTGCACGCGAGT 518
61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACATATATCTGCC 120
519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACATATATCTGCC 578
121 ACGGAGGTGTTATATACCGAAGAAATGCGCGGCACTTTTGGACCACTGATCGAAGAG 180
579 ACGGAGGTGTTATATACCGAAGAAATGCGCGGCACTTTTGGACCACTGATCGAAGAG 638
181 TACTGCGATGATATCTTCCACCTCTAGCACTTTTGAACCACTAACCTTACGCACTGT 240
639 TACTGCGATGATATCTTCCACCTCTAGCACTTTTGAACCACTAACCTTACGCACTGT 698
241 ATGATTTAGACGTGACGCGCCCGAAGATCCCAACGAGAGCGGTTTCGAGATTTTTC 300
699 ATGATTTAGACGTGACGCGCCCGAAGATCCCAACGAGAGCGGTTTCGAGATTTTTC 758
301 CCGACTCTGATATGTTGGCGGTGACGAGAGGATTTGACTTACTCATCTTTCCGCGGCGC 360
759 CCGACTCTGATATGTTGGCGGTGACGAGAGGATTTGACTTACTCATCTTTCCGCGGCGC 818
361 CCGGTTCTCCGAGCGCGCTCACCTTCCGCGAGCCGAGACGCGGAGAGAGAGCT 420
819 CCGGTTCTCCGAGCGCGCTCACCTTCCGCGAGCCGAGACGCGGAGAGAGAGCT 878
421 TGGGTCGCGTTTCTATGCGCAACCTTGTACCGAGAGTATGATCTTACCTGCCACGAG 480
879 TGGGTCGCGTTTCTATGCGCAACCTTGTACCGAGAGTATGATCTTACCTGCCACGAG 938
481 CTGCTTCCACCGACGACGACGATGAAGAGGATGAAGAGGATGATGATTAATG 540
939 CTGCTTCCACCGACGACGACGATGAAGAGGATGAAGAGGATGATGATTAATG 998
541 TGGAGCAACCCCGGAGCGGTTGACAGTCTTGTCACTTATCACCGAGAGAAATCGGGGAGC 600
999 TGGAGCAACCCCGGAGCGGTTGACAGTCTTGTCACTTATCACCGAGAGAAATCGGGGAGC 1058
601 CAGATATATATGTTGCTTGTATATAGAGACCTGTGATCTTGTCTACAGTAAGT 660
1059 CAGATATATATGTTGCTTGTATATAGAGACCTGTGATCTTGTCTACAGTAAGT 1118
661 GAAATATATGAGGACGTGGGTATAGAGTGTGGTGTGTGTATATTTTATTTTAT 720
1119 GAAATATATGAGGACGTGGGTATAGAGTGTGGTGTGTGTATATTTTATTTTAT 1178
721 TTTTACAGTTTGTGGTTTAAAGAAATTTGATATGATTTTATTTTAAAGTCTGTGTC 780
1179 TTTTACAGTTTGTGGTTTAAAGAAATTTGATATGATTTTATTTTAAAGTCTGTGTC 1238
781 TGAACCTGAGCTGAGCCGAGCAAGAACCGAGACCTGCAAGACTTACCCGCTCTTAA 840
1239 TGAACCTGAGCTGAGCCGAGCAAGAACCGAGACCTGCAAGACTTACCCGCTCTTAA 1298
841 AATGGCGCTGTCTATCTGAGAGCGCGGACATCACTGTGTCTAGAGATCAATAGTAG 900
1299 AATGGCGCTGTCTATCTGAGAGCGCGGACATCACTGTGTCTAGAGATCAATAGTAG 1358
901 TAGGATATGCTGTGATCTCGGCTCTTCTAACAACCTCTGAGATACACCGGCTGTCCC 960

1359 TAGGATATGCTGTGATCTCGGCTCTTCTAACAACCTCTGAGATACACCGGCTGTCCC 1418
961 GCTGTGCCCATTAACCAAGTTCGAGAGTGTGTGGCGTGCAGAGCTGTGAAATG 1020
1419 GCTGTGCCCATTAACCAAGTTCGAGAGTGTGTGGCGTGCAGAGCTGTGAAATG 1478
1021 TATGAGAGACTTGTCTTAAACGAGCTGTGGCAACTTTTGGACTTGAAGCTTGAACGCCCCAG 1080
1479 TATGAGAGACTTGTCTTAAACGAGCTGTGGCAACTTTTGGACTTGAAGCTTGAACGCCCCAG 1538
1081 GCCATTAAGTGTAAACCTGTGATTCGAGTGTGGTTAAGCTTGTGTGTAATGAGT 1140
1539 GCCATTAAGTGTAAACCTGTGATTCGAGTGTGGTTAAGCTTGTGTGTAATGAGT 1598
1141 TGATGTAAGTTTAAATAAGGAGTGAATGTTTAACTTGATGATGCGTGTAAATGGGCGC 1200
1599 TGATGTAAGTTTAAATAAGGAGTGAATGTTTAACTTGATGATGCGTGTAAATGGGCGC 1658
1201 GGGGCTTAAAGGATATTAATGCGCGCTGAGCTTATCTTGTTATCTGACTGATGGA 1260
1659 GGGGCTTAAAGGATATTAATGCGCGCTGAGCTTATCTTGTTATCTGACTGATGGA 1718
1261 GGGTGTGGAAGTGTGGAAGATTTTCTGCTGTGCTGATCACTTGCTGGAACGAGCTCTAA 1320
1719 GGGTGTGGAAGTGTGGAAGATTTTCTGCTGTGCTGATCACTTGCTGGAACGAGCTCTAA 1778
1321 CAGTACCTCTTGTGTTGAGAGTTCGTGTGGGCTCATCCAGGCAAGTATGCTGACAG 1380
1779 CAGTACCTCTTGTGTTGAGAGTTCGTGTGGGCTCATCCAGGCAAGTATGCTGACAG 1838
1381 AATTAAAGAGATTTACAAGTGGGAATTTGAAGCTTTGAAATCTGTGTGAGCTGTT 1440
1839 AATTAAAGAGATTTACAAGTGGGAATTTGAAGCTTTGAAATCTGTGTGAGCTGTT 1898
1441 TGATTTCTTGAATCTGGGTACACAGGCGCTTTCAGAGAGGTCATCAAGACTTTTGA 1500
1899 TGATTTCTTGAATCTGGGTACACAGGCGCTTTCAGAGAGGTCATCAAGACTTTTGA 1958
1501 TTTTTCACACCGGGGCGCGCTGTGGCTGTGCTTTTGTGAGTTTAAAGATTA 1560
1959 TTTTTCACACCGGGGCGCGCTGTGGCTGTGCTTTTGTGAGTTTAAAGATTA 2018
1561 ATGAGAGGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTCTGGCATGACTCT 1620
2019 ATGAGAGGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTCTGGCATGACTCT 2078
1621 GTGAGAGCGGTTGTGAGACAAAGAAATGCTGTGCTTGTGCTTCCGCTCGGCGCGG 1680
2079 GTGAGAGCGGTTGTGAGACAAAGAAATGCTGTGCTTGTGCTTCCGCTCGGCGG 2138
1681 GATTAATCCGACGAGAGAGAGACGACGACGAGAGGAAACGAGCGGGGCGGAGGA 1740
2139 GATTAATCCGACGAGAGAGAGACGACGACGAGAGGAAACGAGCGGGGCGGAGGA 2198
1741 GCAAGCCCATGGAACCGGAGAGCGGCTGTGACCTCGGGAATGAATGTTGTACAGGTG 1800
2199 GCAAGCCCATGGAACCGGAGAGCGGCTGTGACCTCGGGAATGAATGTTGTACAGGTG 2258
1801 GCTGAATCTGATCCAGAACTGAGACGCAATTTGACAAATTAACAGAGATGAGGCGGGCTA 1860
2259 GCTGAATCTGATCCAGAACTGAGACGCAATTTGACAAATTAACAGAGATGAGGCGGGCTA 2318
1861 AAGGGGTTAAAGAGAGAGCGGGGGCTTGTGAGGCTTACAGAGAGGCTAGAAATTAAGCT 1920
2319 AAGGGGTTAAAGAGAGAGCGGGGGCTTGTGAGGCTTACAGAGAGGCTAGAAATTAAGCT 2378
1921 TTTTACCTTAATGACCAAGACCGCTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
2379 TTTTACCTTAATGACCAAGACCGCTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
1981 TGCGCTTAATGAGCTGATCTGCTGGCGAGAGATTTTCCATAGAGAGCTGACCACTTAC 2040

Dp	2439	TGGCTAATAGACTGATCTGATCTGCTGGCCGACAAAGATTTCCATAGACGAGCTGACCACTTAC	2498
Qy	2041	TGCGTCGACGACGAGGGATGATTTTGGAGAGGCTATTAAGGATATATGCAAAAGTGGCACTT	2100
Dp	2499	TGGCTGACGCGCAGGGAGTGAATTTTGAGAGAGGCTATTAGGGATATATGCAAAAGTGGCACTT	2558
Qy	2101	AGGCCAATATTGCAAAGTACAAAGATCAGCAAACTTGTAAATATCAGAAATTTGTGTCTACATT	2160
Dp	2559	AGGCCAATATTGCAAAGTACAAAGATCAGCAAACTTGTAAATATCAGAAATTTGTGTCTACATT	2618
Qy	2161	TTCTGGAAACGGGGCCGAGGTGAGATGATATACGAGGATAGAGGTGGCTTTTGAATGTAGC	2220
Dp	2619	TTCTGGAAACGGGGCCGAGGTGAGATGATATACGAGGATAGAGGTGGCTTTTGAATGTAGC	2678
Qy	2221	ATGATAAATATGTGTGCGGGGGGTCTTGGCATGGAACGGGGGTGTATTATATGAAATGTAAAG	2280
Dp	2679	ATGATAAATATGTGTGCGGGGGGTCTTGGCATGGAACGGGGGTGTATTATATGAAATGTAAAG	2738
Qy	2281	TTTACTGAGCCCAATTTTAAAGCGATACGGTATTCTTGCCCAATATCAAACTTATCTTACAC	2340
Dp	2739	TTTACTGAGCCCAATTTTAAAGCGATACGGTATTCTTGCCCAATATCAAACTTATCTTACAC	2798
Qy	2341	GGTGTAAAGCTTCTATGAGGTTTAAACAATACCTGTGTGAAAGCTGGAACCGATGTAAAGGTT	2400
Dp	2799	GGTGTAAAGCTTCTATGAGGTTTAAACAATACCTGTGTGAAAGCTGGAACCGATGTAAAGGTT	2858
Qy	2401	CGGGGCGTGTGCTTTTACTGTGTGGAAGGGGGTGGTGTGTGGCCCAAAAGAGGGGCT	2460
Dp	2859	CGGGGCGTGTGCTTTTACTGTGTGGAAGGGGGTGGTGTGTGGCCCAAAAGAGGGGCT	2918
Qy	2461	TCAATTAAGAAATGCTCTTTTGAAAGGTGTACCTTGGGTATCTGTGTGAGGGTAACTCC	2520
Dp	2919	TCAATTAAGAAATGCTCTTTTGAAAGGTGTACCTTGGGTATCTGTGTGAGGGTAACTCC	2978
Qy	2521	AGGCTGGCCCAACAATGTGGGCTCCGACTGTGTGTTGCTTATGCTAATGTGAAAGCGTGGCT	2580
Dp	2979	AGGCTGGCCCAACAATGTGGGCTCCGACTGTGTGTTGCTTATGCTAATGTGAAAGCGTGGCT	3038
Qy	2581	GTGATTTAAGCAATAATGTGATGTGTGGGACCTGCGAGGACAGGGGCTCTCAGATCTGAAC	2640
Dp	3039	GTGATTTAAGCAATAATGTGATGTGTGGGACCTGCGAGGACAGGGGCTCTCAGATCTGAAC	3098
Qy	2641	TGCTCGGACGGCAACTGTCACTGTGTAAGAACAATTCACTGAGCAGCACTCTCGCAG	2700
Dp	3099	TGCTCGGACGGCAACTGTCACTGTGTAAGAACAATTCACTGAGCAGCACTCTCGCAG	3158
Qy	2701	GCCTGGCAGGTGTTTGAGCAATAATACTGACCCGCTTCTTGCAATTTGGGTAAACAG	2760
Dp	3159	GCCTGGCAGGTGTTTGAGCAATAATACTGACCCGCTTCTTGCAATTTGGGTAAACAG	3218
Qy	2761	AGGGGGGTGTCTCACTTACCAATGTGCAATTTGAGTCACTAAGATATTGCTTGAAGCC	2820
Dp	3219	AGGGGGGTGTCTCACTTACCAATGTGCAATTTGAGTCACTAAGATATTGCTTGAAGCC	3278
Qy	2821	GAGAGCAATGTCCAAAGGTGAACCTGAAAGGGGTGTTTGAATGATCAATGAAGATCTGAAAG	2880
Dp	3279	GAGAGCAATGTCCAAAGGTGAACCTGAAAGGGGTGTTTGAATGATCAATGAAGATCTGAAAG	3338
Qy	2881	GTGTGTAGGTATCAGATGAGACCCGACAGAGGTGCAGACCTTGCGAGTGTGGCGTAACAT	2940
Dp	3339	GTGTGTAGGTATCAGATGAGACCCGACAGAGGTGCAGACCTTGCGAGTGTGGCGTAACAT	3398
Qy	2941	ATTAGGAACCAAGCTGTGATGTCTGATGTGTGACCGAGGAGCTGAGGCCGATCATCTTGGTG	3000
Dp	3399	ATTAGGAACCAAGCTGTGATGTCTGATGTGTGACCGAGGAGCTGAGGCCGATCATCTTGGTG	3458
Qy	3001	CTGGCCCTGCACCCGGCGTGAATTTGGCTTATGCGATGAAGTATCAAGATTGAG	3052
Dp	3459	CTGGCCCTGCACCCGGCGTGAATTTGGCTTATGCGATGAAGTATCAAGATTGAG	3510

ID	AC61116	standard; DNA; 35935 BP.
XX	AC	AC61116;
XX	DT	09-JUL-2003 (first entry)
XX	DE	Adenovirus serotype 6 genome.
XX	KM	ds; non-structural protein; NS3; NS4A; NS4B; NS5A; NS5B; genome;
XX	KW	adenoviral vector; HCV infection; vaccine; gene therapy; protease.
XX	OS	Adenovirus serotype 6.
XX	PN	MO2003031588-A2.
XX	PD	17-APR-2003.
XX	PE	10-OCT-2002; 2002WO-US032512.
XX	FR	11-OCT-2001; 2001US-0328655P.
XX	PR	13-MAR-2002; 2002US-0363774P.
XX	PA	(MERI) MERCK & CO INC.
XX	PI	(RICE-) 1ST RICERCH BIOL MOLECOLARE ANGELTETTI.
XX	P1	Emini EA, Kaslow DC, Bett AJ, Shiver JW, Nicotia A, Lahm A;
XX	P1	Lunzago A, Cortese R, Colloca S;
XX	DR	WPI; 2003-381708/36.
XX	PT	New nucleic acid encoding a Met-NS3-NS4A-NS4B-NS5A polypeptide,
XX	PT	useful as a component of an adenovector or DNA plasmid vaccine for
XX	PT	preventing or treating hepatitis C virus.
XX	XX	Claim 19; Fig 7; 231pp; English.
XX	XX	The invention relates to a nucleic acid encoding a Met-NS3-NS4A-NS4B-NS5A
XX	XX	-NS5B (NS stands for non-structural protein from HCV) polypeptide
XX	XX	appearing as AB009574. The encoded polypeptide has sufficient protease
XX	XX	activity to process itself to produce an NS5B protein that is
XX	XX	enzymatically inactive. Also included are a cultured recombinant cell
XX	XX	comprising the novel nucleic acid, making an adenovector (comprising: (a)
XX	XX	producing an adenovirus genome plasmid comprising a gene expression
XX	XX	cassette by homologous recombination between the novel nucleic acid and a
XX	XX	nucleic acid comprising a first adenovirus region from base pair 1-450
XX	XX	corresponding to either Ad5 or Ad6, a second adenovirus region from base
XX	XX	pair 3511-5548 corresponding to Ad5 or from base pair 3508-5541
XX	XX	corresponding to Ad6, joined to the first region, a third adenovirus
XX	XX	region from base pair 5549-28133 corresponding to Ad5 or from base pair
XX	XX	5542-28156 corresponding to Ad6, joined to the second region, a fourth
XX	XX	adenovirus region from base pair 30818-33966 corresponding to Ad5 or from
XX	XX	base pair 30789-33784 corresponding to Ad6, joined to the third region,
XX	XX	and a fifth adenovirus region from base pair 33967-35935 corresponding to
XX	XX	Ad5 or from base pair 33785-35759 corresponding to Ad6, joined to the
XX	XX	fourth region; and (b) rescuing the recombinant adenovirus from the
XX	XX	recombinant adenovirus plasmid), an adenoviral vector that is produced by
XX	XX	method above appearing as AC61113 which has a humanised version of the
XX	XX	polynucleotide of the invention and encodes the HCV inactivated
XX	XX	polyprotein, a recombinant nucleic acid comprising one or more Ad6
XX	XX	regions and a region not present in Ad6, where at least one Ad6 region is
XX	XX	selected from E1A, E1B, E2B, E2A, E4, L1, L2, L4 and L5. The nucleic acid
XX	XX	is useful as a component of an adenoviral vector or a DNA plasmid vaccine
XX	XX	providing a broad range of antigens for generating an HCV-specific cell
XX	XX	mediated immune response. The nucleic acid may also be used in treating
XX	XX	patients infected with HCV. The present sequence is the Ad6 genome
XX	XX	Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;
XX	XX	Query Match 100.0%; Score 3052; DB 8; Length 35935;
XX	XX	Best Local Similarity 100.0%; Pred. No. 0;
XX	XX	Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2221	ATGATAAATATATGTCGCGGGGGTGCTTGAGCATGGAACGGGGGGTATTATTAAGATGTAAG	2280
Db	2679	ATGATTAATATATGTCGCGGGGGTGCTTGAGCATGGAACGGGGGGTATTATTAAGATGTAAG	2738
QY	2281	TTTACTGCGCCCAATTTTAAAGCGTACGGTATTTCTGCGCAATACCAACTTATCTTACAC	2340
Db	2739	TTTTACTGCGCCCAATTTTAAAGCGTATGCTTTCTGCGCAATACCAACTTATCTTACAC	2798
QY	2341	GGTGTAGCTTCTATGCGTTTAAACAAATCTGTGTGGAAGCTTGACCGATGTAAAGGTT	2400
Db	2799	GGGTAAAGCTTCTATGCGTTTAAACAAATCTGTGTGGAAGCTTGACCGATGTAAAGGTT	2858
QY	2401	CGGGGCGTGTGCTTTTACTGTCTGTGGAAGGGGGTGGTGTGTGCGCCCAAAAGCAGGACT	2460
Db	2859	CGGGGCGTGTGCTTTTACTGTCTGTGGAAGGGGGTGGTGTGTGCGCCCAAAAGCAGGACT	2918
QY	2461	TCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGGGTATCTGTGTGAGGGTAACTCC	2520
Db	2919	TCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGGGTATCTGTGTGAGGGTAACTCC	2978
QY	2521	AGGGTGGCCACAAATGTGGCCTCCGACCTGTGGTTCTTCAATGCTAATGTAAGAAAGGTGGCT	2580
Db	2979	AGGGTGGCCACAAATGTGGCCTCCGACCTGTGGTTCTTCAATGCTAATGTAAGAAAGGTGGCT	3038
QY	2581	GTGATTTAAGCATTAATCATGTATGTGGAACAATCGCAGAGACAGGGGCTCTCAGATCTGACC	2640
Db	3039	GTGATTTAAGCATTAATCATGTATGTGGAACAATCGCAGAGACAGGGGCTCTCAGATCTGACC	3098
QY	2641	TGCTCGGACGGCAACTGTCACTGTCTGTAGAGCAATTCAGTGAACGACCACTCTGCGAAG	2700
Db	3099	TGCTCGGACGGCAACTGTCACTGTCTGTAGAGCAATTCAGTGAACGACCACTCTGCGAAG	3158
QY	2701	GCCTGGGCAAGTGTGAGCAATTAATCATGTACCGGCTGTCTCTGCAATTTGGGTAAACAG	2760
Db	3159	GCCTGGGCAAGTGTGAGCAATTAATCATGTACCGGCTGTCTCTGCAATTTGGGTAAACAG	3218
QY	2761	AGGGGGGTGTCTTCTTACCTTACCAATGCAATTTGAGTCAACTAAGATATTTGCTTGAAGCC	2820
Db	3219	AGGGGGGTGTCTTCTTACCTTACCAATGCAATTTGAGTCAACTAAGATATTTGCTTGAAGCC	3278
QY	2821	GAGAGCATGTTCGAAGGTGAACCTGGAACGGGGTGTGTCATGATCAATGAAGATCTGGAG	2880
Db	3279	GAGAGCATGTTCGAAGGTGAACCTGGAACGGGGTGTGTCATGATCAATGAAGATCTGGAG	3338
QY	2881	GTGCTGAAGTTCAGATGAGAACCCGCAACAGGTGCGAGAACCTTCGAGGTGGCGGTAAACAT	2940
Db	3339	GTGCTGAAGTTCAGATGAGAACCCGCAACAGGTGCGAGAACCTTCGAGGTGGCGGTAAACAT	3398
QY	2941	ATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGAGAGCTGAAGCCCGATCACTTGGTG	3000
Db	3399	ATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGAGAGCTGAAGCCCGATCACTTGGTG	3458
QY	3001	CTGGCCTTGCAACCCCGCTGAAGTTTGGCTTATGCAATGAAGTAAAGTAAAGTTGAG	3052
Db	3459	CTGGCCTTGCAACCCCGCTGAAGTTTGGCTTATGCAATGAAGTAAAGTAAAGTTGAG	3510

WO2003031586-A2.
 17-APR-2003.
 10-OCT-2002; 2002WO-US032512.
 11-OCT-2001; 2001US-0328655P.
 13-MAR-2002; 2002US-0363774P.
 (MERI) MERCK & CO INC.
 (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
 Emimi EA, Kaslow DC, Belt AJ, Shiver JW, Nicotia A, Lahm A;
 Luzzago A, Correse R, Colloca S;
 WPI; 2003-381708/36.
 New nucleic acid encoding a Met-NS3-NS4A-NS4B-NS5A-NS5B polypeptide,
 useful as a component of an adenovector or DNA plasmid vaccine for
 preventing or treating hepatitis C virus.
 Claim 19; Fig 8; 231pp; English.
 The invention relates to a nucleic acid encoding a Met-NS3-NS4A-NS4B-NS5A-
 NS5B (NS stands for non-structural protein from HCV) polypeptide
 appearing as AB009574. The encoded polypeptide has sufficient protease
 activity to process itself to produce an NS5B protein that is
 enzymatically inactive. Also included are a cultured recombinant cell
 comprising the novel nucleic acid, making an adenovector (comprising: (a)
 producing an adenovirus genome plasmid comprising a gene expression
 cassette by homologous recombination between the novel nucleic acid and a
 nucleic acid comprising a first adenovirus region from base pair 1-450
 corresponding to either Ad5 or Ad6, a second adenovirus region from base
 pair 3511-5548 corresponding to Ad5 or from base pair 3508-5541
 corresponding to Ad6, joined to the first region, a third adenovirus
 region from base pair 5549-2813 corresponding to Ad5 or from base pair
 5542-2815 corresponding to Ad6, joined to the second region, a fourth
 adenovirus region from base pair 30818-33966 corresponding to Ad5 or from
 base pair 30789-33784 corresponding to Ad6, joined to the third region,
 and a fifth adenovirus region from base pair 33967-35935 corresponding to
 Ad5 or from base pair 33785-35753 corresponding to Ad6, joined to the
 fourth region; and (b) rescuing the recombinant adenovirus from the
 recombinant adenovirus plasmid), an adenoviral vector that is produced by
 method above appearing as ACA61113 which has a humanised version of the
 polynucleotide of the invention and encodes the HCV inactivated
 polypeptide, a recombinant nucleic acid comprising one or more Ad6
 regions and a region not present in Ad6, where at least one Ad6 region is
 selected from E1A, E1B, E2B, E2A, E4, L1, L2, L4 and L5. The nucleic acid
 is useful as a component of an adenoviral vector or a DNA plasmid vaccine
 providing a broad range of antigens for generating an HCV-specific cell
 mediated immune response. The nucleic acid may also be used in treating
 patients infected with HCV. The present sequence is the Ad5 genome
 Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;

AC	RESULT 10
XX	ACA61117
ID	ACA61117 standard; DNA; 35935 BP.
XX	
AC	ACA61117;
XX	
DT	09-JUL-2003 (first entry)
XX	
DE	Adenovirus serotype 5 genome.
XX	
XX	ds; non-structural protein; NS3; NS4A; NS4B; NS5A; NS5B; genome;
KM	adenoviral vector; HCV infection; vaccine; gene therapy; protease.
XX	
OS	Adenovirus serotype 5.
XX	

QY	CGGTAGTGAATTTATACCGGCTAGTTCCTCAAGAGGCACTCTGATGCTCAGCAGGT	60
Db	CGTGTAGTGAATTTATACCGGCTAGTTCCTCAAGAGGCACTCTGATGCTCAGCAGGT	518
QY	AGAGTTTTCTCTCCGAGCCGCTCCGAACCGGAGCTGAAATATGACATTTATCTGCC	120
Db	AGAGTTTTCTCTCCGAGCCGCTCCGAACCGGAGCTGAAATATGACATTTATCTGCC	578
QY	ACGAGGCTGTTATTAACCGAAGAAATGGCCGCGCAGTCTTTTGGACAGCTGATCGAAGAG	180
Db	ACGAGGCTGTTATTAACCGAAGAAATGGCCGCGCAGTCTTTTGGACAGCTGATCGAAGAG	638
QY	TACTGCGTGAATATCTTCCACTCTTGACCATTTTGAACCACTTACCTTCACGAATCTGT	240

Db 639 TACTGGCTGATATATCTTCCACCTCTCCTAGCCATTTTGAACAACCTTACCGTCTGACGACTGT 698
Qy 241 ATGATTTTAGCTGACGCGCCCCCGAAGATCCCAACGAGAGAGCGGTTTCGAGATTTTTC 300
Db 699 ATGATTTTAGAGTACGCGCCCCCGAAGATCCCAACGAGAGAGCGGTTTCGAGATTTTTC 758
Qy 301 CCGACTCTGTATGTGGCGGTTGACGAGAGGGAATTGACTTACTCACTTTTCCGCGCGGC 360
Db 759 CCGACTCTGTATGTGGCGGTTGACGAGAGGGAATTGACTTACTCACTTTTCCGCGCGGC 818
Qy 361 CCGGTTCTCCGAGCGCGCTCACTTTTCCGCGAGCCCGAGACCGGAGAGAGAGGCT 420
Db 819 CCGGTTCTCCGAGCGCGCTCACTTTTCCGCGAGCCCGAGACCGGAGAGAGAGGCT 878
Qy 421 TGGGTCGGGTTTCTATGCAAACTTTGTAACGAGGTGATGATCTTAACTTGCCACGAGG 480
Db 879 TGGGTCGGGTTTCTATGCAAACTTTGTAACGAGGTGATGATCTTAACTTGCCACGAGG 938
Qy 481 CTGGCTTTCCACCGAGTACGACGAGATGAAAGGCGTGAAGAGTTTGTATGATTTATG 540
Db 939 CTGGCTTTCCACCGAGTACGACGAGATGAAAGGCGTGAAGAGTTTGTATGATTTATG 998
Qy 541 TGAAGACCCCGGACCGGTTGACAGTCTTGTCAATTATCACCGAGAGAAATACGGGGAGCC 600
Db 999 TGAAGACCCCGGACCGGTTGACAGTCTTGTCAATTATCACCGAGAGAAATACGGGGAGCC 1058
Qy 601 CAGATTAATATGTGTTCCGTTTGTCTATATGAGACCTGTGCGATGTTTGTCTACAGTAAGT 660
Db 1059 CAGATTAATATGTGTTCCGTTTGTCTATATGAGACCTGTGCGATGTTTGTCTACAGTAAGT 1118
Qy 661 GAAATTAATGCGGACGTGGTGTATAGAGTGGGTTGGTGTGTAATTTTTTTTTTAAAT 720
Db 1119 GAAATTAATGCGGACGTGGTGTATAGAGTGGGTTGGTGTGTAATTTTTTTTTTAAAT 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATTGTGATTTTTTAAAGGTCCTGTGTC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATTGTGATTTTTTAAAGGTCCTGTGTC 1238
Qy 781 TGAACCTGAGCTTGAGCCCGAGCAAGAACCGAGCCTTGCAAGACTTACCCGCGCTCTAA 840
Db 1239 TGAACCTGAGCTTGAGCCCGAGCAAGAACCGAGCCTTGCAAGACTTACCCGCGCTCTAA 1298
Qy 841 AATGGGCGCTGCTATCCCTGAGACGCGCGACATCACTGTCTGAGAGATGCAATTAAGT 900
Db 1299 AATGGGCGCTGCTATCCCTGAGACGCGCGACATCACTGTCTGAGAGATGCAATTAAGT 1358
Qy 901 TACGATAGCTGTGACTCCGGTCTTCTAAACAACACTTCTGAGATCAACCCGGTGTGCC 960
Db 1359 TACGATAGCTGTGACTCCGGTCTTCTAAACAACACTTCTGAGATCAACCCGGTGTGCC 1418
Qy 961 GCTGTGCCCCATTAAACCAAGTTGCGTGAAGATTGTGGGCGTGCAGGCTGTGAATG 1020
Db 1419 GCTGTGCCCCATTAAACCAAGTTGCGTGAAGATTGTGGGCGTGCAGGCTGTGAATG 1478
Qy 1021 TATCGAGAGACTTGTCTTAAACGAGCCTTGAGCAACTTTGAGCTTGAAGCTTAAAGCCCCAG 1080
Db 1479 TATCGAGAGACTTGTCTTAAACGAGCCTTGAGCAACTTTGAGCTTGAAGCTTAAAGCCCCAG 1538
Qy 1081 GCCATAAGTGTAAACCTGTGATTTGCGTGTGGTTAAACGCTTTGTTTGTGTAATGAGT 1140
Db 1539 GCCATAAGTGTAAACCTGTGATTTGCGTGTGGTTAAACGCTTTGTTTGTGTAATGAGT 1598
Qy 1141 TGATGTAAATTAAAGGAGTGAATGCTTTAACTTGATGGCGGTGTTAAATGGGCGC 1200
Db 1599 TGATGTAAATTAAAGGAGTGAATGCTTTAACTTGATGGCGGTGTTAAATGGGCGC 1658
Qy 1201 GGGGCTAAAGGAGTGAATTAATGCGCGGTGCTAATCTGTGTTCACTGACCTTCAATGGA 1260
Db 1659 GGGGCTAAAGGAGTGAATTAATGCGCGGTGCTAATCTGTGTTCACTGACCTTCAATGGA 1718
Qy 1261 GGGCTTGAAGTGTGGAAGATTTTCTGCTGTGCTGAATCTTGCTGGAACGAGACTCTAA 1320
Db 1719 GGGCTTGAAGTGTGGAAGATTTTCTGCTGTGCTGAATCTTGCTGGAACGAGACTCTAA 1778

Qy 1321 CAGTACCTCTTGTGTTTGAAGGTTTCTGTGGGCTCATCCAGGCAAGTATGTCGAG 1380
Db 1779 CAGTACCTCTTGTGTTTGAAGGTTTCTGTGGGCTCATCCAGGCAAGTATGTCGAG 1838
Qy 1381 AATTAAGAGAGATTACAGAGTGGGAATTGGAAGACTTTTGAATCCCTGTGTGAGCTTT 1440
Db 1839 AATTAAGAGAGATTACAGAGTGGGAATTGGAAGACTTTTGAATCCCTGTGTGAGCTTT 1898
Qy 1441 TGATTTCTTGAATCTGGGTCAACGAGCGCTTTTCAAGAGAGTCAATCAAGACTTTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACGAGCGCTTTTCAAGAGAGTCAATCAAGACTTTTGA 1958
Qy 1501 TTTTTCACACCGGGGCGCGCTGCGTCTGTGCTTTTGAAGTTTAAAGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGTCTGTGCTTTTGAAGTTTAAAGATTA 2018
Qy 1561 ATGAGAGGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTCTGGCCATGCACTT 1620
Db 2019 ATGAGAGGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTCTGGCCATGCACTT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACAAAGAAATCGCTGCTATGTTGTCTTCCGTCGCGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACAAAGAAATCGCTGCTATGTTGTCTTCCGTCGCGC 2138
Qy 1681 GATTAATCCGACGAGAGACAGCAGCAGCAGAGAGAAACGAGCGCGCGCGCAGGA 1740
Db 2139 GATTAATCCGACGAGAGACAGCAGCAGCAGAGAGAAACGAGCGCGCGCGCAGGA 2198
Qy 1741 GCAGAGCCCATGGAACCCGAGAGCCCGGCTGAGACCCCTCGGGAATGTAATGTTGTA 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCCCGGCTGAGACCCCTCGGGAATGTAATGTTGTA 2258
Qy 1801 GCTGAACCTGATCCAGAACTGAGACGATTTTGAATTTACAGAGATGGGACAGGCTA 1860
Db 2259 GCTGAACCTGATCCAGAACTGAGACGATTTTGAATTTACAGAGATGGGACAGGCTA 2318
Qy 1861 AAGGGGTTAAAGAGAGAGCGGGGGCTTGTAGGCTTACAGAGAGGCTAAGAACTTAC 1920
Db 2319 AAGGGGTTAAAGAGAGAGCGGGGGCTTGTAGGCTTACAGAGAGGCTAAGAACTTAC 2378
Qy 1921 TTTAGCTTAATGACCAACAACCCGCTGAGATTTTCTTTTCAAGATCAAGGAATAT 1980
Db 2379 TTTAGCTTAATGACCAACAACCCGCTGAGATTTTCTTTTCAAGATCAAGGAATAT 2438
Qy 1981 TGCGCTAATGAGCTTGAATCTGTGCGCGCAGAAAGTATCCATAGAGAGCTGACCACTTAC 2040
Db 2439 TGCGCTAATGAGCTTGAATCTGTGCGCGCAGAAAGTATCCATAGAGAGCTGACCACTTAC 2498
Qy 2041 TGGCTGAGCCAGGGAGATGATTTTGAAGAGGCTAATTAAGGTTAATGCAAAAGTGGCACTT 2100
Db 2499 TGGCTGAGCCAGGGAGATGATTTTGAAGAGGCTAATTAAGGTTAATGCAAAAGTGGCACTT 2558
Qy 2101 AGGCGAATTTGCAAGTCAAGATCAAGAACTTGTAAATTCAGGAATTTGTGTAACTT 2160
Db 2559 AGGCGAATTTGCAAGTCAAGATCAAGAACTTGTAAATTCAGGAATTTGTGTAACTT 2618
Qy 2161 TCTGGAAACGGGCGCGAGTGTGAGATAGATACGAGAGATAGGGTGGCTTTAAGTGAAGC 2220
Db 2619 TCTGGAAACGGGCGCGAGTGTGAGATAGATACGAGAGATAGGGTGGCTTTAAGTGAAGC 2678
Qy 2221 ATGATTAATATGTGGCCGGGGGTGCTTTGCAATGACCGGGGTGTTAATGAATGAAG 2280
Db 2679 ATGATTAATATGTGGCCGGGGGTGCTTTGCAATGACCGGGGTGTTAATGAATGAAG 2738
Qy 2281 TTTTACGGGCCCCAATTTTACGGGTACGGTTTCTGCGCAATTCGAACCTTAATCTTAC 2340
Db 2739 TTTTACGGGCCCCAATTTTACGGGTACGGTTTCTGCGCAATTCGAACCTTAATCTTAC 2798
Qy 2341 GGTGTAAAGCTTCTATAGGTTTAAACAATACCTGTGTGGAACCTTGACCGATGTAAGGTT 2400
Db 2799 GGTGTAAAGCTTCTATAGGTTTAAACAATACCTGTGTGGAACCTTGACCGATGTAAGGTT 2858

Qy	2401	CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGTGTGCTCGCCCAAAAGCAGGCT	2460
Db	2859	CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGTGTGCTCGCCCAAAAGCAGGCT	2918
Qy	2461	TCAATTAAAGAAATGCGCTCTTTGAAAGAGTATCCTTGGGTATCCGTCTGAAGGTATCC	2520
Db	2919	TCATTTAAAGAAATGCGCTCTTTGAAAGAGTATCCTTGGGTATCCGTCTGAAGGTATCC	2978
Qy	2521	AGGGTGGCCCAATATGTGGCCCTCCGACTGTGGTGTCTTATGCTAAGTAAAGCGTGGCT	2580
Db	2979	AGGGTGGCCCAATATGTGGCCCTCCGACTGTGGTGTCTTATGCTAAGTAAAGCGTGGCT	3038
Qy	2581	GTCATTAAAGCATATACATGTATATGTGTGGCAACTGCGAGGACAGGGCTCTCAGATGCTAAC	2640
Db	3039	GTCATTAAAGCATATACATGTATATGTGTGGCAACTGCGAGGACAGGGCTCTCAGATGCTAAC	3098
Qy	2641	TGCTGTGGACCGGCACTGTCACTGCTGTGAAGACATTCAGTGAAGCACTCTCGCAAG	2700
Db	3099	TGCTGTGGACCGGCACTGTCACTGCTGTGAAGACATTCAGTGAAGCACTCTCGCAAG	3158
Qy	2701	GCCTGGCCAGTGTGTTGAGCATTAACATCTGACCCGCTGTCTTCCTTCATTTGGGTAAAGG	2760
Db	3159	GCCTGGCCAGTGTGTTGAGCATTAACATCTGACCCGCTGTCTTCCTTCATTTGGGTAAAGG	3218
Qy	2761	AGGGGGGTGTTCTTACTTACCTTAACTCAATTGAGTCACTAAGATATGCTTGAAGCC	2820
Db	3219	AGGGGGGTGTTCTTACTTACCTTAACTCAATTGAGTCACTAAGATATGCTTGAAGCC	3278
Qy	2821	GAGAGCATGTCCCAAGGTAACTGTAAAGGGGGTGTGACATGACATGAAGAATCTGGAA	2880
Db	3279	GAGAGCATGTCCCAAGGTAACTGTAAAGGGGGTGTGACATGACATGAAGAATCTGGAA	3338
Qy	2881	GTGCTGAGGTATCGATGAGACCCGCAACAGTGTGACAGCCCTGAGTGTGGGTAAACAT	2940
Db	3339	GTGCTGAGGTATCGATGAGACCCGCAACAGTGTGACAGCCCTGAGTGTGGGTAAACAT	3398
Qy	2941	ATTAGGAACACAGCTGTGATGCTGATGTGACCGAGAGCTGAGGCCCGATCACTTGGTG	3000
Db	3399	ATTAGGAACACAGCTGTGATGCTGATGTGACCGAGAGCTGAGGCCCGATCACTTGGTG	3458
Qy	3001	CTGGGCTGCACCCGGGCTGAGTGGTGTGCTTACGCAATGAAGATPACAGATTGAG	3052
Db	3459	CTGGGCTGCACCCGGGCTGAGTGGTGTGCTTACGCAATGAAGATPACAGATTGAG	3510
RESULT 11			
ACA60761			
ID	ACA60761	standard; DNA; 35935 BP.	
AC	ACA60761;		
XX			
XX			
DT	11-AUG-2003	(first entry)	
XX			
DE	Human adenovirus type 5 DNA sequence.		
XX			
XX			
KW	Neoplasm; ds; tumour; malignant tumour; metastatic tumour; cancer;		
XX			
XX	liver tumour; colorectal cancer; melanoma.		
OS	Human adenovirus type 5.		
XX			
XX			
Key	Location/Qualifiers		
FT	promoter		
FT	1..491		
FT	/*tag= a		
FT	/standard_name= "Promoter"		
FT	/note= "E1A promoter"		
FT	1..103		
FT	repeat_region		
FT	/*tag= b		
FT	/rpt_type= OTHER		
FT	/note= "OTHER = Inverted terminal repeat (ITR)"		
FT	1..51		
FT	misc_feature		
FT	/*tag= C		
FT	/note= "Region of max DNA replication"		
FT	63..69		
FT	misc binding		

FT	misc_feature	110.119	/*tag= f	/not= "labelled as E1A-F in Figure 9 no further details given"
FT	enhancer	149.174	/*tag= g	/standard_name= "Enhancer"
FT	misc_feature	153.162	/*tag= h	/not= "labelled as E1A-F in Figure 9 no further details given"
FT	misc_feature	167.206	/*tag= i	/not= "labelled as E1A-F in Figure 9 no further details given"
FT	misc_feature	211.219	/*tag= j	/not= "labelled as E2F in Figure 9 no further details given"
FT	misc_feature	227.236	/*tag= k	/not= "labelled as E1A-F in Figure 9 no further details given"
FT	misc_feature	245.258	/*tag= l	/not= "labelled as A1 in Figure 9 no further details given"
FT	misc_feature	266.273	/*tag= m	/not= "labelled as A11 in Figure 9 no further details given"
FT	misc_feature	274.279	/*tag= n	/not= "labelled as E2F in Figure 9 no further details given"
FT	misc_feature	295.304	/*tag= o	/not= "labelled as E1A-F in Figure 9 no further details given"
FT	misc_feature	318.335	/*tag= p	/not= "labelled as AV in Figure 9 no further details given"
FT	misc_feature	343.356	/*tag= q	/not= "labelled as AVI in Figure 9 no further details given"
FT	misc_feature	364.387	/*tag= r	/not= "labelled as AI in Figure 9 no further details given"
FT	misc_feature	456.461	/*tag= s	/bound_motety= "ATP"
FT	TATA_signal	468.475	/*tag= t	/standard_name= "TATA box"
FT	promoter	35596.35935	/*tag= u	/standard_name= "Promoter"
FT	misc_feature	35605	/*tag= v	/not= "E4 promoter"
FT	TATA_signal	35631.35638	/*tag= w	/standard_name= "TATA box"
FT	misc_feature	35650.35658		

```
FT      /tag= x
FT      /note= "Labelled as B4F1 in Figure 9 no further details
FT      given"
FT      misc_binding
FT      /tag= y
FT      /bound_molecly= "ATP"
FT      misc_feature
FT      /tag= z
FT      /note= "Labelled as B4F1 in Figure 9 no further details
FT      given"
FT      repeat_region
FT      /tag= aa
FT      /rpt_type= OTHER
FT      /note= "OTHER = Inverted terminal repeat (ITR)"
FT      misc_binding
FT      /tag= ab
FT      /bound_molecly= "ATP"
FT      misc_binding
FT      /tag= ac
FT      /bound_molecly= "ATP"
FT      misc_feature
FT      /tag= ad
FT      /note= "Region of max DNA replication"
FT      MO2003006662-A1.
FT      23-JAN-2003.
FT      12-JUL-2002; 2002MO-GB003211.
FT      13-JUL-2001; 2001GB-00017198.
FT      (BTGI-) BTG INT LTD.
FT      I990 RD, Fuierer C, Homicsko KG;
FT      WPI; 2003-221752/21.
FT      New viral DNA construct having one or more tumor specific transcription
FT      factor binding sites controlling expression of the E1A open reading
FT      frame, useful in the treatment of malignant and metastatic tumors of the
FT      colon.
FT      PS      Disclosure; Page 70-87; 97BP; English.
XX      CC      The invention relates to a new viral DNA construct encoding for an
XX      CC      adenovirus capable of replication in a human or animal tumour cell, that
XX      CC      comprises one or more transcription factor (TF) binding sites operatively
XX      CC      positioned together with the E1A open reading frame to promote expression
XX      CC      of E1A proteins in the presence of the TF. The viral construct and/or
XX      CC      virus is useful in the manufacture of a medicament in the therapy of
XX      CC      patients having neoplasm, where they are capable of causing death to
XX      CC      tumour cell. They are useful in treating malignant and metastatic tumours
XX      CC      derived from colon cells particularly liver tumours also for treating
XX      CC      colorectal cancers and melanomas. The present sequence represents the DNA
XX      CC      sequence of human adenovirus type 5
XX      SQ      Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;
XX      Query Match      100.0%; Score 3052; DB 10; Length 35935;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1      CGGTAGTATTATATACCGGTAGTCTCTCAAGAGCCACTCTTGAAGTCCAGCGAGT 60
DB      459      CGTGTAGTATTATATACCGGTAGTCTCTCAAGAGCCACTCTTGAAGTCCAGCGAGT 518
QY      61      AGAGTTTCTCTCGAGACCGCTCCGACACCGGAGCTGAAAATGAGACATTTATCTGCC 120
DB      519      AGAGTTTCTCTCGAGACCGCTCCGACACCGGAGCTGAAAATGAGACATTTATCTGCC 578
QY      121      ACGGAGGTATTATACGGAAGAAATGCGCGCAGTCTTTGACCAGCTGATCGAAGAG 180
DB      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
DB      579      ACGGAGGTATTATACGGAAGAAATGCGCGCAGTCTTTGACCAGCTGATCGAAGAG 638
QY      181      TACTGGCTGATTAATCTTCACTCTCTAGCCATTTTGAACCACTTACCCTTACGAACTGT 240
DB      639      TACTGGCTGATTAATCTTCACTCTCTAGCCATTTTGAACCACTTACCCTTACGAACTGT 698
QY      241      ATGATTTAGAGTACGCGCCCGCAAGATCCCAACGAGAGAGCGGTTTGCAGATTTTTC 300
DB      699      ATGATTTAGAGTACGCGCCCGCAAGATCCCAACGAGAGAGCGGTTTGCAGATTTTTC 758
QY      301      CCGACTCTGTAATGTGGCGGTGAGAGAAAGGATTGACTTACTACTTTTCCGCGCGGC 360
DB      759      CCGACTCTGTAATGTGGCGGTGAGAGAAAGGATTGACTTACTACTTTTCCGCGCGGC 818
QY      361      CCGGTTCTCGGAGCCGCTCACCCTTTCCCGGACCCCGAGACCCGAGAGAGAGCCT 420
DB      819      CCGGTTCTCGGAGCCGCTCACCCTTTCCCGGACCCCGAGACCCGAGAGAGAGCCT 878
QY      421      TGGGTCCGGTTCTATGTCGAAACCTTGTATCCGAGGTATGATCTTACCTGCCACGAG 480
DB      879      TGGGTCCGGTTCTATGTCGAAACCTTGTATCCGAGGTATGATCTTACCTGCCACGAG 938
QY      481      CTGGCTTTCCACCCGAGTACGAGAGTGAAGAGGATGAGAGATTGTGTAGATTATG 540
DB      939      CTGGCTTTCCACCCGAGTACGAGAGTGAAGAGGATGAGAGATTGTGTAGATTATG 998
QY      541      TGAGACACCCCGGACGAGTTGACAGTCTTGTCTATATCAACCGAGGAATAACGGGGAGC 600
DB      999      TGAGACACCCCGGACGAGTTGACAGTCTTGTCTATATCAACCGAGGAATAACGGGGAGC 1058
QY      601      CAGATATTATATGTTCGCTTGTCTATATGAGAGACTGTGCAATGTTGTCTACAGTAA 660
DB      1059      CAGATATTATATGTTCGCTTGTCTATATGAGAGACTGTGCAATGTTGTCTACAGTAA 1118
QY      661      GAAATTTATGGGACAGTGGTATAGAGTGTGGGTTTGTGTGGTAATTTTTTTTAT 720
DB      1119      GAAATTTATGGGACAGTGGTATAGAGTGTGGGTTTGTGTGGTAATTTTTTTTAT 1178
QY      721      TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTAAAGAGTCTGTGTC 780
DB      1179      TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTAAAGAGTCTGTGTC 1238
QY      781      TGAACCTGAGGCTTGAAGCCCGACGAGAACCGGAGCTTGCAGAGACTTACCCCGTCTTA 840
DB      1239      TGAACCTGAGGCTTGAAGCCCGACGAGAACCGGAGCTTGCAGAGACTTACCCCGTCTTA 1298
QY      841      AATGGCGCTGTCTTCTGAGAGCCCGACATCACTGTGCTTGAAGATCAATATGATG 900
DB      1299      AATGGCGCTGTCTTCTGAGAGCCCGACATCACTGTGCTTGAAGATCAATATGATG 1358
QY      901      TACGATAGCTGTGACTCCGCTCTTCTTAACACACTCTTGAATACACCCGAGTGTCC 960
DB      1359      TACGATAGCTGTGACTCCGCTCTTCTTAACACACTCTTGAATACACCCGAGTGTCC 1418
QY      961      GCTGTGCCCCATTAAACCAAGTGGCGTGAAGTGTGGGCGTCCAGAGCTGTGAGATG 1020
DB      1419      GCTGTGCCCCATTAAACCAAGTGGCGTGAAGTGTGGGCGTCCAGAGCTGTGAGATG 1478
QY      1021      TATCGAGGACTTGTCTTAACGAGCTTGGGCAACTTTTGAATCTTGAAGCTGTAAACGCCAG 1080
DB      1479      TATCGAGGACTTGTCTTAACGAGCTTGGGCAACTTTTGAATCTTGAAGCTGTAAACGCCAG 1538
QY      1081      GCATTAAGGTGTAACCTGTGATTTGCGTGTGTGTTAACCGCTTTTGTCTGATGAGT 1140
DB      1539      GCATTAAGGTGTAACCTGTGATTTGCGTGTGTGTTAACCGCTTTTGTCTGATGAGT 1598
QY      1141      TGATGTAGTTTAAATGAAGGTGATATATCTTAACTGATGCGCGTTAAATGTGGGC 1200
DB      1599      TGATGTAGTTTAAATGAAGGTGATATATCTTAACTGATGCGCGTTAAATGTGGGC 1658
QY      1201      GGGGCTTAAAGGATATATATGCGCGTGGCTAATCTTGGTTACATCTGACTCATGGA 1260
DB      1659      GGGGCTTAAAGGATATATATGCGCGTGGCTAATCTTGGTTACATCTGACTCATGGA 1718
```

Qy 1261 GCGTTGGGAGCTTTTGGAGAAATTTTCTGCTGTGCTTAACCTTGTGGAAACAGACTCTAA 1320
Db 1719 GCGTTGGGAGGTTTGGAGAAATTTTCTGCTGTGCTTAACCTTGTGGAAACAGACTCTAA 1778
Qy 1321 CAGTACCTCTGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAAGTATGCTGAG 1380
Db 1779 CAGTACCTCTGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAAGTATGCTGAG 1838
Qy 1381 AATTAAAGAGATTACAAGTGGGAAATTTGAAAGCTTTGAAATCTGTGTGAGCTGT 1440
Db 1839 AATTAAAGAGATTACAAGTGGGAAATTTGAAAGCTTTGAAATCTGTGTGAGCTGT 1898
Qy 1441 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAAAGAAAGTCAATCAAGCTTTGGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAAAGAAAGTCAATCAAGCTTTGGA 1958
Qy 1501 TTTTTCACACCGGGGCGCGCTGCGGCTGTGTTGCTTTTGGAGTTTATTAAGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGGCTGTGTTGCTTTTGGAGTTTATTAAGATTA 2018
Qy 1561 ATGAGCCGAGAAACCCATCTGAGCGGGGGTACCTGTGAAATTTTCTGGCCATGATCT 1620
Db 2019 ATGAGCCGAGAAACCCATCTGAGCGGGGGTACCTGTGAAATTTTCTGGCCATGATCT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACAACAAGATCGCTGCTACTGTGTTCTTCCGTCGCGCCG 1680
Db 2079 GTGAGAGCGGTTGTGAGACAACAAGATCGCTGCTACTGTGTTCTTCCGTCGCGCCG 2138
Qy 1681 GATAATACCGACGAGAGACAGACAGACAGAGAGAAACCCAGCGCGGCGAGGA 1740
Db 2139 GATAATACCGACGAGAGACAGACAGACAGAGAGAAACCCAGCGCGGCGAGGA 2198
Qy 1741 GCAGAGCCCATGGAACCCGAGAGCCGCTGGAACCTTGGGAAATGATGTTGTAACAGGTG 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCCGCTGGAACCTTGGGAAATGATGTTGTAACAGGTG 2258
Qy 1801 GCTGAACGTATCCAGAACTGAGAGCATTTTGAACATTAACAAGATGGGCAAGGGCTA 1860
Db 2259 GCTGAACGTATCCAGAACTGAGAGCATTTTGAACATTAACAAGATGGGCAAGGGCTA 2318
Qy 1861 AAGGGGATTAAGAGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTACT 1920
Db 2319 AAGGGGATTAAGAGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTACT 2378
Qy 1921 TTTAGCTTAATGACCAACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATAT 1980
Db 2379 TTTAGCTTAATGACCAACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATAT 2438
Qy 1981 TGCGCTAATGAGCTTGAATCTGTGGCGCAAGATATTCATAGAGACAGTCAACCTTAC 2040
Db 2439 TGCGCTAATGAGCTTGAATCTGTGGCGCAAGATATTCATAGAGACAGTCAACCTTAC 2498
Qy 2041 TGCGCTGAGCCAGGGGATGATTTTGAAGAGCTATTAAGGATATGCAAAAGGTGCACTT 2100
Db 2499 TGCGCTGAGCCAGGGGATGATTTTGAAGAGCTATTAAGGATATGCAAAAGGTGCACTT 2558
Qy 2101 AGGCCAGATTGCAAGTACAAAGATCGAAACTTGTAAATATCAGGAATTTGCTACAT 2160
Db 2559 AGGCCAGATTGCAAGTACAAAGATCGAAACTTGTAAATATCAGGAATTTGCTACAT 2618
Qy 2161 TCTGGGAAACGGGGCGGAGGTGAGATTAATACAGAGGATAGGGTGGCTTTTGAATGAG 2220
Db 2619 TCTGGGAAACGGGGCGGAGGTGAGATTAATACAGAGGATAGGGTGGCTTTTGAATGAG 2678
Qy 2221 ATGATTAATATGTGCGCGGGGGTGTGGCATGAGCGGGGTGATTAATGATTAAGG 2280
Db 2679 ATGATTAATATGTGCGCGGGGGTGTGGCATGAGCGGGGTGATTAATGATTAAGG 2738
Qy 2281 TTTTACGGCCCCCAATTTTACGGGTACGGTTTCTGCGCAATACCACTTATCTTACAC 2340
Db 2739 TTTTACGGCCCCCAATTTTACGGGTACGGTTTCTGCGCAATACCACTTATCTTACAC 2798

Qy 2341 GGTGTAGACTTCTATGGGTTTAAACAATACCTGTGTGGAAGCTGGAACGATGTAAGGTT 2400
Db 2799 GGTGTAGACTTCTATGGGTTTAAACAATACCTGTGTGGAAGCTGGAACGATGTAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGTGTGTGCGCCCAAAAGCAGGCT 2460
Db 2859 CGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGTGTGTGCGCCCAAAAGCAGGCT 2918
Qy 2461 TCAATTAAGAAATGCCCTTTTGAAGGTATACCTTGGGTATCCGTGTGAGGGGTAACTCC 2520
Db 2919 TCAATTAAGAAATGCCCTTTTGAAGGTATACCTTGGGTATCCGTGTGAGGGGTAACTCC 2978
Qy 2521 AGGGTGGCCACAATGTGGGCTCCGACTGTGTGTTGCTTCAATGTAGTAAAGCGTGGCT 2580
Db 2979 AGGGTGGCCACAATGTGGGCTCCGACTGTGTGTTGCTTCAATGTAGTAAAGCGTGGCT 3038
Qy 2581 GTGATTAAGCATTAACATGTATGTGGCACTGCGAGGACAGGGCTTCAAGATCTGACC 2640
Db 3039 GTGATTAAGCATTAACATGTATGTGGCACTGCGAGGACAGGGGCTTCAAGATCTGACC 3098
Qy 2641 TGCTCGAGCGGCAACTGTCTCACTGTGAAGACCAATTACGTAAGCAACCTCCGGAAG 2700
Db 3099 TGCTCGAGCGGCAACTGTCTCACTGTGAAGACCAATTACGTAAGCAACCTCCGGAAG 3158
Qy 2701 GCTGCGCAGTGTGATGACATTAACATGACCGGCTGTTCTTGTGATTTGGGTAAAGG 2760
Db 3159 GCTGCGCAGTGTGATGACATTAACATGACCGGCTGTTCTTGTGATTTGGGTAAAGG 3218
Qy 2761 AGGGGGGTGTCTTCACTTCACTTCAATGCAATTTGATGACACTAAGATATTTGAGCCC 2820
Db 3219 AGGGGGGTGTCTTCACTTCACTTCAATGCAATTTGATGACACTAAGATATTTGAGCCC 3278
Qy 2821 GAGAGCATGTCCAAAGTGAACCTGGAACGGGGTGTGTAACATGACCAATGAAGATCTGGAAG 2880
Db 3279 GAGAGCATGTCCAAAGTGAACCTGGAACGGGGTGTGTAACATGACCAATGAAGATCTGGAAG 3338
Qy 2881 GTGCTGAGTACGATGAGACCCGCAACGAGTGCAGACCTTGCAGAGTGTGGCGTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGACCCGCAACGAGTGCAGACCTTGCAGAGTGTGGCGTAAACAT 3398
Qy 2941 ATTAGAACCAAGCTGTGATGCTGATGTGAACCGAGAGCTGAGGCCGATCACTTGGTG 3000
Db 3399 ATTAGAACCAAGCTGTGATGCTGATGTGAACCGAGAGCTGAGGCCGATCACTTGGTG 3458
Qy 3001 CTGGCCCTGCACCCGCGCTGATGTTGGCTCTAGCGATGAATTAAGATTGAG 3052
Db 3459 CTGGCCCTGCACCCGCGCTGATGTTGGCTCTAGCGATGAATTAAGATTGAG 3510

RESULT 12
ADR41672
ID ADR41672 standard; DNA; 35935 BP.
XX
XX ADR41672;
AC
XX
DT 04-NOV-2004 (first entry)
XX
DE Wild type Ad5 adenovirus.
XX
XX
XX Lytic agent; ds; chaperone; heat shock protein; stimulin;
KW tumour shrinkage; oncolysis; HSP; HSP-CRA; cancer reactive antigen;
KW nasopharyngeal carcinoma; chondrosarcoma; colon cancer; breast; prostate;
KW ovarian; stomach carcinoma; rectum; malignant hepatoma; melanoma; p53;
KW tumour suppressor gene; Ad5; S98-002; E1b region; E3; E1b-55KD; gene;
KW ascites.
XX
OS Human adenovirus type 5.
XX
FH Key Location/Qualifiers
FT misc_feature 2501..3328 /*tag=a
FT /note="Partial E1b region"
FT misc_feature 27865..30995

FT /*tag= b
XX /note= "E3 region"
XX WO2004066947-A2.
XX
XX 12-AUG-2004.
XX
XX 28-JAN-2004; 2004WO-US002330.
XX
XX 28-JAN-2003; 2003US-0443095P.
XX
XX (SHAN-) SHANGHAI SUNWAY BIOTECH CO LTD.
XX
XX Hu F, Wu B;
XX WPI; 2004-580848/56.
XX
XX Ablating tumor cells in a subject having at least one tumor site by
PT contacting the tumor cells in at least one tumor with a lytic agent in
PT vivo and applying a sufficient in vivo stimulus to the created tumor
PT forming a stimulated tumor.
XX
XX Example 1; SEQ ID NO 4; 129bp; English.
XX
XX The present invention relates to the compositions and methods for
XX ablating tumor cells in a subject having one or more tumor sites. The
XX method includes introduction of a lytic agent into a tumor (which forms
XX a treated tumor) and application of stimulus to the treated tumor. The
XX stimulus (physical, chemical or biological) induces the level of
XX chaperone proteins (heat shock proteins) in the tumor cells. The
XX combination of the lytic agent and tumor cell stimulus leads to tumor
XX shrinkage. The invention relates to the synchronization between oncolysis
XX and elevated expression of a heat shock protein (HSP), which results in
XX sufficient release of HSP-CRA (cancer reactive antigen). The sufficient
XX levels of HSP-CRA exhibit a signal immunogenic enough to the immune
XX system in order to elicit an immune response against the cancer. The
XX method of the invention is useful in ablating tumor cells for treating
XX nasopharyngeal carcinoma, chondrosarcoma, colon cancer, breast cancer,
XX prostate cancer, ovarian cancer, stomach carcinoma, rectum cancer,
XX malignant hepatoma, melanoma, ascites etc. Mutations of the p53 gene
XX exist in more than half of cancer cases. The treated or non-treated
XX cancers which consist of a defective p53 tumor suppressor gene or an
XX activated oncogene are good candidates for this method of therapy. The
XX oncolytic viruses of this invention comprise genetically modified Ad5
XX variants. This oncolytic adenovirus selectively replicates in cancer
XX cells with a p53 mutation and lyses cancer cells with high specificity.
XX The genome of a wild type Ad5 is composed of 35,935 bps. Genetically
XX modified variant Ad5 (S98-001) has an extra stop codon at position 2025
XX (E1b region) and possesses deletions in E1b region (in between 2,501 and
XX 3,328) and in E3 (in between 27865 and position 30,995) region. In normal
XX cells E1b-55KD binds and inactivates the protein encoded by the p53 gene
XX and initiates viral replication. The S98-001 variant is not able to
XX replicate in normal cells, but replicates rapidly in cancer cells in
XX which the p53 protein is dysfunctional. The function of E3 is related to
XX the ability of an adenovirus to escape from the surveillance of the
XX immune system. The complete deletion of the E3 region in S98-001 enables
XX the immune system easier recognition and elimination of this virus. S98
XX -002 is another genetically modified variant Ad5. It has deletions in the
XX region encoding E1b-55KD (in between 2,501 and 3,328) and of the entire
XX E3 region (in between 27865 and position 30,995). The variant sequences
XX of Ad5 are unable to integrate into the human genome, but selectively
XX replicate in cancer cells. So, S98-001 and S98-002 are safe for use in
XX humans and animals. The presented sequence is shown as SEQ ID No 4 in the
XX adenovirus DNA. Note: This sequence is shown as SEQ ID No 4 in the
XX sequence listing, however, this does not correspond to the description of
XX the sequence in example 1 of the specification. This sequence is referred
XX as SEQ ID No 3 in example 1.
XX
XX Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;
Query Match 100.0%; Score 3052; DB 13; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTGTAGTATTTTAAACCCGCTGAGTTCTTCAAGAGCCACTTGTAGTCCAGCAGT 60
DB 459 CGTGTAGTATTTTAAACCCGCTGAGTTCTTCAAGAGCCACTTGTAGTCCAGCAGT 518
QY 61 AGAGTTTTCCTCCGAGCCGCTCCGACACCGGAGACTGAAATGAAATATTTATCTG 120
DB 519 AGAGTTTTCCTCCGAGCCGCTCCGACACCGGAGACTGAAATGAAATATTTATCTG 578
QY 121 ACGAGGTGTTATTAACGAAAGAAATGCGCCAGTCTTTTGAACCACTGATCGAAGG 180
DB 579 ACGAGGTGTTATTAACGAAAGAAATGCGCCAGTCTTTTGAACCACTGATCGAAGG 638
QY 181 TACTGCTGATTAATCTTCACTCTCTTACGATTTTGAACCACTTCACTGACTGT 240
DB 639 TACTGCTGATTAATCTTCACTCTCTTACGATTTTGAACCACTTCACTGACTGT 698
QY 241 ATGATTTAGACGTGACGCGCCCGGAGATCCCAACGAGGAGCGGTTTGCAGATTTTC 300
DB 699 ATGATTTAGACGTGACGCGCCCGGAGATCCCAACGAGGAGCGGTTTGCAGATTTTC 758
QY 301 CCGACTCTGTAATGTGGCGGTGAGAGGATTTGACTTACTTCTTCCGCGGCGC 360
DB 759 CCGACTCTGTAATGTGGCGGTGAGAGGATTTGACTTACTTCTTCCGCGGCGC 818
QY 361 CCGGTTCTCGGAGCGGCTTCACTTTCCCGGACCCCGAGACCGGAGAGAGCTT 420
DB 819 CCGGTTCTCGGAGCGGCTTCACTTTCCCGGACCCCGAGACCGGAGAGAGAGCTT 480
QY 421 TGGTCCGTTTCTATGACCAACCTTTTACCGGAGTATGATCTTACCTGACAGG 480
DB 879 TGGTCCGTTTCTATGACCAACCTTTTACCGGAGTATGATCTTACCTGACAGG 938
QY 481 CTGGCTTTCAACCGAGAGAGAGAGATGAGAGGTTGTTAGATTTATG 540
DB 939 CTGGCTTTCAACCGAGAGAGAGAGATGAGAGGTTGTTAGATTTATG 998
QY 541 TGGAGACCCCGGAGCGGTTGACGCTTGTCTATTCACCGAGAAATACGGGAGAC 600
DB 999 TGGAGACCCCGGAGCGGTTGACGCTTGTCTATTCACCGAGAAATACGGGAGAC 1058
QY 601 CAGATATTATGTGCTTGTCTATTCAGAGACCTGAGATGTTGTCTACAGTAAGT 660
DB 1059 CAGATATTATGTGCTTGTCTATTCAGAGACCTGAGATGTTGTCTACAGTAAGT 1118
QY 661 GAAATATTATGAGAGAGGATGATGAGTGTGTTGTGTGTAATTTTATTTTAT 720
DB 1119 GAAATATTATGAGAGAGGATGATGAGTGTGTTGTGTGTAATTTTATTTTAT 1178
QY 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATTTTAAAGAGTCTCTGTGTC 780
DB 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATTTTAAAGAGTCTCTGTGTC 1238
QY 781 TGAACCTGAGACCTGAGCCGAGCCAGAACCGGAGCCGCAAGACTTCCGCTCTAA 840
DB 1239 TGAACCTGAGACCTGAGCCGAGCCAGAACCGGAGCCGCAAGACTTCCGCTCTAA 1298
QY 841 AATGGCCCTGCTATCTGAGACGCGCGACATCACTGTGCTAGAGAAATGCAATAG 900
DB 1299 AATGGCCCTGCTATCTGAGACGCGCGACATCACTGTGCTAGAGAAATGCAATAG 1358
QY 901 TACGATAGCTGTGATCTCGGCTCTTAAACACACTCTGAGATACACCGGCTGCC 960
DB 1359 TACGATAGCTGTGATCTCGGCTCTTAAACACACTCTGAGATACACCGGCTGCC 1418
QY 961 GCTGTGCCCATTAACAGATGCGGAGAGTTGTGGGCGTGCAGGCTGTGATG 1020
DB 1419 GCTGTGCCCATTAACAGATGCGGAGAGTTGTGGGCGTGCAGGCTGTGATG 1478
QY 1021 TATCGAGACTTGTGTTAACAAGCTGAGCAACTTTTGAATGAGCTGTAAACGCCAG 1080
DB 1479 TATCGAGACTTGTGTTAACAAGCTGAGCAACTTTTGAATGAGCTGTAAACGCCAG 1538

QY	1081	GCCATAAGGGTAAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTGTTGCTGAATGACT	1140
Db	1539	GCCATAAGGGTAAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTGTTGCTGAATGACT	1598
QY	1141	TGATGTAAAGTTAATAAAGGGTGAATATAATTAACTTGATAGGCGGTAAATGGGGC	1200
Db	1599	TGATGTAAAGTTAATAAAGGGTGAATATAATTAACTTGATAGGCGGTAAATGGGGC	1658
QY	1201	GGGGCTTAAAGGGTATATAATATGCGCGGTGGCTAATCTTGTTACATCTGACCTCATGGA	1260
Db	1659	GGGGCTTAAAGGGTATATAATATGCGCGGTGGCTAATCTTGTTACATCTGACCTCATGGA	1718
QY	1261	GGCTTGGGAGCTTTTGGAAAGTTTTTCTGCTGTGTGCTTAACCTTGGTGAACAGAGCTCTAA	1320
Db	1719	GGCTTGGGAGCTTTTGGAAAGTTTTTCTGCTGTGTGCTTAACCTTGGTGAACAGAGCTCTAA	1778
QY	1321	CAGTAACTCTTGTTTTGGAGGTTTCTGTGGGGCTCATCCAGGCAAAAGTAAGCTGAG	1380
Db	1779	CAGTAACTCTTGTTTTGGAGGTTTCTGTGGGGCTCATCCAGGCAAAAGTAAGCTGAG	1838
QY	1381	AATTAAAGAGGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGACTGTT	1440
Db	1839	AATTAAAGAGGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGACTGTT	1898
QY	1441	TGATTTCTTTGAATCTGGGTCAACAGCGGCTTTTCCAAGAAAGTCAATCAAGACTTTTGA	1500
Db	1899	TGATTTCTTTGAATCTGGGTCAACAGCGGCTTTTCCAAGAAAGTCAATCAAGACTTTTGA	1958
QY	1501	TTTTTCCACACCGGGGGGCGCTGTGGGCTGCTGTTGCTTTTGAAGTTTAAAGGATTA	1560
Db	1959	TTTTTCCACACCGGGGGGCGCTGTGGGCTGCTGTTGCTTTTGAAGTTTAAAGGATTA	2018
QY	1561	ATGAGAGGAAGAAACCCATCTGAGCGGGGGGTACCTGTGATTTTCTGAGCATGACATCT	1620
Db	2019	ATGAGAGGAAGAAACCCATCTGAGCGGGGGGTACCTGTGATTTTCTGAGCATGACATCT	2078
QY	1621	GTGAGAGACGGTGTGTGACACACAAGAAATCCGCTGTACTGTGTCTTCGTCGCGCGGCG	1680
Db	2079	GTGAGAGACGGTGTGTGACACACAAGAAATCCGCTGTACTGTGTCTTCGTCGCGCGGCG	2138
QY	1681	GATTAATCCCGACGGAGGACGACAGCAGCAGAGGAAACCAAGGGCGGCGGCGAGGA	1740
Db	2139	GATTAATCCCGACGGAGGACGACAGCAGCAGCAGAGGAAACCAAGGGCGGCGGCGAGGA	2198
QY	1741	GCAGAGCCCATGGAACCCGAGAGCGGCGCTGGAACCTTCGGAAATGAATGTGTGACAGGTG	1800
Db	2199	GCAGAGCCCATGGAACCCGAGAGCGGCGCTGGAACCTTCGGAAATGAATGTGTGACAGGTG	2258
QY	1801	GCTGAACCTGTATCCAGAACTGAGACGCAATTTGACAAATTAACAAGAGATGGCAGGGGCTA	1860
Db	2259	GCTGAACCTGTATCCAGAACTGAGACGCAATTTGACAAATTAACAAGAGATGGCAGGGGCTA	2318
QY	1861	AAGGGGGTAAAGAGGAGCGGGGGGCTTGTAGGCTACAGAGAGGCTAAGGAATCTAGCT	1920
Db	2319	AAGGGGGTAAAGAGGAGCGGGGGGCTTGTAGGCTACAGAGAGGCTAAGGAATCTAGCT	2378
QY	1921	TTTAACTTAATAGACAGACACCGTCTGTAGGTATTAATCTTTTCAACAGATCAAGATTAAT	1980
Db	2379	TTTAACTTAATAGACAGACACCGTCTGTAGGTATTAATCTTTTCAACAGATCAAGATTAAT	2438
QY	1981	TGCGCTAATGAGCTTGAATCTGTGTGGCGCAGAAATTCATATAGAGCAGCTGACCACTTAC	2040
Db	2439	TGCGCTAATGAGCTTGAATCTGTGTGGCGCAGAAATTCATATAGAGCAGCTGACCACTTAC	2498
QY	2041	TGCGTGCACCAAGGGAGTATTTTGAAGAGCTATTAAGGATTAATGCAAAAGTGGCACTT	2100
Db	2499	TGCGTGCACCAAGGGAGTATTTTGAAGAGCTATTAAGGATTAATGCAAAAGTGGCACTT	2558
QY	2101	AGGCGAGATTSCAAGTACAAAGATCAGCAAACTTGTAAATATCAAGAAATGTGTGCAACTT	2160
Db	2559	AGGCGAGATTSCAAGTACAAAGATCAGCAAACTTGTAAATATCAAGAAATGTGTGCAACTT	2618
QY	2161	TCTGGGAACGGGGCCGAGGTGAGATAGATACGAGAGATAGAGTGCGCTTTTGAATGTAGC	2220

Db	2619	TCGCGGAAACGGGGCCGAGGTGAGATAGATACGAGGATAGGGTGGCTTTAGATGAGC	2676
Qy	2221	ATGATTAATATATGTGGCCGGGGGTGCTTGGCATGAGACGGGGTGTATATTATGATGTAAAG	2288
Db	2679	ATGATTAATATATGTGGCCGGGGGTGCTTGGCATGAGACGGGGGTGTATATTATGATGTAAAG	2738
Qy	2281	TTTACTGGCCCCCAATTTTAAAGGGTACGGTTTCTCGGCCAATTAACCACTTATCTTACAC	2344
Db	2739	TTTACTGGCCCCCAATTTTAAAGGGTACGGTTTCTCGGCCAATTAACCACTTATCTTACAC	2798
Qy	2341	GGTGTAAAGCTTCTATGGGTTTAAACAATACCGTGTGTGAAAGCTGTGACCGATGTAAAGGTT	2406
Db	2799	GGTGTAAAGCTTCTATGGGTTTAAACAATACCGTGTGTGAAAGCTGTGACCGATGTAAAGGTT	2858
Qy	2401	CGGGGCTGTGCTTTTAACTGTCTGTGAGAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT	2466
Db	2859	CGGGGCTGTGCTTTTAACTGTCTGTGAGAGGGGGTGTGTGTGCGCCCAAAAGCAGGGCT	2918
Qy	2461	TCAATTAAGAAATGCTCTTTTGAAGGTGATCCTTGGGTATCTGTCTGTAGGGTAACTCC	2522
Db	2919	TCAATTAAGAAATGCTCTTTTGAAGGTGATCCTTGGGTATCTGTCTGTAGGGTAACTCC	2976
Qy	2521	AGGGTGGCCCAATATGTGGCCTCCGACGTGTGGTTCCTTCAAGCTAATGTAAGACGTGGCT	2588
Db	2979	AGGGTGGCCCAATATGTGGCCTCCGACGTGTGGTTCCTTCAAGCTAATGTAAGACGTGGCT	3038
Qy	2581	GTGATTAAGCATTAACATGTATGTGTGCAACTGTGAGAGCAGGGGCTCTCAGATGCTGACC	2644
Db	3039	GTGATTAAGCATTAACATGTATGTGTGCAACTGTGAGAGCAGGGGCTCTCAGATGCTGACC	3098
Qy	2641	TGCTTGGACGGCACTGTCACTGTCTGTAGAGCAATTCAGGTAGCCACCTCTTGGCAAG	2700
Db	3099	TGCTTGGACGGCACTGTCACTGTCTGTAGAGCAATTCAGGTAGCCACCTCTTGGCAAG	3158
Qy	2701	GCCGTGGCAGGTGTTTGAAGCATATCTGACCCGCTGTTCCTTGCATTGGGTAAACAGG	2766
Db	3159	GCCGTGGCAGGTGTTTGAAGCATATCTGACCCGCTGTTCCTTGCATTGGGTAAACAGG	3218
Qy	2761	AGGGGGGTGTTCCTACCTTACCAATGTGCAATTGTGATGACACATAAGATATTTGCTTGAGCC	2822
Db	3219	AGGGGGGTGTTCCTACCTTACCAATGTGCAATTGTGATGACACATAAGATATTTGCTTGAGCC	3276
Qy	2821	GAGAGCATGTCCAAAGTGAACCTTGAACGGGGTGTGTCATGATGACCATGAAAGATCTGAAAG	2888
Db	3279	GAGAGCATGTGTCCAAAGTGAACCTTGAACGGGGTGTGTCATGATGACCATGAAAGATCTGAAAG	3338
Qy	2881	GTGCTGAGGTACGATGAGAACCCGCAACAGGTGTGACACCTTCGAGATGTGGCGGTAAACAT	2944
Db	3339	GTGCTGAGGTACGATGAGAACCCGCAACAGGTGTGACACCTTCGAGATGTGGCGGTAAACAT	3398
Qy	2941	ATTAGAACAACGAGCTGTGATGCTGATGTGTGACCAAGAGAGCTGAGGCCCGCATCACTTGGTG	3000
Db	3399	ATTAGAACAACGAGCTGTGATGCTGATGTGTGACCAAGAGAGCTGAGGCCCGCATCACTTGGTG	3458
Qy	3001	CTGGCCTGTGCAACCGCGCTGAGTTTGGCTCTAGCGATGAAGAATACAGATTGAG	3052
Db	3459	CTGGCCTGTGCAACCGCGCTGAGTTTGGCTCTAGCGATGAAGAATACAGATTGAG	3510
RESULT 13			
AAD27971 standard; DNA, 35978 BP.			
XX	AAD27971;		
XX	AC		
XX	16-JUN-2002 (first entry)		
XX	DT		
XX	DE		
XX	Recombinant adenovirus vector G23-TERT.		
KM	Recombinant adenovirus vector; adenovirus death protein; Adp; telomerase;		
KM	human; telomerase reverse transcriptase promoter; TERT; neoplastic cell;		
KM	cancer; G23-TERT; E3 region; mutant; ds.		

XX Mastradenovirus.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX US2002028785-A1.
XX 07-MAR-2002.
PD 19-SEP-2001; 2001US-00956335.
PF 12-JUN-1999; 98US-00351778.
PR 20-SEP-2000; 2000US-0233872P.
XX (UWSL-) UNIV SAINT LOUIS.
XX
PI Moid WSM, Toch K, Tollefson AE, Kuppuewamy M,
XX WPI; 2002-328910/36.
XX
PT Novel recombinant adenovirus vector useful for destroying neoplastic
PT cells, comprises a human telomerase reverse transcriptase promoter, and at
PT least one inactivation mutation in the E3 region.
XX
PS Claim 2; Page 12-28; 64pp; English.
XX
CC The invention relates to a recombinant adenovirus vector which
CC overexpresses an adenovirus death protein (ADP) and which is replication-
CC restricted to cells expressing telomerase, comprises a human telomerase
CC reverse transcriptase promoter (hERT) and at least one inactivating
CC mutation in the E3 region. The vector of the invention is useful in vitro
CC for promoting death of a cell expressing telomerase, and for promoting
CC death of neoplastic cells in a patient. The adenovirus vector is an
CC efficient and effective anticancer agent that could specifically target
CC neoplastic cells, while replicating poorly or not at all in normal
CC tissue, and efficiently spreading to neighbouring neoplastic cells,
CC thereby maximizing its cancer-killing ability. The presence of human
CC telomerase reverse transcriptase promoter allows restriction of
CC replication of the adenovirus to cells expressing telomerase without the
CC need for complementation to achieve replication competence in these
CC cells. The present sequence is adenovirus vector G23-ERT which comprises
CC an ADP gene, a hERT promoter, and a mutation in the E3 region
XX
SQ Sequence 35978 BP; 8265 A; 10141 C; 10026 G; 7546 T; 0 U; 0 Other;
Query Match 100.0%; Score 3052; DB 6; Length 35978;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGTAGTGTATTTATACCCGGTGAATTCCTCAAGAGCCACTTGAAGTCCAGCGAGT 60
DB 459 CGTGAAGTGTATTTATACCCGGTGAATTCCTCAAGAGCCACTTGAAGTCCAGCGAGT 518
QY 61 AGAGTTTCTCTCCGAGCCCGCTCCGACACCGGAGCTGAATATGACATATATCTCC 120
DB 519 AGAGTTTCTCTCCGAGCCCGCTCCGACACCGGAGCTGAATATGACATATATCTCC 578
QY 121 ACGGAGGTGTATTACCGAAGAAATGCGCAGCTTTTGAACAGGCTGATCGAAGAG 180
DB 579 ACGGAGGTGTATTACCGAAGAAATGCGCAGCTTTTGAACAGGCTGATCGAAGAG 638
QY 181 TACTGGCTGATATCTTCACTCTTACGCCATTTTGAACACCTTACCGAAGCTGT 240
DB 639 TACTGGCTGATATCTTCACTCTTACGCCATTTTGAACACCTTACCGAAGCTGT 698
QY 241 ATGATTTAGAGTGAGCGCCCGCCGAAGATCCCAAGAGAGCGGTTTCCGAGATTTTC 300
DB 699 ATGATTTAGAGTGAGCGCCCGCCGAAGATCCCAAGAGAGCGGTTTCCGAGATTTTC 758
QY 301 CCGACTCTGTATATGTTGGCGGTGACGAAAGGATGACTTCACTTTCCGCGCGCGC 360
DB 759 CCGACTCTGTATATGTTGGCGGTGACGAAAGGATGACTTCACTTTCCGCGCGCGC 818

QY 361 CCGGTTCTCCGAGCCGCTCACTTTTCCCGGACGCCGAGCAGCGGAGAGAGCCT 420
DB 819 CCGGTTCTCCGAGCCGCTCACTTTTCCCGGACGCCGAGCAGCGGAGAGAGCCT 878
QY 421 TGGGTCGGGTTTCTATGCGAAACCTTGTACCGGAGGTGATGATCTTACCGCAGAG 480
DB 879 TGGGTCGGGTTTCTATGCGAAACCTTGTACCGGAGGTGATGATCTTACCGCAGAG 938
QY 481 CTGGCTTCCACCCAGTGAAGAGAGATGAAAGAGGATGAGGATTTGTAGATTATG 540
DB 939 CTGGCTTCCACCCAGTGAAGAGATGAAAGAGGATGAGGATTTGTAGATTATG 998
QY 541 TGAAGACCCCGGAGCGGTTGACAGTCTTGTCAATATACCGAAGAAACCGGAGAC 600
DB 999 TGAAGACCCCGGAGCGGTTGACAGTCTTGTCAATATACCGAAGAAACCGGAGAC 1058
QY 601 CAGATATTATATGTTCCGTTTGTCTATATAGAGACCTGTGCGATGTTGTCTACAGT 660
DB 1059 CAGATATTATGTTCCGTTTGTCTATATAGAGACCTGTGCGATGTTGTCTACAGT 1118
QY 661 GAAATTTAGGCAAGTGGGTATAGAGTGGGTTGGTGGTAAATTTTTTTTAT 720
DB 1119 GAAATTTATGGGCAAGTGGGTATAGAGTGGGTTGGTGGTAAATTTTTTTTAT 1178
QY 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATTGTGATTTTTTAAAGGTCCTGTG 780
DB 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATTGTGATTTTTTAAAGGTCCTGTG 1238
QY 781 TGAACCTGAGCTGACCCCGGAGCCAGAACCGGAGCTGCAAGCTACCCCGCTCA 840
DB 1239 TGAACCTGAGCTGACCCCGGAGCCAGAACCGGAGCTGCAAGCTACCCCGCTCA 1298
QY 841 AATGGCGCTCTATATCTGAGACCCCGACATCACTGTCTAGAGATCAATATAG 900
DB 1299 AATGGCGCTCTATATCTGAGACCCCGACATCACTGTCTAGAGATCAATATAG 1358
QY 901 TACGATAGCTGTGATCTCCGCTCTTCAACACCTCTGAGATACACCGGTGTGCTC 960
DB 1359 TACGATAGCTGTGATCTCCGCTCTTCAACACCTCTGAGATACACCGGTGTGCTC 1418
QY 961 GCTGCGCCCATTAACAGATGCGGAGAGTGGTGGGCGGCGAGGCTGTGGAATG 1020
DB 1419 GCTGCGCCCATTAACAGATGCGGAGAGTGGTGGGCGGCGAGGCTGTGGAATG 1478
QY 1021 TATCGAGACTTGTCTTAACGAGCTGGGCAACTTTTGAAGCTGTAAACGCCCGAG 1080
DB 1479 TATCGAGACTTGTCTTAACGAGCTGGGCAACTTTTGAAGCTGTAAACGCCCGAG 1538
QY 1081 GCCATTAAGTGTAAACCTGTGATTCGCTGTGTAAACGCTTTTGTCTGAATAGT 1140
DB 1539 GCCATTAAGTGTAAACCTGTGATTCGCTGTGTAAACGCTTTTGTCTGAATAGT 1598
QY 1141 TGAATGATTTTAAAGGTTGAGATTAAGTTTAACTGTGATGCGCGTTTAAATGGG 1200
DB 1599 TGAATGATTTTAAAGGTTGAGATTAAGTTTAACTGTGATGCGCGTTTAAATGGG 1658
QY 1201 GGGGCTTAAAGGTTATTAATGCGCGCTGTATCTTGTGTACATCTGACCTCATGA 1260
DB 1659 GGGGCTTAAAGGTTATTAATGCGCGCTGTATCTTGTGTACATCTGACCTCATGA 1718
QY 1261 GGGTGGAGGTGTTGGAAGATTTTCTGCTGTGCTTAAGTCTGGAACAGAGCTTAA 1320
DB 1719 GGGTGGAGGTGTTGGAAGATTTTCTGCTGTGCTTAAGTCTGGAACAGAGCTTAA 1778
QY 1321 CAGTACCTCTGTTTGGAGGTTTCTGTGGGGCTCATCCAGGCAAGTTAGTCTGAG 1380
DB 1779 CAGTACCTCTGTTTGGAGGTTTCTGTGGGGCTCATCCAGGCAAGTTAGTCTGAG 1838
QY 1381 AATTAAAGAGATTACAAGTGGAAATTTGAAGACTTTTGAATCTGTGTGAGCTGT 1440
DB 1839 AATTAAAGAGATTACAAGTGGAAATTTGAAGACTTTTGAATCTGTGTGAGCTGT 1898

QY	1441	TGATTTCTTTGAATCTGGGTCACACAGCGGCTTTTCCAMAGAAAGTCATCAAGACTTTTGGAA	1500
Db	1899	TGATTTCTTTGAATCTGGGTCACACAGCGGCTTTTCCAMAGAAAGTCATCAAGACTTTTGGAA	1958
QY	1501	TTTTTCCACACCGGGGCGCGCTGGGCGCTGTCGTTTCTTTTGGATTATTAAGATPA	1560
Db	1959	TTTTTCCACACCGGGGCGCGCTGGGCGCTGTCGTTTCTTTTGGATTATTAAGATPA	2018
QY	1561	ATGAGCGAAGAAAACCCATCTGAGCGGGGGGTACCTGCTGATTTTCTGCGCATGATCT	1620
Db	2019	ATGAGCGAAGAAAACCCATCTGAGCGGGGGGTACCTGCTGATTTTCTGCGCATGATCT	2078
QY	1621	GTGAGAGCGGTTGTGAGACACAMAGATCGCTCTGTACTGTTGTCTTCGTCGCGCGGC	1680
Db	2079	GTGAGAGCGGTTGTGAGACACAMAGATCGCTCTGTACTGTTGTCTTCGTCGCGCGGC	2138
QY	1681	GATATATACCGACCGAGGAGACAGACACACAGAGAGAAACCGAGGGGCGGCGAGAA	1740
Db	2139	GATATATACCGACCGAGGAGACAGACACACAGAGAGAAACCGAGGGGCGGCGAGAA	2198
QY	1741	GCAGAGCCCATAGAACCCGAGAGCGGCGCTGAGACCTCGGGAAATGAAATGTTGTACAGGTG	1800
Db	2199	GCAGAGCCCATAGAACCCGAGAGCGGCGCTGAGACCTCGGGAAATGAAATGTTGTACAGGTG	2258
QY	1801	GCTGAACCTGTATCCAGAACTGAGACGCATTTTGACATTAACAGAGATGGGACAGGGCTA	1860
Db	2259	GCTGAACCTGTATCCAGAACTGAGACGCATTTTGACATTAACAGAGATGGGACAGGGCTA	2318
QY	1861	AAGGGGGTAAAGAGGAGACGGGGGGCTTGTAGAGCTACAGAGAGGCTAGAGAACTAGCT	1920
Db	2319	AAGGGGGTAAAGAGGAGACGGGGGGCTTGTAGAGCTACAGAGAGGCTAGAGAACTAGCT	2378
QY	1921	TTTGAAGCTTAATAGACACAGACACCGCTCTGAGTGTATTACTTTTCAACAGATCAAGATPAAT	1980
Db	2379	TTTGAAGCTTAATAGACACAGACACCGCTCTGAGTGTATTACTTTTCAACAGATCAAGATPAAT	2438
QY	1981	TGCGCTAATAGACTTGATCTGCTGGCGCAAGATTTTCATAGACAGCTGACCACTTAC	2040
Db	2439	TGCGCTAATAGACTTGATCTGCTGGCGCAAGATTTTCATAGACAGCTGACCACTTAC	2498
QY	2041	TGGCTGCAGCCAGGGGATGATTTTGGAGAGGCTATTAGGGATATAGCAAAAGTGGCACTT	2100
Db	2499	TGGCTGCAGCCAGGGGATGATTTTGGAGAGGCTATTAGGGATATAGCAAAAGTGGCACTT	2558
QY	2101	AGGCGAATTCGAAGTACAGATCAGCAAACTTGTAAATATACAGAAATTTGTGCTACATT	2160
Db	2559	AGGCGAATTCGAAGTACAGATCAGCAAACTTGTAAATATACAGAAATTTGTGCTACATT	2618
QY	2161	TCTGGGAAACGCGGCGGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTAGATGTAGC	2220
Db	2619	TCTGGGAAACGCGGCGGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTAGATGTAGC	2678
QY	2221	ATGATAAATATGTGGCCGGGGGTGCTTGGCANTGACGGGGGTGTATTAATGAATGTAAAG	2280
Db	2679	ATGATAAATATGTGGCCGGGGGTGCTTGGCANTGACGGGGGTGTATTAATGAATGTAAAG	2738
QY	2281	TTTACTGAGCCCAATTTTAAAGCGGTACGGTTTTCCTGCGCAATATCAACTTATCTACAC	2340
Db	2739	TTTACTGAGCCCAATTTTAAAGCGGTATTTTTCCTGCGCAATATCAACTTATCTACAC	2798
QY	2341	GGGTGTAAGCTTCTATGGGTTTAAACATATCTGTGTGAAAGCTGTGACCGATGTAAAGGTT	2400
Db	2799	GGGTGTAAGCTTCTATGGGTTTAAACATATCTGTGTGAAAGCTGTGACCGATGTAAAGGTT	2858
QY	2401	CGGGGCTGTGCTTTTACTGTCTGTGANAAGGGGGTGTGTGTCCGCCCAAAAGCAGGGCT	2460
Db	2859	CGGGGCTGTGCTTTTACTGTCTGTGANAAGGGGGTGTGTGTCCGCCCAAAAGCAGGGCT	2918
QY	2461	TCAATTAAGAATATGCTCTTTTGAAGAAGTGTACCTTGGGTATTCCTGTCTGAGAGGTATACCC	2520
Db	2919	TCAATTAAGAATATGCTCTTTTGAAGAAGTGTACCTTGGGTATTCCTGTCTGAGAGGTATACCC	2978
QY	2521	AGGGTGCACCAATATGTGGCCTCCGACTGTGGTGTCTTCATGCTAGTGAAGAAAGCGTGGCT	2580

Db	2979	AGGGTGGCCCAACTGTCCTCCGACTGTGGTTGCTTCATGTAGTAAAGGCGTGCT	3038
Oy	2581	GTGATTAAGCATTAACATGATGTATGTGGCAACTGCAGAGACAGGGGCTCTCAGATCTGACC	2640
Db	3039	GTGATTAAGCATTAACATGTATGTGGCACTGCAGAGACAGGGGCTCTCAGATCTGACC	3098
Oy	2641	TGCTTCGACGGCAACTGTCACTGCTGTGAAGCACTTCACTGACCGCACTTCGCAAG	2700
Db	3099	TGCTTCGACGGCAACTGTCACTGCTGTGAAGCACTTCACTGACCGCACTTCGCAAG	3158
Oy	2701	GCCCTGCGCAGTGTTTGAAGCATTAATATCTGACCCGCTGTTCTCTTGCAATTGCGTAAACAG	2760
Db	3159	GCCCTGCGCAGTGTTTGAAGCATTAATATCTGACCCGCTGTTCTCTTGCAATTGCGTAAACAG	3218
Oy	2761	AGGGGGGGTGTTCTCTACCTTACCAATGCAATTGTAGTCACTAAGATATTGCTTGAGCCC	2820
Db	3219	AGGGGGGGTGTTCTCTACCTTACCAATGCAATTGTAGTCACTAAGATATTGCTTGAGCCC	3278
Oy	2821	GAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTTTGAATGACCATGACATCTGGAG	2880
Db	3279	GAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTTTGAATGACCATGACATCTGGAG	3338
Oy	2881	GTGCTGAGGTACGATGAGTGAACCCCGACAGAGTGCAGACCTCGAGTGTGGCGTAAACAT	2940
Db	3339	GTGCTGAGGTACGATGAGTGAACCCCGACAGAGTGCAGACCTCGAGTGTGGCGTAAACAT	3398
Oy	2941	ATTAGGAACACAGCCTGTGATCTGATGTGACCGAGAGCTGAAGGCCGATCATCTTGGTG	3000
Db	3399	ATTAGGAACACAGCCTGTGATCTGATGTGACCGAGAGCTGAAGGCCGATCATCTTGGTG	3458
Oy	3001	CTGGCGCTGCACCCGCGCTGAGTTTGGCTCTTACGATGAAGATACAGATTGAG	3052
Db	3459	CTGGCGCTGCACCCGCGCTGAGTTTGGCTCTTACGATGAAGATACAGATTGAG	3510
RESULT 14			
AAH20746	AAH20746 standard; DNA; 7090 BP.		
AC	AAH20746;		
XX	13-AUG-2001 (first entry)		
DT	Plasmid STK146 DNA fragment.		
DE	Gene therapy: amniocyte; cytotstatic; Ad5; E1A region; E1B region;		
XX	modified tropism; tumor; PCR primer; ss.		
KW	Synthetic.		
OS	WO200136615-A2.		
XX	25-MAY-2001.		
PN	07-NOV-2000; 2000WO-EP010992.		
XX	18-NOV-1999; 99DE-0105558.		
PR	(KOCH/) KOCHANNEK S.		
XX	Kochanek S, Schiedner G;		
XX	WPI; 2001-343817/36.		
DR	New permanent amniocyte cell lines, useful for producing viral gene		
PT	therapy vectors or mutant adenoviruses, express the adenoviral E1A and		
PT	E1B gene products.		
XX	Example 1; Page 67-72; 72pp; German.		
PS	This invention describes novel permanent amniocyte cell lines (A), the		
XX	containing at least one nucleic acid (I) that causes expression of		

CC gene products (ii) of the adenoviral E1A and E1B regions. (A) are used to
CC produce gene therapy vectors, especially adeno, adeno-associated, retro
CC or lentiviral vectors, particularly first- or second generation, large-
CC capacity or deleted adenoviral vectors. (A) are also used to produce
CC adenoviral mutants, optionally with modified tropism. The vectors may
CC express a wide range of therapeutic proteins or antisense RNAs.
CC Adenoviral mutants, unable to express the E1B 55 kDa protein, are useful
CC for treating tumors, they can replicate in the cells but not significantly in
CC normal primary cells. (A) can be made efficiently, simply and
CC reproducibly. The products of the invention have cytototoxic activity.
CC This sequence represents a PCR primer used in the amplification of
CC Adenovirus A45 DNA which is described in the method of the invention
XX

Sequence 7090 BP; 1696 A; 1685 C; 1882 G; 1827 T; 0 U; 0 Other;

Query Match 98.5%; Score 3006.8; DB 5; Length 7090;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3008; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 43 TCCTGATGCGCAGGAGTAAAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAA 102
DB 2749 TATGAGAGCCAGGAGAGTATCTCTCCGAGCCGCTCCGACACCGGAGCTGAAA 2808
QY 103 TGAACATATTATCTGCGCAGGAGTATTAACCGAAGAAATGCGCGCAGTCTTTGG 162
DB 2809 TGAACATATTATCTGCGCAGGAGTATTAACCGAAGAAATGCGCGCAGTCTTTGG 2868
QY 163 ACAGCTGATGAGAGGATGCTGATTAATCTTCCACCTCTAGCCATTTTGAACAC 222
DB 2869 ACCAGCTGATGAGAGGATGCTGATTAATCTTCCACCTCTAGCCATTTTGAACAC 2928
QY 223 CTACCTTCACGAACTGTATGATTTTGAAGCGGCGCCCGAAGATCCACAGAGAG 282
DB 2929 CTACCTTCACGAACTGTATGATTTTGAAGCGGCGCCCGAAGATCCACAGAGAG 2988
QY 283 CGGTTTGCAGATTTTTCGCACTCTGTATGTTGGCGGTGACAGAAAGGATTAAC 342
DB 2989 CGGTTTGCAGATTTTTCGCACTCTGTATGTTGGCGGTGACAGAAAGGATTAAC 3048
QY 343 TCACCTTTTCGCGCGCGCGGTTCTCGAGCGCGCTCACCTTTCCGCGAGCCGAGC 402
DB 3049 TCACCTTTTCGCGCGCGCGGTTCTCGAGCGCGCTCACCTTTCCGCGAGCCGAGC 3108
QY 403 AGCGGAGACAGAGAGCTTGGGTCCGGTTCTATGCGCAACCTTGTACCGGAGGTATCG 462
DB 3109 AGCGGAGACAGAGAGCTTGGGTCCGGTTCTATGCGCAACCTTGTACCGGAGGTATCG 3168
QY 463 ATCTTACCTGCGCAGAGGCTGTTTCCACCCAGTGAACGAGAGATGAAGAGGTAG 522
DB 3169 ATCTTACCTGCGCAGAGGCTGTTTCCACCCAGTGAACGAGAGATGAAGAGGTAG 3228
QY 523 AGTTTGTGTAGATTATGTGAGACACCGCGGCAAGTTTGAGGTCTTGTATATAC 582
DB 3229 AGTTTGTGTAGATTATGTGAGACACCGCGGCAAGTTTGAGGTCTTGTATATAC 3288
QY 583 GAGAGATACGCGGAGACCCAGATTTATGTGTTGGCTTGTATATGAGACTGTGCA 642
DB 3289 GAGAGATACGCGGAGACCCAGATTTATGTGTTGGCTTGTATATGAGACTGTGCA 3348
QY 643 TGTGTGTACAGTAAAGTAAATTAAGGAGGTGGGTATGAGTGGTGGTGGT 702
DB 3349 TGTGTGTACAGTAAAGTAAATTAAGGAGGTGGGTATGAGTGGTGGTGGTGGT 3408
QY 703 GGTAAATTTTATTTTAAATTTTATAGTTTGTGTTTAAAGATTTTGTATGTGATTT 762
DB 3409 GGTAAATTTTATTTTAAATTTTATAGTTTGTGTTTAAAGATTTTGTATGTGATTT 3468
QY 763 TTTTAAAGTGTCTGTGTGAACTGAGCTGAGCCGAGCAGACACCGAGCTGCAAG 822
DB 3469 TTTTAAAGTGTCTGTGTGAACTGAGCTGAGCCGAGCAGACACCGAGCTGCAAG 3528
QY 823 ACCTACCGCGCTCTAAATATGCGGCTGTATCTGAGAGCGCCGACATCACTGTGTC 882

DB 3529 ACCTACCGCGCTCTAAATATGCGGCTGTATCTGAGAGCGCCGACATCACTGTGTC 3588
QY 883 TAGAAGATGCAATAGTATGATACGATACCTGATCTCCGCTCTTCTTAACACACCTCTGA 942
DB 3589 TAGAAGATGCAATAGTATGATACGATACCTGATCTCCGCTCTTCTTAACACACCTCTGA 3648
QY 943 GATACACCGGCTGTCCCGCTGTGCGCCATTAACCGAGTTGCCGTGAGATTTGGTGGCG 1002
DB 3649 GATACACCGGCTGTCCCGCTGTGCGCCATTAACCGAGTTGCCGTGAGATTTGGTGGCG 3708
QY 1003 TCGCAGGCTGTGGAATGATATGAGACTGTGCTTAACGAGCTGCGGACCTTTGGA 1062
DB 3709 TCGCAGGCTGTGGAATGATATGAGACTGTGCTTAACGAGCTGCGGACCTTTGGA 3768
QY 1063 GAGCTGTAACGCGCCGAGGCTATAGGTGTAACCTGTGATTTGCTGTGTGTTAACGCC 1122
DB 3769 GAGCTGTAACGCGCCGAGGCTATAGGTGTAACCTGTGATTTGCTGTGTGTTAACGCC 3828
QY 1123 TTTGTTGCTGATGATGATTGATGATTAATTAAGGCTGATTAATGTTTAACTTGA 1182
DB 3829 TTTGTTGCTGATGATGATTGATGATTAATTAAGGCTGATTAATGTTTAACTTGA 3888
QY 1183 TGGCGTTTAAATGAGGCGGGGCTTAAAGGATATATATGCGCGGTGATTAACCTTGGT 1242
DB 3889 TGGCGTTTAAATGAGGCGGGGCTTAAAGGATATATATGCGCGGTGATTAACCTTGGT 3948
QY 1243 TACATCTGACCTCATGAGAGCTTGGAGTGTGGAAGATTTTCTGCTGTGCTTA 1302
DB 3949 TACATCTGACCTCATGAGAGCTTGGAGTGTGGAAGATTTTCTGCTGTGCTTA 4008
QY 1303 GCTGGAACAGAGCTTAAACAGTACTTGGTTTGAAGTTTCTGTGGGCTCATCCA 1362
DB 4009 GCTGGAACAGAGCTTAAACAGTACTTGGTTTGAAGTTTCTGTGGGCTCATCCA 4068
QY 1363 GGCAAGTTAGTCTGCAAGTAAAGAGATTAACAGTGGGAATTTGAAGCTTTTGA 1422
DB 4069 GGCAAGTTAGTCTGCAAGTAAAGAGATTAACAGTGGGAATTTGAAGCTTTTGA 4128
QY 1423 ATCTGTGTGAGCTGTTTGAATCTTGAATCTTGGGTCAACAGGCGCTTTTCAAGAGAA 1482
DB 4129 ATCTGTGTGAGCTGTTTGAATCTTGAATCTTGGGTCAACAGGCGCTTTTCAAGAGAA 4188
QY 1483 GGTATCAAGCTTTGATTTTCCACACCGGGCGCGCTGCTGTGCTTTT 1542
DB 4189 GGTATCAAGCTTTGATTTTCCACACCGGGCGCGCTGCTGTGCTTTT 4248
QY 1543 GAGTTTATTAAGATTAATGAGACGAAGAAACCATCTGAGCGGGGGTACCTGCTGA 1602
DB 4249 GAGTTTATTAAGATTAATGAGACGAAGAAACCATCTGAGCGGGGGTACCTGCTGA 4308
QY 1603 TTTTCTGCGCATGATCTGTGAGAGCGGTTGTGAGACACAAGATGCGCTGACTGTT 1662
DB 4309 TTTTCTGCGCATGATCTGTGAGAGCGGTTGTGAGACACAAGATGCGCTGACTGTT 4368
QY 1663 GTCTTCCGTCCGCGCGCATTAATCCGACGAGAGACAGACAGACAGAGAGAGAGC 1722
DB 4369 GTCTTCCGTCCGCGCGCATTAATCCGACGAGAGACAGACAGAGAGAGAGAGC 4428
QY 1723 CAGCGCGCGGCGAGAGAGAGAGCCCATGGAACCGAGAGCGGCGCTGAGCCCTCGGGA 1782
DB 4429 CAGCGCGCGGCGAGAGAGAGAGCCCATGGAACCGAGAGCGGCGCTGAGCCCTCGGGA 4488
QY 1783 ATGAATGTTTGAAGTGTGATCTGATCCAGAACTGAGACGCAATTTTGA 1842
DB 4489 ATGAATGTTTGAAGTGTGATCTGATCCAGAACTGAGACGCAATTTTGA 4548
QY 1843 GAGGATGAGGAGGAGGCTTAAAGGAGGCTTAAAGGAGGAGGAGGAGGCTTGTGAGCTACAGAG 1902
DB 4549 GAGGATGAGGAGGAGGCTTAAAGGAGGCTTAAAGGAGGAGGAGGAGGCTTGTGAGCTACAGAG 4608
QY 1903 GAGGCTAGAAATCTAGCTTTTATGCTTAATGACAGACACGCTCTGAGTATTA 1962
DB 4609 GAGGCTAGAAATCTAGCTTTTATGCTTAATGACAGACACGCTCTGAGTATTA 4668

```

Oy 1963 CAACAGATCAAGGATTAATTGGCTTAATGAGCTTGAATCTGGCGGACAGATATTCCATA 2022
Db 4669 CAACGATCAAGGATTAATTGGCTTAATGAGCTTGAATCTGGCGGACAGATATTCCATA 4728
Oy 2023 GAGCAGCTGACCACTTACTGCTGAGCCAGGAGGATGATTTTGAAGAGGCTATTAGGCTA 2082
Db 4729 GAGCAGCTGACCACTTACTGCTGAGCCAGGAGGATGATTTTGAAGAGGCTATTAGGCTA 4788
Oy 2083 TATGCAAGGCTGACCTTATAGCCAGATTTGCAAGTCAAGATCAGCAAACTTGTAATATC 2142
Db 4789 TATGCAAGGCTGACCTTATAGCCAGATTTGCAAGTCAAGATCAGCAAACTTGTAATATC 4848
Oy 2143 AGGATTTGCTCATTTCTGGGAAAGGAGCCGAGGAGTGAATGATTAAGGAGGATAGG 2202
Db 4849 AGGATTTGCTCATTTCTGGGAAAGGAGCCGAGGAGTGAATGATTAAGGAGGATAGG 4908
Oy 2203 GTGGCTTTAGATGATGATGATTAATATATGAGCCGAGGAGTGTCTTGGCATGAGCGGGTG 2262
Db 4909 GTGGCTTTAGATGATGATGATTAATATATGAGCCGAGGAGTGTCTTGGCATGAGCGGGTG 4968
Oy 2263 GTTATTATGAATGTAAGGTTTACTGAGCCCAATTTTACGGGTACGGTTTCTTGGCCAT 2322
Db 4969 GTTATTATGAATGTAAGGTTTACTGAGCCCAATTTTACGGGTACGGTTTCTTGGCCAT 5028
Oy 2323 ACCAACCCTTATCTTACAGAGGTGTAAGCTTCTATGGGTTTAACAATACCTGATGGAAGCC 2382
Db 5029 ACCAACCCTTATCTTACAGAGGTGTAAGCTTCTATGGGTTTAACAATACCTGATGGAAGCC 5088
Oy 2383 TGAACCGATGTAAGGTTTCTGGGAGTGTGCTTCTTAACTGCTGTGAAAGGAGGTGTGT 2442
Db 5089 TGAACCGATGTAAGGTTTCTGGGAGTGTGCTTCTTAACTGCTGTGAAAGGAGGTGTGT 5148
Oy 2443 CGCCCCCAAAAGCAGAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTAACCTTGGGTATC 2502
Db 5149 CGCCCCCAAAAGCAGAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTAACCTTGGGTATC 5208
Oy 2503 CTGCTGAGGGTAACTCCAGAGGTGCGCACAATGAGGCTCCGACTGTGTTGCTTCACTG 2562
Db 5209 CTGCTGAGGGTAACTCCAGAGGTGCGCACAATGAGGCTCCGACTGTGTTGCTTCACTG 5268
Oy 2563 CTAGTGAAGAAAGCGTGTGATTAAGCATTAACATGATGATGAGCACTGCGAGGACAGG 2622
Db 5269 CTAGTGAAGAAAGCGTGTGATTAAGCATTAACATGATGATGAGCACTGCGAGGACAGG 5328
Oy 2623 GCCTCTCAGATGCTGACCTGCTCGGACGCAACGTGTCACTGCTGAAGACATTCACGTA 2682
Db 5329 GCCTCTCAGATGCTGACCTGCTCGGACGCAACGTGTCACTGCTGAAGACATTCACGTA 5388
Oy 2683 GCCAGCCACTCTCGCAAGGCTGAGCACTGTTTGAAGCATTAACATTAACCCGCTGTCC 2742
Db 5389 GCCAGCCACTCTCGCAAGGCTGAGCACTGTTTGAAGCATTAACATTAACCCGCTGTCC 5448
Oy 2743 TTGCATTTGGGTAAACAGAGGAGGAGGTGTTCTTACCTTAACAATGCAATTTGATCACT 2802
Db 5449 TTGCATTTGGGTAAACAGAGGAGGAGGTGTTCTTACCTTAACAATGCAATTTGATCACT 5508
Oy 2803 AAGATATTGCTTGAAGCCGAGAGCATGTCCTCAAGGTGAACCTGAACGGGCTTTTGAACATG 2862
Db 5509 AAGATATTGCTTGAAGCCGAGAGCATGTCCTCAAGGTGAACCTGAACGGGCTTTTGAACATG 5568
Oy 2863 ACCATGAAGATCTGGAAGGTCTGAGTACATGAGACCCGCAACAGGCTGACAGCCCTGC 2922
Db 5569 ACCATGAAGATCTGGAAGGTCTGAGTACATGAGACCCGCAACAGGCTGACAGCCCTGC 5628
Oy 2923 GAGTGTGCGGTAAACATATTAGAACAGGCTGTGATGCTGATGATGACGAGAGAGCTG 2982
Db 5629 GAGTGTGCGGTAAACATATTAGAACAGGCTGTGATGCTGATGATGACGAGAGAGCTG 5688
Oy 2983 AGGCCCGATCACTTGGTGTCTGCGCAGCCGCGTGAAGTTGGTCTTAAGGATGAAGAT 3042
Db 5689 AGGCCCGATCACTTGGTGTCTGCGCAGCCGCGTGAAGTTGGTCTTAAGGATGAAGAT 5748

```

```

Oy 3043 ACAGATTGAG 3052
Db 5749 ACAGATTGAG 5758

RESULT 15
ACCT0006
ID ACC70006 standard; cDNA; 3408 BP.
XX
AC ACC70006;
XX
DT 29-JUL-2003 (first entry)
XX
DE Nucleotide sequence of the E1a protein of human adenovirus type 5.
XX
KW Cancer; hyperproliferative disorder; viral vector; H19 promoter;
KW carcinoma; sarcoma; adenoma; ganglioblastoma; bladder carcinoma; E1a;
KW gene; 88.
XX
OS Human adenovirus type 5.
XX
Key Location/Qualifiers
FH 44..1029
FT /*tag= a
FT /product= "E1a protein"
FT /note= "contains an intron"
FT 44..598
FT /*tag= b
FT /number= 1
FT intron 599..714
FT /*tag= c
FT /number= 1
FT exon 715..1026
FT /*tag= d
FT /number= 2
PN MO2003035883-A2.
XX
PD 01-MAY-2003.
XX
PF 22-OCT-2002; 2002MO-IL000843.
XX
PR 22-OCT-2001; 2001US-00012131.
XX
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI Hochberg A, Ayesh S;
XX
DR WPI; 2003-441263/41.
XX
DR P-PSDB; ABR55301.
XX
PT Treating cancer or hyperproliferative disorder comprises administering a
PT conditionally replicative viral vector, where the viral nucleic acid
PT encoding a product essential for its replication is operably linked to
PT H19 regulatory sequence.
XX
PS Example; Fig 7; 122pp; English.
XX
CC The specification describes a method of treating cancer or
CC hyperproliferative disorders. The method comprises administering a
CC conditionally replicative viral vector, where at least one of the viral
CC nucleic acids encoding a product essential for its replication is
CC operably linked to an H19 regulatory sequence. The method is useful for
CC treating cancer or hyperproliferative disorders. The cancer is selected
CC from many different types, for example, carcinoma, sarcoma, adenoma and
CC ganglioblastoma. Preferably, the cancer is bladder carcinoma. The present
CC sequence encodes the E1a protein of human adenovirus type 5. It was
CC linked to a H19 regulatory sequence, and used to produce vectors for use
CC in the method of the invention
XX
SQ Sequence 3408 BP; 767 A; 764 C; 1007 G; 870 T; 0 U; 0 Other;

```

Query Match

98.1%; Score 2994; DB 9; Length 3408;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 GTAGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGACTGAAATGAGACATATTATCTG 118
Db 1 GTAGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGACTGAAATGAGACATATTATCTG 60
QY 119 CCAGGAGGTGTTATTAACGAGAAATGCGCCGCTCTTTTGGACCAAGCTGATGGAAGA 178
Db 61 CCAGGAGGTGTTATTAACGAGAAATGCGCCGCTCTTTTGGACCAAGCTGATGGAAGA 120
QY 179 GGTACTGCTGATTAATCTTCACTCTAGACATTTTGAACCACTTACCTTACAGAACT 238
Db 121 GGTACTGCTGATTAATCTTCACTCTAGACATTTTGAACCACTTACCTTACAGAACT 180
QY 239 GTATGATTTAGACGTGACGCGCCCGGAGAGTCCAAACGAGAGGCGTTTGGCAGATTTT 298
Db 181 GTATGATTTAGACGTGACGCGCCCGGAGAGTCCAAACGAGAGGCGTTTGGCAGATTTT 240
QY 299 TCCGACCTCTGTAATGTTGGCGGTGACAGAAAGGATTTGACTTACTACTTTTCCGCGGC 358
Db 241 TCCGACCTCTGTAATGTTGGCGGTGACAGAAAGGATTTGACTTACTACTTTTCCGCGGC 300
QY 359 GCCCGGTTCTCCGAGCCGCTCACCTTTCCCGGAGCCCGAGCAGCCGAGCAGAGAGC 418
Db 301 GCCCGGTTCTCCGAGCCGCTCACCTTTCCCGGAGCCCGAGCAGCCGAGCAGAGAGC 360
QY 419 CTGGGTCGCGTTTCTGATGCAAACTTGTATCGGAGGTGATGATCTTACCTGACAGA 478
Db 361 CTGGGTCGCGTTTCTGATGCAAACTTGTATCGGAGGTGATGATCTTACCTGACAGA 420
QY 479 GGTCTGGCTTTTCCACCGATGACGAGAGATGAAAGGTTGAGGATTTGTGTAGATTA 538
Db 421 GGTCTGGCTTTTCCACCGATGACGAGAGATGAAAGGTTGAGGATTTGTGTAGATTA 480
QY 539 TGTGAGACACCCCGGAGCAGGTTGACAGGCTTGTCAATTACACCGAGAAATACGGGAGA 598
Db 481 TGTGAGACACCCCGGAGCAGGTTGACAGGCTTGTCAATTACACCGAGAAATACGGGAGA 540
QY 599 CCCAGATATATGTTGCTTGTCTATATGAGACCTGTGAGCATGTTGTCTACAGTAA 658
Db 541 CCCAGATATATGTTGCTTGTCTATATGAGACCTGTGAGCATGTTGTCTACAGTAA 600
QY 659 GTGAAATTAATGAGGAGTGGGTGATGAGAGTGGGTTGGTGTGTATTTTATTTT 718
Db 601 GTGAAATTAATGAGGAGTGGGTGATGAGAGTGGGTTGGTGTGTATTTTATTTT 660
QY 719 ATTTTACAGTTTGTGTTTAAAGATTTTGTATTTGATTTTAAAGGTCGCTG 778
Db 661 ATTTTACAGTTTGTGTTTAAAGATTTTGTATTTGATTTTAAAGGTCGCTG 720
QY 779 TCTGAACCTGAGCCGAGCCCGAGCCGAGACCGAGCCGTCGAAAGACTTACCGCGCTCT 838
Db 721 TCTGAACCTGAGCCGAGCCCGAGCCGAGACCGAGCCGTCGAAAGACTTACCGCGCTCT 780
QY 839 AAAATGCGGCTGCTATCTTGAAGACCCCGACATCACTGTGTCTAGAGATGCAATGT 898
Db 781 AAAATGCGGCTGCTATCTTGAAGACCCCGACATCACTGTGTCTAGAGATGCAATGT 840
QY 899 AGTACGATAGCTGATGATCTCGGTCCTTCTAACACACCTGAGAGATACACCGGTCGTC 958
Db 841 AGTACGATAGCTGATGATCTCGGTCCTTCTAACACACCTGAGAGATACACCGGTCGTC 900
QY 959 CCGGCTGCCCCATTAACCAAGTTGCGGTGAGAGTTGTTGGCGCTGCGCAGAGCTGTGAA 1018
Db 901 CCGGCTGCCCCATTAACCAAGTTGCGGTGAGAGTTGTTGGCGCTGCGCAGAGCTGTGAA 960
QY 1019 TGTATCGAGACTTGTCTTAAGAGGCTGGGCAACTTTGAGACTTGAAGCTGTTAAACGCCCC 1078
Db 961 TGTATCGAGACTTGTCTTAAGAGGCTGGGCAACTTTGAGACTTGAAGCTGTTAAACGCCCC 1020
QY 1079 AGGCCATAGAGTGTAAACCTGTGATTTGGGTGTGTTAAAGCCCTTTGTTGAGATGA 1138
Db 1138 AGGCCATAGAGTGTAAACCTGTGATTTGGGTGTGTTAAAGCCCTTTGTTGAGATGA 1080

Db 1021 AGGCCATAGAGTGTAAACCTGTGATTTGGGTGTGTTAAAGCCCTTTGTTGAGATGA 1080
QY 1139 GTTATGTAAAGTTTAAATTAAGAGGTGAGATTAATGTTTAACTTGCATGCGGTGTTAATGGG 1198
Db 1081 GTTATGTAAAGTTTAAATTAAGAGGTGAGATTAATGTTTAACTTGCATGCGGTGTTAATGGG 1140
QY 1199 GCGGGGCTTAAAGGATATTAATGCGCGGTGGCTAATCTTGGTTACATCTGACTCATG 1258
Db 1141 GCGGGGCTTAAAGGATATTAATGCGCGGTGGCTAATCTTGGTTACATCTGACTCATG 1200
QY 1259 GAGGCTGGAGGTGTTGGAAGATTTTCTGTGCGTAACTTGTCTGGAACAGAGCTCT 1318
Db 1201 GAGGCTGGAGGTGTTGGAAGATTTTCTGTGCGTAACTTGTCTGGAACAGAGCTCT 1260
QY 1319 AACAGTACCTTGTGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAAGTTAGTCTGC 1378
Db 1261 AACAGTACCTTGTGTTTGGAGGTTTCTGTGGGCTCATCCAGGCAAAAGTTAGTCTGC 1320
QY 1379 AGAATTAAGAGATTTACAAATGAGGAAATTTGAAGAGCTTTGAAATCCTGTGTGAGCTG 1438
Db 1321 AGAATTAAGAGATTTACAAATGAGGAAATTTGAAGAGCTTTGAAATCCTGTGTGAGCTG 1380
QY 1439 TTTGATTTCTTGAATCTGAGTCAACAGGCGCTTTTCCAGAGAAAGTCAACAGCTTTC 1498
Db 1381 TTTGATTTCTTGAATCTGAGTCAACAGGCGCTTTTCCAGAGAAAGTCAACAGCTTTC 1440
QY 1499 GATTTTTCACACCGGGCGGCTGCGGCTGCTGTGCTTTTGTGATTTTAAAGAT 1558
Db 1441 GATTTTTCACACCGGGCGGCTGCGGCTGCTGTGCTTTTGTGATTTTAAAGAT 1500
QY 1559 AAATGAGCCGAAAGAAACCATCTGAGCGGGGGGTACCTGCTGATTTTCTGCGCATGAT 1618
Db 1501 AAATGAGCCGAAAGAAACCATCTGAGCGGGGGGTACCTGCTGATTTTCTGCGCATGAT 1560
QY 1619 CTGTGAGAGCGGTTGTGAGACAAAGATGCGCTGACTGTGTCTTCCGTCGCGCCG 1678
Db 1561 CTGTGAGAGCGGTTGTGAGACAAAGATGCGCTGACTGTGTCTTCCGTCGCGCCG 1620
QY 1679 GCGATTAATCCGACGAGAGAGCAGACAGCAGAGAGAGAGCAGCGCGGCGGCGAG 1738
Db 1621 GCGATTAATCCGACGAGAGAGCAGACAGCAGAGAGAGAGCAGCGCGGCGGCGAG 1680
QY 1739 GAGCAGAGCCCATGAGAACCCGAGAGCCGCTGAGACCTTGGGGAATGAATTTTCAAG 1798
Db 1681 GAGCAGAGCCCATGAGAACCCGAGAGCCGCTGAGACCTTGGGGAATGAATTTTCAAG 1740
QY 1799 TGCGTGAACCTGATCCAGAACTGAGACGCAATTTTGAACAATTAACAGAGATGGGAGGCG 1858
Db 1741 TGCGTGAACCTGATCCAGAACTGAGACGCAATTTTGAACAATTAACAGAGATGGGAGGCG 1800
QY 1859 TAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTTAGAATCTAG 1918
Db 1801 TAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTTAGAATCTAG 1860
QY 1919 CTTTACCTTAATGACAGACACCTGCTGAGTATTTACTTTTCAACAGATCAAGATA 1978
Db 1861 CTTTACCTTAATGACAGACACCTGCTGAGTATTTACTTTTCAACAGATCAAGATA 1920
QY 1979 ATTGCGCTAATGACCTTGATCTGCTGGGCGAGAGTATTCATAGAGAGCTGACCACTT 2038
Db 1921 ATTGCGCTAATGACCTTGATCTGCTGGGCGAGAGTATTCATAGAGAGCTGACCACTT 1980
QY 2039 ACTGCTGACAGCCAGGGAGTATTTTGAAGAGCTATTAAGGATATGCAAGGTGAC 2098
Db 1981 ACTGCTGACAGCCAGGGAGTATTTTGAAGAGCTATTAAGGATATGCAAGGTGAC 2040
QY 2099 TTAGCCAGATTTGCAATGACAGATCAAGCAACTTGTAAATATAGAGATTTGTGCTACA 2158
Db 2041 TTAGCCAGATTTGCAATGACAGATCAAGCAACTTGTAAATATAGAGATTTGTGCTACA 2100
QY 2159 TTTCTGGGAACGCGGGCGAGGTGAGATGATACAGAGAGATAGGAGTGGCTTTTGAATGTA 2218
Db 2101 TTTCTGGGAACGCGGGCGAGGTGAGATGATACAGAGAGATAGGAGTGGCTTTTGAATGTA 2160

QY	2219	GCATGATTAATATATGCGCGGGGGTCTGGGCATGAGACGGGTATGTTATTAATGATTA	2278
Dp	2161	GCATGATTAATATATGCGCGGGGGTCTGGGCATGAGACGGGTATGTTATTAATGATTA	2220
QY	2279	GGTTTACTGCGCCCAATTTTAGCGGTACGATTTTCTGGCCAAATACCAACCTTATCTTAC	2338
Dp	2221	GGTTTACTGCGCCCAATTTTAGCGGTACGATTTTCTGGCCAAATACCAACCTTATCTTAC	2280
QY	2339	ACGGGTATACGTTCTATAGGGTTTAAACAATACCTGTGTGGAGACCTTGACCCGATATAGGG	2398
Dp	2281	ACGGGTATACGTTCTATAGGGTTTAAACAATACCTGTGTGGAGACCTTGACCCGATATAGGG	2340
QY	2399	TTCCGGGGCTGTGCTTTTATCTGCTGTGGAGAGGGGGTGTGTGTGCGCCCAAAAGCAGGG	2458
Dp	2341	TTCCGGGGCTGTGCTTTTATCTGCTGTGGAGAGGGGGTGTGTGTGCGCCCAAAAGCAGGG	2400
QY	2459	CTTCAATTTAAGAAATGCTCTTTTGAAGAGTATACCTTGGGTATCTCTGTCTGAGGGTAACT	2518
Dp	2401	CTTCAATTTAAGAAATGCTCTTTTGAAGAGTATACCTTGGGTATCTCTGTCTGAGGGTAACT	2460
QY	2519	CCAGGGTCCGCCACAATGTGGCTTCCGACTGTGTGTGTTTCAATCTATGTAAGACGCTGG	2578
Dp	2461	CCAGGGTCCGCCACAATGTGGCTTCCGACTGTGTGTGTTTCAATCTATGTAAGACGCTGG	2520
QY	2579	CTGTGATTTAACATTAACAATGTGATGTGGCAACTGCGAGAGCAGGGCCTCTCAGATGTCTGA	2638
Dp	2521	CTGTGATTTAACATTAACAATGTGATGTGGCAACTGCGAGAGCAGGGCCTCTCAGATGTCTGA	2580
QY	2639	CTGTGCTGCGACGGCAACTGTCACTGTGTGAGAGCACTTACAGTATGCCAGCACTCTGTGCA	2698
Dp	2581	CTGTGCTGCGACGGCAACTGTCACTGTGTGAGAGCACTTACAGTATGCCAGCACTCTGTGCA	2640
QY	2699	AGGCTGTGGCCAGTGTTTGAGCATTAACAATGACACCGCTGTTCCTGTGATTTGGGTAAACA	2758
Dp	2641	AGGCTGTGGCCAGTGTTTGAGCATTAACAATGACACCGCTGTTCCTGTGATTTGGGTAAACA	2700
QY	2759	GGAGGGGGGTGTCTCTACCTTACCAATGCAATTTGAGTCAACATTAAGTATATTTGCTTGAGC	2818
Dp	2701	GGAGGGGGGTGTCTCTACCTTACCAATGCAATTTGAGTCAACATTAAGTATATTTGCTTGAGC	2760
QY	2819	CCGAGAGCATGTCTCAAGGTGAACCTTGAAACGGGGGTTTTGACATGACCATTAAGATCTTGA	2878
Dp	2761	CCGAGAGCATGTCTCAAGGTGAACCTTGAAACGGGGGTTTTGACATGACCATTAAGATCTTGA	2820
QY	2879	AGGTGCTCAGGTACGATAGACCCGCAACAAGTGTGACACTGTGACAGTGTGCGCGTAAAC	2938
Dp	2821	AGGTGCTCAGGTACGATAGACCCGCAACAAGTGTGACACTGTGACAGTGTGCGCGTAAAC	2880
QY	2939	ATATTTAGGAACCAAGCTGTGATGCTGTGATGTGACCGAGAGACTGAGGCCGATCACTTTGG	2998
Dp	2881	ATATTTAGGAACCAAGCTGTGATGCTGTGATGTGACCGAGAGACTGAGGCCGATCACTTTGG	2940
QY	2999	TGCTGCGCTCTGACCCGCGCTAGTGTGGCTCTTACGATGAAGAGTACAGATTTGAG	3052
Dp	2941	TGCTGCGCTCTGACCCGCGCTAGTGTGGCTCTTACGATGAAGAGTACAGATTTGAG	2994

Search completed: October 28, 2005, 02:58:45
Job time : 1498 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 28, 2005, 02:07:07 ; Search time 8768 Seconds
(without alignments)
13249.561 Million cell updates/sec

Title: US-10-790-562-33

Sequence: 1 cggctactgctcttatacc.....cgatgaagatcacagatcgag 3052

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: gb_est1.*
2: gb_est2.*
3: gb_hlc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gse1.*
9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	615.8	20.2	648	4	BM655780	170006873
2	615.6	20.2	766	6	CD742927	UI-H-FT1
3	607	19.9	750	6	CD370352	UI-H-FT1
4	592.8	19.4	625	7	CK624194	ml18c08.Y
5	587.4	19.2	743	6	CA306892	UI-H-FT1
6	573	18.8	726	6	CA307899	UI-H-FT1
7	460	15.1	602	6	CD370856	UI-H-FT1
8	335.4	11.0	337	2	BM591710	170006870
9	249.8	8.2	347	2	BF915148	IL3-UT011
10	224.2	7.3	323	2	BF914577	IL3-UT011
11	223.8	7.3	321	2	BF915126	IL3-UT011
12	222.4	7.3	741	6	CD366021	UI-H-FT1
13	173.6	5.7	667	6	CD742922	UI-H-FT2
14	167	5.5	661	6	CD365243	UI-H-FT2
15	162	5.3	173	4	BM600614	170006877
16	131.8	4.3	229	2	BF915892	IL3-UT011
17	100.8	3.3	198	2	BP914321	IL3-UT011
18	50.2	1.6	884	9	CNS00600	Protophila
19	48.6	1.6	942	9	CNS00601	Protophila
20	48.2	1.6	940	9	CNS03004	AL255325
21	47.6	1.6	1101	9	CNS00100	Tetradodon
22	47.2	1.5	732	7	CK305430	Protophila
23	46.8	1.5	1220	6	CD504965	SB02029B1
24	46.6	1.5	1032	9	CU505993	CDA71-A08 SATL_759_

25	46.4	1.5	519	4	BM439574
26	46.2	1.5	1101	9	CNS017M2
27	46	1.5	670	9	CNS04K72
28	46	1.5	807	9	CNS0128R
29	46	1.5	1511	9	CG753350
30	45.8	1.5	662	5	BU303489
31	45.8	1.5	891	5	BU842949
32	45.6	1.5	556	9	CR335545
33	45.6	1.5	1003	9	CNS017UQ
34	45.6	1.5	1042	9	CNS0039B
35	45.4	1.5	922	9	CNS0073M
36	45.4	1.5	1101	9	CNS00LT2
37	45	1.5	861	9	CNS0075A
38	45	1.5	1098	9	CNS015EM
39	45	1.5	1101	9	CNS000D1
40	44.8	1.5	564	9	CNS01711
41	44.8	1.5	768	7	CK306519
42	44.6	1.5	455	2	BE208710
43	44.6	1.5	713	9	AG506778
44	44.6	1.5	939	9	CNS00CNG
45	44.6	1.5	1101	9	CNS0100X

ALIGNMENTS

RESULT 1
BM655780 648 bp mRNA linear EST 26-FEB-2002
LOCUS 17000687386917 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION 19600449669374 5', mRNA sequence.
ACCESSION BM655780
VERSION BM655780.1 GI:18955291
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anophelinae;
1 (bases 1 to 648)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
JOURNAL Unpublished (2002)
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: N001004A9S row: M column: 20
Seq primer: M13 Reverse.
FEATURES
source location/Qualifiers
1..648
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
/clone="19600449669374"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_id="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
ORIGIN
Query Match 20.2%; Score 615.8; DB 4; Length 648;
Best Local Similarity 97.7%; Pred. No. 5.4e-157;

Matches	636;	Conservative	0;	Mismatches	12;	Indels	3;	Gaps	1;
Qy	1126	GTTTGCTGAATGAGTTGATGTAATTAATAAGGGTGAATATGTTTAACTTGATCG							1185
Db	1	GTTTGCTGAATGAGTTGATGTAATTAATAAGGGTGAATATGTTTAACTTGATCG							60
Qy	1186	CGTGTAAATGAGGGGGCTTTAAAGGATTAATATATGCGCGTGGCTTAATCTGGTTAC							1245
Db	61	CGTGTAAATGAGGGGGCTTTAAAGGATTAATATATGCGCGTGGCTTAATCTGGTTAC							120
Qy	1246	ATTCGACCTCATGAGAGCTTGGAGAGTGTGTTGGAAGATTTTCTGCTGTCGCTAACTTGCT							1305
Db	121	ATTCGACCTCATGAGAGCTTGGAGAGTGTGTTGGAAGATTTTCTGCTGTCGCTAACTTGCT							180
Qy	1306	GGAACAGAGCTCTTAACAGTACTCTTGTTGTTGAGGTTTCTGCGGGCTCATCCAGGC							1365
Db	181	GGAACAGAGCTCTTAACAGTACTCTTGTTGTTGAGGTTTCTGCGGGCTCATCCAGGC							240
Qy	1366	AAAGTTAGTCTGCAATTAAGAGGATTAACAGTGGGAATTTGAGAGCTTTGGAATC							1425
Db	241	AAAGTTAGTCTGCAATTAAGAGGATTAACAGTGGGAATTTGAGAGCTTTGGAATC							300
Qy	1426	CTGTGTGAGCTGTTTGAATCTTGAATCTGGTCAACAGGCGCTTTTCAAGAGAAAGT							1485
Db	301	CTGTGTGAGCTGTTTGAATCTTGAATCTGGTCAACAGGCGCTTTTCAAGAGAAAGT							360
Qy	1486	CATCAAGCTTTGATTTTTCACACCGGGGCGGCTGCGCTGTGTTGCTTTTGTAG							1545
Db	361	CATCAAGCTTTGATTTTTCACACCGGGGCGGCTGCGCTGTGTTGCTTTTGTAG							420
Qy	1546	TTTATATAAGATTAATGAGCGAAGAAACCATGTGAGCGGGGGTACCTGTGATTT							1605
Db	421	TTTATATAAGATTAATGAGCGAAGAAACCATGTGAGCGGGGGTACCTGTGATTT							480
Qy	1606	TCTGGCCATGATCTGTGAGAGCGGTTGTGAGACACAGAATCGCTTACTTGTGTC							1665
Db	481	TCTGGCCATGATCTGTGAGAGCGGTTGTGAGACACAGAATCGCTTACTTGTGTC							540
Qy	1666	TTCCGTCGCGCCCGGATTAATACCGAGAGAGAGACAGACAGACAGAGAAACCG							1725
Db	541	TTCCGTCGCGCCCGGATTAATACCGAGAGAGAGAGACAGACAGACAGAGAAACCG							597
Qy	1726	GCGGCGGCGGAG							1776
Db	598	GCGGCGGCGGAG							648

FEATURES	source
location/Qualifiers	
1..766	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="UI-H-FT1-Bka-m-09-0-UI"	
/tissue_type="Alveolar Macrophage"	
/dev_stage="Adult"	
/lab_host="DH10B (Life Technologies)"	
/clone_lib="NCI-CGAP FT1"	
/note="Organ: Lung; Vector: pFTT3-Pac (Pharmacia) with a modified polylinker; Site 1: Bcl I; Site 2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The RNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions). The RNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; we adenovirus moi 500, 3 hours; we adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; we adenovirus + LPS 3 hours; we adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Bcl I adaptor, digested with Not I, and cloned directionally into the pFTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dfr)18 tail. The sequence tag for this library is GGCATGCGG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.	
TAG_LIB=UI-H-FT1	
TAG_LIB=Human Lung Alveolar Macrophage	
TAG_SEQ=GGCCATGCGG"	
ORIGIN	
Query Match	20.2%; Score 615.6; DB 6; Length 766;
Best Local Similarity	85.9%; Pred. No. 6.4e-157;
Matches 744;	Conservative 0; Mismatches 6; Indels 116; Gaps 1;
Qy	311 AATGTGGCGTGAGAGAGGATTAATTAATCTTTCGCGGAGCCGGTTCTCC
Db	766 AATGTGGCGTGAGAGAGGATTAATTAATCTTTCGCGGAGCCGGTTCTCC
Qy	371 GAGACCGCTTCACCTTTTCCGGAGCCCGAGACAGCGAGAGAGAGAGAGAGAG
Db	706 GAGACCGCTTCACCTTTTCCGGAGCCCGAGAGCGAGAGAGAGAGAGAGAG
Qy	431 TTCTATGCCAACTTTTACCGAGGATGATCTTAACCTTCCAGAGAGTGGCTTCC
Db	646 TTCTATGCCAACTTTTACCGAGGATGATCTTAACCTTCCAGAGAGTGGCTTCC
Qy	491 ACCAGTGAAGAGAGATGAAGAGGAGGAGGTTGTGTTAGATTATGAGACACC
Db	586 ACCAGTGAAGAGAGATGAAGAGGAGGAGGTTGTGTTAGATTATGAGACACC
Qy	551 CGGCGACGGTTGACAGTCTTGTCTATTATCACCGAGAGAAATACGGGGAGACCA
Db	526 CGGCGACGGTTGACAGTCTTGTCTATTATCACCGAGAGAAATACGGGGAGACCA

Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
 Seq primer: M13 FORWARD
 POLYA=Yes.

Qy	611	GTGTTGCTTTGCTATATAGAGAACCTGTGGGATGTTTGCTACAGTAAAGTAAATATAG	670
Db	466	GTGTTCCGCTTTGCTATATAGAGAACCTGTGGGATGTTTGCTACAGTAAAGTAAATATAG	423
Qy	671	GGCAGTGGGTATAGAGTGTGGGTTTGGTGTGTAATTTTTTTTAATTTTACAGTT	730
Db	422	-----	423
Qy	731	TTGTGCTTTAAGAAATTTTGTATTTGTATTTTTTTTAAAAAGTCCTGTGTCTGAACCTGAG	790
Db	422	----- -GTCTGTGTCTGAACCTGAG	403
Qy	791	CCTGAGCCCGAGCCGAGAACCGGAGCCTGCAAGACCTACCGCGCGCTCAAAATGGCGCT	850
Db	402	CTTGAAGCCCGAGCCGAGAACCGGAGCCTGCAAGACCTACCGCGCGCTCAAAATGGCGCT	343
Qy	851	GCTATCTCTGAGACGGCCGACATCACTGTGTCTAGAGATGCAATAGTAGTACGGATAGC	910
Db	342	GCTATCTCTGAGACGGCCGACATCACTGTGTCTAGAGATGCAATAGTAGTACGGATAGC	283
Qy	911	TGTGATCTCCGGTCCTTTTAAACACACCTTCTTGAGATACACCGGTGTGTCGCTGTGCCCC	970
Db	282	TGTATCTCCGGTCCTTTTAAACACACCTTCTTGAGATACACCGGTGTGTCGCTGTGCCCC	223
Qy	971	ATTAAACACAGTTGCGGTGAGAGTTGTGTGGGGGTGSCAGGCTGTGAGATGTATGAGAAC	1030
Db	222	ATTAAACACAGTTGCGGTGAGAGTTGTGTGGGGGTGSCAGGCTGTGAGATGTATGAGAAC	163
Qy	1031	TTGCTTAAACGAGCCTGTGGCAACTTTGAGACTTGAACGCCCCAGGCCATTAAGT	1090
Db	162	TTGCTTAAACGAGCCTGTGGCAACTTTGAGACTTGAACGCCCCAGGCCATTAAGT	103
Qy	1091	GTAAACCTGTGATTCGCTGTGTGTTAACGSCCTTTGTTGCTGAATGAGTTGATGAAGT	1150
Db	102	GTAAACCTGTGATTCGCTGTGTGTTAACGSCCTTTGTTGCTGAATGAGTTGATGAAGT	43
Qy	1151	TTAATTAAGGCTGAGATTAATGTTTAA	1176
Db	42	TTAATTAAGGCTGAGATTAATGTTTAA	17

```

RESULT 3
LOCUS CD370352/c
DEFINITION UT-H-FT1-bkb-j-17-0-UI .g1 NCI CGAP_FTI Homo sapiens CDNA clone
ACCESSION CD370352
VERSION CD370352
KEYWORDS CD370352.1 GI:31154442
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
COMMENT 1 (bases 1 to 750)
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
COMMENT Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
COMMENT Email: CGAPbs-rc@mail.nih.gov
COMMENT Tissue Procurement: Dr. Gary W. Hummingsake, U of I
COMMENT CDNA library preparation: Dr. M. Bento Soares, University of Iowa
COMMENT CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
COMMENT DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
COMMENT CDNA Distribution: Distribution Information can be found at
COMMENT http://genome.uiowa.edu/distribution/cgap.html
COMMENT Seq primer: M13 FORWARD
FEATURES
SOURCE POLYA=yes.
location/Qualifiers
1..750
/organism="Homo sapiens"
/mol_type="mRNA"

```

/db_xref="taxon:9606"
 /clone="UI-H-Frt1-bkb-j-17-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP FPI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/mL, 3 hours; LPS 100 ng/mL, 24 hours; PMA 10 ng/mL, 3 hours; PMA 10 ng/mL, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG_TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-Frt1
 TAG_SEQ=GGCCATGCCG"

Query Match	19.9%	Score 607	DB 6	Length 750
Best Local Similarity	86.2%	Pred. No. 1, 4e-154		
Matches 733	Conservative 0	Mismatches 1	Indels 116	Gaps 1
QY	327	GAAAGGATTGACTTACTGACTTTTCCGCGCGCGCCGGTTCTCCGAGCGGCTGACTT	386	
Db	750	GAAAGGATTGACTTACTGACTTTTCCGCGCGCGCCGGTTCTCCGAGCGGCTGACTT	691	
QY	387	TCCCGGCAAGCCGAGCAGCGCCGAGCAGAGGCGTTGGGTCCGGTTCTATGCCAAACCTT	446	
Db	690	TCCCGGCAAGCCGAGCAGCGCCGAGCAGAGGCGTTGGGTCCGGTTCTATGCCAAACCTT	631	
QY	447	GTAACGGAGGTGATTCGACTTTACCTGCGACGAGGCTGGCTTTCACCCAGTGAAGAGAG	506	
Db	630	GTAACGGAGGTGATTCGACTTTACCTGCGACGAGGCTGGCTTTCACCCAGTGAAGAGAG	571	
QY	507	GATGAAGAAGGTGAGGAGCTTTGTGTGATTAATGTGAGACACCCCGGACAGGTTGCAGG	566	
Db	570	GATGAAGAAGGTGAGGAGCTTTGTGTGATTAATGTGAGACACCCCGGACAGGTTGCAGG	511	
QY	567	TCTTGTCAATATGACCGGAGGAATACGGGGGAGCCAGATTTATATGTGTGGCTTGGCTAT	626	
Db	510	TCTTGTCAATATGACCGGAGGAATACGGGGGAGCCAGATTTATATGTGTGGCTTGGCTAT	451	
QY	627	ATGAGGACCTGTGGCATGTTTGTCTACAGTAAGTGAATAATATGGGCGAGTGGGTGATAGA	686	
Db	450	ATGAGGACCTGTGGCATGTTTGTCTACA-----	423	
QY	687	GTGTGTGGTTGGTGTGTGTAATTTTTTTTTTAATTTTACAGTTTGTGTGTTAAAGAT	746	
Db	422	-----	423	

QY 747 TTGTATTGATTTTTTAAAGTCTGTCTGAACTGAGCTGAGCCGAGCCAG 806
Db 422 -----GTCTGTGTCTGAACCTGAGCCGAGCCAG 387
QY 807 AACGGAGCCTGCAAGACTACCCGCGCTCTAAATGGCCCTGTATCTCTGAGAGCC 866
Db 386 AACGGAGCCTGCAAGACTACCCGCGCTCTAAATGGCCCTGTATCTCTGAGAGCC 327
QY 867 CGAATACCTGTCTTGAAGAAATGCAATAGTACCGAATGCTGATCTCCGCTCTT 926
Db 326 CGAATACCTGTCTTGAAGAAATGCAATAGTACCGAATGCTGATCTCCGCTCTT 267
QY 927 CTAACACACTCTCTGAGATACCCGCGGTCTCCGCTTAAACAGTTGCCG 986
Db 266 CTAACACACTCTCTGAGATACCCGCGGTCTCCGCTTAAACAGTTGCCG 207
QY 987 TGAGAGTTGTGGCGCTGCGCAGGCTGTGAATGTATGAGAGACTTGTCTTAACGAGCTG 1046
Db 206 TGAGAGTTGTGGCGCTGCGCAGGCTGTGAATGTATGAGAGACTTGTCTTAACGAGCTG 147
QY 1047 GGCAACTTTGAGCTTGAGCTGTAAAGCCCGAGCCCTAAGGTGTAACTGTGATTGC 1106
Db 146 GGCAACTTTGAGCTTGAGCTGTAAAGCCCGAGCCCTAAGGTGTAACTGTGATTGC 87
QY 1107 GTGTGTGTAAAGCTTTGTTGCTGAATGATGTATGATTTAATAAGGAGTGA 1166
Db 86 GTGTGTGTAAAGCTTTGTTGCTGAATGATGTATGATTTAATAAGGAGTGA 27
QY 1167 TAATGTTTAA 1176
Db 26 TAATGTTTAA 17

RESULT 4
CK624194 625 bp mRNA linear EST 26-JAN-2004
DEFINITION m18c08.y1 Mouse RPE/choroid, unamplified: ml/mj Mus musculus cDNA
LOCUS m18c08 5', mRNA sequence.
ACCESSION CK624194
VERSION CK624194.1 GI:41345080
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 625)
AUTHORS Ida,H., Boylan,S., Weigel,A., Smit-McBride,Z., Chao,A., Gao,J.,
Buchoff,P., Wistow,G. and Hjelmelund,L.
TITLE Unpublished sequence tag analysis of mouse RPE/choroid
JOURNAL Contact: Wistow G
COMMENT Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 18 row: c column: 08
Seq primer: M13Rpl reverse primer (ABI).
Location/Qualifiers
1..625
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57Bl6J"
/db_xref="taxon:10090"
/clone="m18c08"
/sex="Male"
/issue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_id="Mouse RPE/choroid, unamplified: ml/mj"
/note="Organ: Eye; Vector: pSPORT1; 64ug total RNA was

extracted from 200 adult male mouse RPE/choroids. A
directionally cloned cDNA library in the pSPORT1
vector (Life Technologies) was constructed at Bioserve
Biotechnology (Laurel MD) essentially following the
protocols of the Superscript Plasmid System full details
of which are contained in the manufacturer's instruction
manual (<http://www.lifetech.com/>). First strand synthesis
was carried out using a Not I primer-adaptor
[5'-pGACTGATTTAGATGCGAGCGCGCCCT(7.15-3')]. cDNA was
cloned in Not I/Sal I sites. EST analysis was performed on
the unamplified library at the NIH Intramural Sequencing
Center (NISC)."

ORIGIN

Query Match 19.4%; Score 592.8; DB 7; Length 625;
Best Local Similarity 97.6%; Pred. No. 1.1e-150;
Matches 613; Conservative 0; Mismatches 12; Indels 3; Gaps 1;
QY 1127 TTGCTGAATGAGTTGATGTATGATTTAATGAAGGTGAGATTAATGTTAACTTGATGCG 1186
Db 1 TTGCTGAATGAGTTGATGTATGATTTAATGAAGGTGAGATTAATGTTAACTTGATGCG 60
QY 1187 GTGTTAAATGAGGCGGCTTAAAGGATATATATGCGCCGTGAGCTAATCTTGTTACA 1246
Db 61 GTGTTAAATGAGGCGGCTTAAAGGATATATATGCGCCGTGAGCTAATCTTGTTACA 120
QY 1247 TGTGACCTCANTGAGGCTTGGAGCTGTTTGAAGATTTTCTGTGTGCGTAATCTTGCTG 1306
Db 121 TGTGACCTCANTGAGGCTTGGAGCTGTTTGAAGATTTTCTGTGTGCGTAATCTTGCTG 180
QY 1307 GAACAGAGCTCTAAACAGTACCTCTTGTTTGAAGTTCTGTGAGGCTCATCCAGGCA 1366
Db 181 GAACAGAGCTCTAAACAGTACCTCTTGTTTGAAGTTCTGTGAGGCTCATCCAGGCA 240
QY 1367 AAGTTAGCTTGAAGATTAAGAGGATTAACAATGAGGATTTGAAGCTTTGAAATCC 1426
Db 241 AAGTTAGCTTGAAGATTAAGAGGATTAACAATGAGGATTTGAAGCTTTGAAATCC 300
QY 1427 TGTGTGAGCTGTTGATTTCTTTGAATCTGTGTCACAGGCGCTTTCCAAAGAAAGTGC 1486
Db 301 TGTGTGAGCTGTTGATTTCTTTGAATCTGTGTCACAGGCGCTTTCCAAAGAAAGTGC 360
QY 1487 ATCAAGACTTGTGATTTTTCACACCGGCGCGCTGCGCTGTGCTTTTGTAGT 1546
Db 361 ATCAAGACTTGTGATTTTTCACACCGGCGCGCTGCGCTGTGCTTTTGTAGT 420
QY 1547 TTTATTAAGATTAATGAGCGGAAGAAACCATCTGAGCGGCGGTACCTGCTGATTTT 1606
Db 421 TTTATTAAGATTAATGAGCGGAAGAAACCATCTGAGCGGCGGTACCTGCTGATTTT 480
QY 1607 CTGGCAGTGCATCTGTGGAAGAGGCTGTGTGACACAAAGAAATGCGCTACCTGTGCT 1666
Db 481 CTGGCAGTGCATCTGTGGAAGAGGCTGTGTGACACAAAGAAATGCGCTACCTGTGCT 540
QY 1667 TCCGTCCGCCCGCGATATATCGACCGAGAGCAGCAGCAGCAGCAGAGGAAGCAAG 1726
Db 541 TCCGTCCGCCCGCGGAATATATCGAGAGG---AGCAACAGCAGCAGGAAGCAAGGCGG 597
QY 1727 CGGCGCGCGAGAGCAGAGCCCATGGA 1754
Db 598 CGGCGCGCGAGAGCAGAGCCCATGGA 625

RESULT 5
CA306892/c 743 bp mRNA linear EST 05-AUG-2004
LOCUS CA306892
DEFINITION UI-H-FT1-bht-p-24-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bht-p-24-0-UI 3', mRNA sequence.
ACCESSION CA306892
VERSION CA306892.1 GI:24469946
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: gcapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLY-A-yes.

FEATURES SOURCE

1. 743 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FTI-bht-p-24-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_id="NCI_CGAP_FTI"
/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI CGAP FTI is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an Ecor I adaptor,
digested with Not I, and cloned directionally into
pRTT3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCGC. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FTI
TAG_SEQ=GGCCATGCGC"

ORIGIN

Query Match 19.2%; Score 587.4; DB 6; Length 743;
Best Local Similarity 86.0%; Pred. No. 3.4e-149;
Matches 725; Conservative 0; Mismatches 1; Indels 117; Gaps 2;
QY 341 ACTACTTTTCCGCGCGCGCGGTTCTCCGAGCGGCTTACTTTTCCGCGCGCGCGA 400
DB 743 ACTACTTTTCCGCGCGCGCGGTTCTCCGAGCGGCTTACTTTTCCGCGCGCGCGA 684
QY 401 GCAGCCGAGAGAGAGCTTGAGTCCGTTTCTATGCAAACTTATACCGAGGATGAT 460
|||||

DB 683 GCAGCCGAGAGAGAGCTTGAGTCCGTTTCTATGCAAACTTATACCGAGGATGAT 624
QY 461 GCATCTTACCTGCCACGAGGCTGCTTTCCACCCAGTAGAGAGATGAGAGGATGA 520
DB 623 GCATCTTACCTGCCACGAGGCTGCTTTCCACCCAGTAGAGAGATGAGAGGATGA 564
QY 521 GGAATTTGTGTATGATATATGATGAGACACCCCGGACGAGTTGACGATCTTATCA 580
DB 563 GGAATTTGTGTATGATATATGATGAGACACCCCGGACGAGTTGACGATCTTATCA 504
QY 581 CCGAGAGAAATACGCGGAGGACCCAGATATATGATGCTTGTATATGAGAGACTGTG 640
DB 503 CCGAGAGAAATACGCGGAGGACCCAGATATATGATGCTTGTATATGAGAGACTGTG 444
QY 641 CATGTTGTCTACAGTAAGTAAATATATGAGGAGTGTGATGAGTGTGCTTGTG 700
DB 443 CATGTTGTCTAC-----
QY 701 GTGCTAATTTTATTTTATTTTATTTTACAGTTTGTGCTTAAAGATTTTGTATGATT 760
DB 429 -----
QY 761 TTTTAAAGGTCCTGTGTGCTGAACTGAGGCTGAGCCGAGACCGAGACTGTGA 820
DB 429 -----GTCTGTGTCTGAACTGTAGCTTGAGCCCGAGACCGAGACTGTGA 380
QY 821 AGACCTTACCGCGCGCTCTTAAATATGAGGCGCTGTATCTGTAGACCGCCGACATCACTGTG 880
DB 379 AGACCTTACCGCGCGCTCTTAAATATGAGGCGCTGTATCTGTAGAGCCCGACATCACTGTG 320
QY 881 TCTTGAGAAATGCAATATGATGATGAGAGATGCTGTGATCTGCTCTTCTTACACACTCTCT 940
DB 319 TCTTGAGAAATGCAATATGATGATGAGAGATGCTGTGATCTGCTCTTCTTACACACTCTCT 260
QY 941 GAGATACACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000
DB 259 GAGATACACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 200
QY 1001 CGTGCGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1060
DB 199 CGTGCGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 140
QY 1061 TTGAGCTGTAAAGCGCCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1120
DB 139 TTGAGCTGTAAAGCGCCGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 80
QY 1121 CCTTGTGCTGAT 1179
DB 79 CCTTGTGCTGAT 20
QY 1180 GCA 1182
DB 19 GAA 17
RESULT 6
CA307899/c 726 bp mRNA linear EST 05-AUG-2004
LOCUS UI-H-FTI-b1b-a-23-0-UI.s1 NCI CGAP FTI Homo sapiens cDNA clone
DEFINITION UI-H-FTI-b1b-a-23-0-UI 3', mRNA sequence.
ACCESSION CA307899 GI:24470953
VERSION CA307899.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Straubeberg, Ph.D.

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-21, >AT-rich#low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES

source

Location/Qualifiers
 1..726
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT1-b1b-a-23-0-UI"
 /cissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="MDH10B (Life Technologies)"
 /clone_lib="NCI CGAP FT1"
 /note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
 modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NCI CGAP FT1 is a normalized cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
 moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
 vector (Ads CMV eGFP), moi 500, 3 hours; Adenoviral vector
 (Ads CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
 hours; wt adenovirus + LPS 24 hours. The library was
 normalized according to Bonaldo, Lennon and Soares, Genome
 Research, 6:791-806, 1996. First strand cDNA synthesis was
 primed with an oligo-dT primer containing a Not I site.
 Double stranded cDNA was ligated to an EcoR I adaptor,
 digested with Not I, and cloned directionally into
 pRTT3-Pac vector. The oligonucleotide used to prime the
 synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 GGCCATGCCG. The tissue was provided by Dr. Gary W.
 Hunninghake of the University of Iowa.
 TAG_TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-FT1
 TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 18.8%; Score 573; DB 6; Length 726;
 Best Local Similarity 85.9%; Pred. No. 3e-145;
 Matches 710; Conservative 0; Mismatches 0; Indels 117; Gaps 2;

350 TCCGCGGCGCGCGGTTCTCCGAGACCGCTCACCTTCCGGCAGCCCGAGACCGCGA 409
 Db TCCGCGGCGCGCGC-GTTCTCCGAGACCGCTCACCTTCCGGCAGCCCGAGACCGCGA 668
 410 GCAGAGACCTTGGGTCCGGTTTCTATSCCAAACCTTGTACCGAGAGTGATCGATCTTAC 469
 Db GCAGAGACCTTGGGTCCGGTTTCTATSCCAAACCTTGTACCGAGAGTGATCGATCTTAC 608
 470 CTGCCACAGAGCTGGCTTTCCACCCAGAGACGAGATGAAGAGGTGAGAGTTTGT 529
 Db CTGCCACAGAGCTGGCTTTCCACCCAGAGACGAGATGAAGAGGTGAGAGTTTGT 548

Db

Qy 530 GTTAGATTATGTGGAGACCCCGGGACAGGTTGACAGTCTTGTCATTATCACCAGGAGA 589
 Db 547 GTTAGATTATGTGGAGACCCCGGGACAGGTTGACAGTCTTGTCATTATCACCAGGAGA 488
 Qy 590 TACGGGGAGACCCAGATATTATGTGTTGCTTGTCTATATAGAGACCTGTGGACATGTTGT 649
 Db 487 TACGGGGAGACCCAGATATTATGTGTTGCTTGTCTATATAGAGACCTGTGGACATGTTGT 428
 Qy 650 CTACAGTAAGTGAATAATTATGGGCAGTGGGTATAGTGTGGGTTTGTGTGTATTT 709
 Db 427 CTACA----- 423
 Qy 710 TTTTAAATTTTAAATTTTACAGTTTGTGTGTTTAAAGATTTGTATTTGATTTTAA 769
 Db 422 ----- 423
 Qy 770 GGTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCAGAACCGAGCCTGCAAGACTTACC 829
 Db 422 -GTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCAGAACCGAGCCTGCAAGACTTACC 364
 Qy 830 CGCGGTCTTAAATGGGCGCTGCTATCTGAGACGCCCGACATACCTGTGTCTAGAGAA 889
 Db 363 CGCGGTCTTAAATGGGCGCTGCTATCTGAGACGCCCGACATACCTGTGTCTAGAGAA 304
 Qy 890 TGCAATAGTAGTACGATAGCTGTAAGCTCCGTCCTTCTAACAACCTCTGAGATACAC 949
 Db 303 TGCAATAGTAGTACGATAGCTGTAAGCTCCGTCCTTCTAACAACCTCTGAGATACAC 244
 Qy 950 CCGGTGTCCCGCTGTGCCCCCATTTAAACAGTTGCGGTGAGAGTTGGTGGCGCTGCCAG 1009
 Db 243 CCGGTGTCCCGCTGTGCCCCCATTTAAACAGTTGCGGTGAGAGTTGGTGGCGCTGCCAG 184
 Qy 1010 GCTGTGAATGTATCGAGACCTTGCTTAAGAGCCTGGGCAACCTTGGACCTTAGGCTGT 1069
 Db 183 GCTGTGAATGTATCGAGACCTTGCTTAAGAGCCTGGGCAACCTTGGACCTTAGGCTGT 124
 Qy 1070 AAACGCCCGCAGCATAGAGTGTAAACCTGTGATGGCTGTGTGTAGAGCTTTGTTT 1129
 Db 123 AAACGCCCGCAGCATAGAGTGTAAACCTGTGATGGCTGTGTGTAGAGCTTTGTTT 64
 Qy 1130 GCTGAATGAGTGTATGTAAGTTTAAATGAAGGCTGAGATTAATGTTTAA 1176
 Db 63 GCTGAATGAGTGTATGTAAGTTTAAATGAAGGCTGAGATTAATGTTTAA 17

RESULT 7
 CD370856/c 602 bp mRNA linear EST 05-AUG-2004
 LOCUS
 DEFINITION
 UI-H-FT1-b1z-n-11-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone
 UI-H-FT1-b1z-n-11-0-UI 3', mRNA sequence.
 CD370856
 ACCESSION
 CD370856.1 GI:31154946
 VERSION
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 602)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/cgap.html
 Seq primer: M13 FORWARD
 POLYA=yes.
 Location/Qualifiers

FEATURES

Source

1. 602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-Fri-bjz-n-11-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FPI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP FPI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; Adenovirus moi 500, 3 hours; Adenovirus + LPS 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; Adenovirus + LPS 3 hours; Adenovirus + LPS 24 hours. The library was normalized according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (d)18 tail. The sequence tag for this library is:
GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=human Lung Alveolar Macrophage
TAG LIB=UI-H-FPI
TAG_SEQ=GGCCATGCCG"

Query Match 15.1%; Score 460; DB 6; Length 602;
Best Local Similarity 83.5%; Pred. No. 2,8e-114;
Matches 586; Conservative 0; Mismatches 0; Indels 116; Gaps 1;

ORIGIN

475 ACGAGGCTGGCTTCCACCAAGTGCAGCAGAGATGAAGAGGAGGAGTTGTGTAG 534
602 ACGAGGCTGGCTTCCACCAAGTGCAGCAGAGATGAAGAGGAGGAGTTGTGTAG 543
535 ATTATGTGACACACCCGGGACCGTTGAGTCTTTCATTATACCGGAGGATACG 594
542 ATTATGTGACACACCCGGGACCGTTGAGTCTTTCATTATACCGGAGGATACG 483
595 GGAACCCAGATATTATGTGTGCTTTCATTATAGAGACCTGTGTCATCTACA 654
482 GGAACCCAGATATTATGTGTGCTTTCATTATAGAGACCTGTGTCATCTACA 423
655 GTAAGTAAATATATGAGCACTGTGTATATAGAGTGTGTGTGTATATTTT 714
422 ----- 423
715 TTTAATTTTACAGTTTGTGTATTAAGAAATTTGTATGTGATTTTAAAGTTC 774
422 -----GTC 419
775 TGTGCTGAACCTGAGCTGAGCCGAGCCGAGACCGAGCTGCAAGACCTACCCGCG 834
418 TGTGCTGAACCTGAGCTGAGCCGAGCCGAGACCGAGCTGCAAGACCTACCCGCG 359

ORIGIN

Query Match 11.0%; Score 335.4; DB 4; Length 337;
Best Local Similarity 99.7%; Pred. No. 3.4e-80;
Matches 336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FEATURES

Source

1. 337
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
/clone="19600449695952"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="A.Gam.ad.cDNA.blood1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mrz.org)"

ORIGIN

835 TCCTAAATGCGCGCTGCTATCTGAGACGCCGACATACCTGTGTAGAGATGCA 894
358 TCCTAAATGCGCGCTGCTATCTGAGACGCCGACATACCTGTGTAGAGATGCA 299
895 TAGTAGTACGAGTATGCTGTGACTCCGGTCTTCTTAACACACTCTGATACACCCGGT 954
298 TAGTAGTACGAGTATGCTGTGACTCCGGTCTTCTTAACACACTCTGATACACCCGGT 239
955 GGTCCCGCTGTGCGCCCATTAACAGATTGCCGTGAGAGTGTGTGCGCGCCAGCTGT 1014
238 GGTCCCGCTGTGCGCCCATTAACAGATTGCCGTGAGAGTGTGTGCGCGCGCTGT 179
1015 GGAATGTTCAGAGACTTGTCTTAACAGACTTGGGCACTTTGGACTTGAACG 1074
178 GGAATGTTCAGAGACTTGTCTTAACAGACTTGGGCACTTTGGACTTGAACG 119
1075 CCCGAGCCCATTAAGTGTAAACCTGTGATTCGTGTGTGTTAAGCCTTTGTGTGCTGA 1134
118 CCCGAGCCCATTAAGTGTAAACCTGTGATTCGTGTGTGTTAAGCCTTTGTGTGCTGA 59
1135 ATGAGTTGATGTAAATTAATTAAGGAGTGAATATGTTAA 1176
58 ATGAGTTGATGTAAATTAATTAAGGAGTGAATATGTTAA 17
RESULT 8
BM591710 337 bp mRNA linear EST 25-FEB-2002
LOCUS 1700068738831 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
DEFINITION 19600449695952 5', mRNA sequence.
ACCESSION BM591710
VERSION BM591710.1 GI:18887571
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
1 (bases 1 to 337)
Holt,R.A., Lin,D.-J., Murphy,S.D., Evans,C.A., Kraft,C.T.,
Cherlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
JOURNAL Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: N001004AB8 row: P column: 18
Seq primer: M13 Reverse.
Location/Qualifiers

Oy 1126 GTTTCGTAATGAGTGTGATGTTAATATAAAGGGTGAATATGTTTAACTTGCAATGG 1185
Db 1 GTTTCGTAATGAGTGTGATGTTAATATAAAGGGTGAATATGTTTAACTTGCAATGG 60
Oy 1186 CGTGTAAATGAGGGGCGGGCTTAAAGGGTATATAATGCGCGGTGCTAATCTTGTTAC 1245
Db 61 CGTGTAAATGAGGGGCGGGCTTAAAGGGTATATAATGCGCGGTGCTAATCTTGTTAC 120
Oy 1246 ATTCGACCTCATGAGAGCTTTGGAGCTGTTTGGAGATTTTTCTGCTGCGCTAATCTTGCT 1305
Db 121 ATTCGACCTCATGAGAGCTTTGGAGATTTTTCTGCTGCGCTAATCTTGCT 180
Oy 1306 GGAACAGAGCTCTAACAAGTACCTCTTGTTTGGAGTTTCTGTCGGGCTCATCCAGGC 1365
Db 181 GGAACAGAGCTCTAACAAGTACCTCTTGTTTGGAGTTTCTGTCGGGCTCATCCAGGC 240
Oy 1366 AAAGTTAGTCTGCAAGATTAAAGAGATTACAAAGTGGGAATTTGAAGACTTTGAAATC 1425
Db 241 AAAGTTAGTCTGCAAGATTAAAGAGATTACAAAGTGGGAATTTGAAGACTTTGAAATC 300
Oy 1426 CTGTGCTGAGCTGTTTGAATCTTGGAATCTGGCTAC 1462
Db 301 CTGTGCTGAGCTGTTTGAATCTTGGAATCTGGCTAC 337

RESULT 9
LOCUS BF915148 347 bp mRNA linear EST 18-JAN-2001
DEFINITION IL3-UT0114-041200-328-H03_1 UT0114 Homo sapiens cDNA, mRNA
sequence.
ACCESSION BF915148
VERSION BF915148
KEYWORDS EST. GI:12306606
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negal,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&ct=IL3-UT0114-
041200-328-H03_1&ct3=2000-12-04&ct4=1)
Seq primer: puc 18 forward
High quality sequence stop: 329.

FEATURES
Location/Qualifiers
1..347

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0114"
/note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 8.2%; Score 249.8; DB 2; Length 347;
Best Local Similarity 95.5%; Pred. No. 1e-56;
Matches 257; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 866 CCGACATCACCTGTGTCTAGAAATGCAATAGTACGATGACTGTGACTCCGGTCT 925
Db 347 CCGACATCACCTGTGTCTAGAAATGCAATAGTACGATGACTGTGACTCCGGTCT 288
Oy 926 TCTAACACACTCTCTGAGATACACCCGGTGTCCCGCTGTGCCCATTAACACAGTTGCC 985
Db 287 TCTAACACACTCTCTGAGATACACCCGGTGTCCCGCTGTGCCCATTAACACAGTTGCC 228
Oy 986 GTGAGAGTGGTGGGCGGTCCGACGCTGTGGATATATCGAGACTTGCTTAAGAGCCT 1045
Db 227 GTGAGAGTGGTGGGCGGTCCGACGCTGTGGATATATCGAGACTTGCTTAAGAGCCT 168
Oy 1046 GGGCAACCTTTGACTTGAAGCTGTAAACGCCCCAGCCATTAAGGTGTAAACCTGTGATTG 1105
Db 167 GGGCAACCTTTGACTTGAAGCTGTAAACGCCCCAGCCATTAAGGTGTAAACCTGTGATTG 108
Oy 1106 CGTGTGCTTAACGCTCTTGTTGCTGA 1134
Db 107 CGTGTGCTTCTTGTTATTGACGCTTA 79

RESULT 10
LOCUS BF914577 323 bp mRNA linear EST 18-JAN-2001
DEFINITION IL3-UT0114-011200-362-G09_1 UT0114 Homo sapiens cDNA, mRNA
sequence.
ACCESSION BF914577
VERSION BF914577
KEYWORDS EST. GI:12306035
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Negal,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&ct=IL3-UT0114-
011200-362-G09_1&ct3=2000-12-01&ct4=1)
Seq primer: puc 18 forward
High quality sequence stop: 322.

FEATURES
Location/Qualifiers
1..323

source
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1ib="UT0114"
/note="Organ: uterus tumor; Vector: puc18; Site 1: Smal;
Site 2: Smal; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 7.3%; Score 224.2; DB 2; Length 321;
Best Local Similarity 94.7%; Pred. No. 1.1e-49;
Matches 232; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 890 TGCATAGTAGTAGGATGAGTGTGACCTCCGCTCTTCTTAACACCTCTGAGATAC 949
DB 323 TGCATAGTAGTAGGATGAGTGTGACCTCCGCTCTTCTTAACACCTCTGAGATAC 264
OY 950 CCGGTGTGTCCTGTCGCCCATTAACCAAGTCCGTGAGAGTTGTGGCGTCGACG 1009
DB 263 CCGGTGTGTCCTGTCGCCCATTAACCAAGTCCGTGAGAGTTGTGGCGTCGACG 204
OY 1010 GCTGTGATGTATGAGAGACTTGTCTTAACGAGCTGGGCAACTTTGAGCTTGT 1069
DB 203 GCTGTGATGTATGAGAGACTTGTCTTAACGAGCTGGGCAACTTTGAGCTTGT 144
OY 1070 AAAGCCCGCAGGCAATAGTGTAACTGTGATGCTGTGTGTGTTAAGCCCTTGT 1129
DB 143 AAAGCCCGCAGGCAATAGTGTAACTGTGATGCTGTGTGTGTTAAGCCCTTGT 84
OY 1130 GCTGA 1134
DB 83 GCTTA 79

RESULT 11
LOCUS BF915126/c 321 bp mRNA linear EST 18-JAN-2001
DEFINITION U3-UT0114-041200-328-A10_1 UT0114 Homo sapiens cDNA, mRNA
sequence.
ACCESSION BF915126
VERSION BF915126.1 GI:12306584
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 321)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongseneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 2002663
PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-

041200-328-A10_1&t3=2000-12-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 159.
Location/Qualifiers
1..321

FEATURES

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1ib="UT0114"
/note="Organ: uterus tumor; Vector: puc18; Site 1: Smal;
Site 2: Smal; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 7.3%; Score 223.8; DB 2; Length 321;
Best Local Similarity 95.1%; Pred. No. 1.4e-49;
Matches 231; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 892 CAATAGTAGTAGGATGAGTGTGACCTCCGCTCTTCTTAACACCTCTGAGATAC 951
DB 321 CAATAGTAGTAGGATGAGTGTGACCTCCGCTCTTCTTAACACCTCTGAGATAC 262
OY 952 GGTGTGTCCTGTCGCCCATTAACCAAGTCCGTGAGAGTTGTGGCGTCGACG 1011
DB 261 GGTGTGTCCTGTCGCCCATTAACCAAGTCCGTGAGAGTTGTGGCGTCGACG 202
OY 1012 TGTGAAATGTATCGAGAGACTTGTCTTAACGAGCTGGGCAACTTTGAGCTTGA 1071
DB 201 TGTGAAATGTATCGAGAGACTTGTCTTAACGAGCTGGGCAACTTTGAGCTTGA 142
OY 1072 ACGCCCGCAGGCAATAGTGTAACTGTGATGCTGTGTGTGTTAAGCCCTTGT 1131
DB 141 ACGCCCGCAGGCAATAGTGTAACTGTGATGCTGTGTGTGTTAAGCCCTTGT 82
OY 1132 TGA 1134
DB 81 TTA 79

RESULT 12
LOCUS CD366021/c 741 bp mRNA linear EST 05-AUG-2004
DEFINITION U3-UT1-bjs-k-22-0-UT 31 NCI CGAP FT1 Homo sapiens cDNA clone
sequence.
ACCESSION CD366021
VERSION CD366021.1 GI:31150111
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 741)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Email: cgaps-remail.nih.gov
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1..741

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-b3a-k-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FTL"
/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI CGAP FTL is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions), other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 7.3%; Score 222.4; DB 6; Length 741;
Best Local Similarity 98.7%; Pred. No. 4.1e-49;
Matches 234; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 2816 AGCCCGAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTTCATGATGACATGAAGATCT 2875
Db 730 AGCCCGAGAGCATGTCCAAAGGT-AACTGAAACGGGGTGTTCATGATGACATGAAGATCT 672
QY 2876 GGAAGGTCTGAAGTACATGAGACCCGACACAGGTGACACCTCGCAGATGTGGCGGTA 2935
Db 671 GGAAGGTCTGAAGTACATGAGACCCGACACAGGTGACACCTCGCAGATGTGGCGGTA 612
QY 2936 AACATATTAGGAACAGAGCTGTGATGTGATGACCGAGAGCTGAGGCCCGATCCT 2995
Db 611 AACATATTAGGAACAGAGCTGTGATGTGATGACCGAGAGCTGAGGCCCGATCCT 552
QY 2996 TGGTGTCTGGCTGCACCCGCGCTGAGTTGGCTCTAGCGATGAAGATACAGATTGAG 3052
Db 551 TGGTGTCTGGCTGCACCCGCGCTGAGTTGGCTCTAGCGATGAAGATACAGATTGAG 495
RESULT 13
CD742922/c 667 bp mRNA linear EST 05-AUG-2004
LOCUS
DEFINITION UI-H-FT1-b3a-k-23-0-UI.s1 NCI CGAP FTL Homo sapiens cDNA clone
ACCESSION CD742922
VERSION CD742922.1 GI:322937772
KEYWORDS EST.

SOURCE
ORGANISM Homo sapiens (human)
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eulhelia; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 667)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA sequence: 546-595, >(CAG)n\$imple_repeat (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.
FEATURES
source
Location/Qualifiers
1..667
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-b3a-k-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FTL"
/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI CGAP FTL is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions), other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 5.7%; Score 173.6; DB 6; Length 667;
Best Local Similarity 97.8%; Pred. No. 9.7e-36;
Matches 176; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1623 GGAGAGGGGTTGTAGACACAAGAAATCGCTCTACTTGTCTTCCGCGCCGGGGA 1682
 Db 667 GGAGAGCGGTTGTGTGACACAAGAAATCGCTCTACTTGTCTTCCGCGCCGGGGA 608
 Oy 1683 TAAATACCGACGAGAGACGAGACGAGACGAGAGAGAACCGAGCGCGCGAGAGC 1742
 Db 607 TAAATACCGACGAGAGACGAGACGAGACGAGAGAGAACCGAGCGCGCGAGAGC 548
 Oy 1743 AGAGCCCATGGAACCCGAGACCGCGCTGTGAACCTCGGGAATGATGTTGTACAGTGGC 1802
 Db 547 AGAGCCCATGGAACCCGAGACCGCGCTGTGAACCTCGGGAATGATGTTGTACAGTGGC 488
 RESULT 14
 CD365243/c 661 bp mRNA linear EST 05-AUG-2004
 LOCUS UI-H-FT2-bj1-c-23-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
 DEFINITION UI-H-FT2-bj1-c-23-0-UI 3', mRNA sequence.
 CD365243
 VERSION CD365243.1 GI:31149333
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 661)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/cgap.html
 Seq Primer: M13 FORWARD
 POLYAyes.

FEATURES

source
 1. 661
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FT2-bj1-c-23-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_id="NCI CGAP FT2"
 /note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
 modified polylinker; Site 1: Ecor I; Site 2: Not I;
 NCI CGAP FT2 is a subcloned cDNA library constructed from
 a pool of 81 RNA samples from Alveolar Macrophages.
 challenged with different treatments. The mRNA samples
 were a mixture of these conditions (times refer to
 incubations following isolation by bronchoalveolar lavage)
 (some normal donor macrophages were cultured in some of
 the conditions, other donor macrophages in different
 conditions). The mRNA samples were pooled for library
 construction. Control 0 hours; control 3 hours; control 24
 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
 PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
 mol 10, 3 hours; Klebsiella mol 10, 24 hours; Staph
 aureus mol 10, 3 hours; Staph aureus mol 10, 24 hours;
 Adenoviral vector (Ad5 CMV egfp), mol 500, 3 hours;
 Adenoviral vector (Ad5 CMV egfp), mol 500, 24 hours;
 Adenoviral vector (Ad5 CMV egfp), mol 500, 24 hours;
 Adenovirus mol 500, 3 hours; wt adenovirus mol 500, 24
 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours;
 wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours.
 The library was subcloned according to Bonaldo, Lennon
 and Soares, Genome Research, 6:791-806, 1996. The tissue

ORIGIN

was provided by Dr. Gary W. Hunninghake of the University
 of Iowa
 TAG_TISSUE=Human Lung Alveolar Macrophage
 TAG_LIB=UI-H-FT2
 TAG_SEQ=GGCCATGCGC"

Query Match 5.5%; Score 167; DB 6; Length 661;
 Best Local Similarity 100.0%; Pred. No. 6.2e-34;
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2886 GAGGTACGATGAGACCCGACACAGATGAGACCTGTGAGTGTGCGGTAAACATATTAG 2945
 Db 661 GAGGTACGATGAGACCCGACACAGATGAGACCTGTGAGTGTGCGGTAAACATATTAG 602
 Oy 2946 GAACACAGCTGTGATGTGTGATGTGACGAGACCTGAGGCCGATCACTTGCTGCTGGC 3005
 Db 601 GAACACAGCTGTGATGTGTGATGTGACGAGACCTGAGGCCGATCACTTGCTGCTGGC 542
 Oy 3006 CTGCACCCGCGCTGATGTTGCTCTTACGATGAAGATACAGATTGAG 3052
 Db 541 CTGCACCCGCGCTGATGTTGCTCTTACGATGAAGATACAGATTGAG 495

RESULT 15

BM600614 173 bp mRNA linear EST 25-FEB-2002
 LOCUS 1700687054399 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
 DEFINITION 19600449720751 5', mRNA sequence.
 BM600614
 VERSION BM600614.1 GI:18898718
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.

REFERENCE 1 (bases 1 to 173)
 AUTHORS Holt,R.A., Jin,J.-D., Murphy,S.D., Evans,C.A., Kraft,C.L.,
 Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
 TITLE Celera Anopheles gambiae EST project
 JOURNAL Unpublished (2002)
 COMMENT Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: NU01004AA1 row: J column: 01
 Seq Primer: M13 Reverse.

FEATURES

source
 1. 173
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449720751"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /clone_id="A.Gam.ad.cDNA.blood1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
 hours after human blood feeding. cDNA inserts >500 bp
 cloned directionally into pSport 1. Not 1 site is 3'.
 Clones available through the Malaria Research and
 Reference Reagent Resource Center (www.malaria.rtrc.org)"

ORIGIN

Query Match 5.3%; Score 162; DB 4; Length 173;
 Best Local Similarity 99.4%; Pred. No. 1e-32;
 Matches 173; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
OY 1126 GTTGTGAATGAGTTGATGTPAAGTTTATTAAGGGTGAGATAAGTTTACTTGCAATGG 1185
Db 1 GTTGCTGAATGAGTTGATGTPAAGTTTATTAAGGGTGAGATAAGTTTACTTGCAATGG 60
OY 1186 CGTGTAAATGGGCGGGGCTTAAAGGGTATATATGCGCGGTGAGCTAATCTTGTTAC 1245
Db 61 CGTGTAAATGGGCGGGGCTTAAAGGGTATATATGCGCGGTGAGCTAATCTTGTTAC 120
OY 1246 ATCTGACCTCATGAGGCTTGGGAGTGTGGAAGATTTTCTGCTGCGGTAA 1299
Db 121 ATCTGACCTCATGAGGCTTGGGAGTGTGGAAG-TTTTCTGCTGCGGTAA 173
```

Search completed: October 28, 2005, 08:56:38
Job time : 8779 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 28, 2005, 02:08:20 ; Search time 516 Seconds

(without alignments)
9678.133 Million cell updates/sec

Title: US-10-790-562-33

Perfect score: 3052

Sequence: 1 cgtgtagtgcattatatacc.....cgtagaagatcacagatcgag 3052

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCtus.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3052	100.0	35935	2	US-08-735-609-1
2	3052	100.0	35935	2	US-08-735-609-1
3	3052	100.0	35935	3	US-08-735-609-1
4	3052	100.0	35935	3	US-08-735-609-1
5	3052	100.0	35935	3	US-08-735-609-1
6	3052	100.0	35935	3	US-08-735-609-1
7	3052	100.0	35935	3	US-08-735-609-1
8	3052	100.0	35935	3	US-08-735-609-1
9	3052	100.0	35935	3	US-08-735-609-1
10	3052	100.0	35935	3	US-08-735-609-1
11	3052	100.0	35935	3	US-08-735-609-1
12	3052	100.0	35935	3	US-08-735-609-1
13	3052	100.0	35935	3	US-08-735-609-1
14	3052	100.0	35935	3	US-08-735-609-1
15	3052	100.0	35935	3	US-08-735-609-1
16	3052	100.0	35935	3	US-08-735-609-1
17	3052	100.0	35935	3	US-08-735-609-1
18	3052	100.0	35935	3	US-08-735-609-1
19	3052	100.0	35935	3	US-08-735-609-1
20	3052	100.0	35935	3	US-08-735-609-1
21	3052	100.0	35935	3	US-08-735-609-1
22	3052	100.0	35935	3	US-08-735-609-1
23	3052	100.0	35935	3	US-08-735-609-1
24	3052	100.0	35935	3	US-08-735-609-1
25	3052	100.0	35935	3	US-08-735-609-1
26	3052	100.0	35935	3	US-08-735-609-1
27	3052	100.0	35935	3	US-08-735-609-1

28	1000	32.8	1000	2	US-08-473-399B-1	Sequence 1, Appli
29	1000	32.8	1000	2	US-08-473-399B-3	Sequence 3, Appli
30	1000	32.8	1000	3	US-08-853-831-1	Sequence 1, Appli
31	1000	32.8	1000	3	US-08-853-831-3	Sequence 1, Appli
32	1000	32.8	1000	4	US-09-510-885-1	Sequence 1, Appli
33	1000	32.8	1000	4	US-09-510-885-3	Sequence 1, Appli
34	1000	32.8	1000	5	PCT-US93-09774-1	Sequence 1, Appli
35	1000	32.8	1000	5	PCT-US93-09774-3	Sequence 1, Appli
36	682.4	22.4	36519	3	US-08-923-137-2	Sequence 3, Appli
37	644.8	21.1	35524	3	US-08-923-137-2	Sequence 1, Appli
38	618.2	20.3	34794	4	US-09-713-678-39	Sequence 39, Appli
39	599.6	19.6	35081	2	US-08-752-760A-1	Sequence 1, Appli
40	546.8	17.9	7507	4	US-08-653-114A-1	Sequence 1, Appli
41	463	15.2	1800	4	US-08-540-077-4	Sequence 1, Appli
42	458.2	15.0	1796	4	US-08-540-077-2	Sequence 2, Appli
43	337	11.0	337	4	US-09-714-550-2	Sequence 2, Appli
44	308.6	10.1	315	3	US-08-945-424-1	Sequence 1, Appli
45	308.6	10.1	315	4	US-09-718-865-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-735-609-1
Sequence 1, Application US/08735609
Patent No. 595360
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735.609
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-735-609-1
Query Match 100.0%; Score 3052; DB 2; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 CCGTACTGATTTATACCGCGTGCAGTTCCTCAAGAGCCACTTGTAGTCCAGCAGT 60

Db	459	CGTGTAGTGAATTTATACCCGGTAGTTCCTCAAGAGCCACTCTTGAGTGCACAGCGT	518
Qy	61	AGAGTTTTCTCTCCGAGCCGCTCCGACACCGGGACTGAAAATGACATATTAATCTCC	120
Db	519	AGAGTTTTCTCTCCGAGCCGCTCCGACACCGGGACTGAAAATGACATATTAATCTCC	578
Qy	121	ACGAGAGTGTATTAACCGAAGAAATGCCCCCAGTCTTTTGGACCACTGATCGAAGG	180
Db	579	ACGAGAGTGTATTAACCGAAGAAATGCCCCCAGTCTTTTGGACCACTGATCGAAGG	638
Qy	181	TACTGCGTGAATATCTTCCACTCTTAGCCATTTTGAACCACTACCTTCACGAACTGT	240
Db	639	TACTGCGTGAATATCTTCCACTCTTAGCCATTTTGAACCACTACCTTCACGAACTGT	698
Qy	241	ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGAGCGGTTTCGACAGATTTTC	300
Db	699	ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGAGCGGTTTCGACAGATTTTC	758
Qy	301	CCGACTCTGTATATGTGGCGGTGACGAGAAAGGATTAATTAATCTCACTTTCCGCGGGC	360
Db	759	CCGACTCTGTATATGTGGCGGTGACGAGAAAGGATTAATTAATCTCACTTTCCGCGGGC	818
Qy	361	CCGGTCTCCGAGAGCCGCTCACTTTCCCGGACGCCGAGAGCCGAGAGAGAGCT	420
Db	819	CCGGTCTCCGAGAGCCGCTCACTTTCCCGGACGCCGAGAGCCGAGAGAGAGCT	878
Qy	421	TGGGTCCGGTTTCTATGCGCAAACTTTGACCGGAGTGAATGATTTTACCTGCCAGAG	480
Db	879	TGGGTCCGGTTTCTATGCGCAAACTTTGACCGGAGTGAATGATTTTACCTGCCAGAG	938
Qy	481	CTGGCTTTCCACCGAGTACGACGAGATGAAGAGGTGAGGAGTTTGTGTAGATTATG	540
Db	939	CTGGCTTTCCACCGAGTACGACGAGATGAAGAGGTGAGGAGTTTGTGTAGATTATG	998
Qy	541	TGGACACCCCGGGACCGTTGCCAGGCTTGTCAATTAACCGAGAAATACGGGGACC	600
Db	999	TGGACACCCCGGGACCGTTGCCAGGCTTGTCAATTAACCGAGAAATACGGGGACC	1058
Qy	601	CAGATATTAATGTGTTGCTTGTGCTAATATAGAGACTGTGGACTGTGTTGCTACAGTAAGT	660
Db	1059	CAGATATTAATGTGTTGCTTGTGCTAATATAGAGACTGTGGACTGTGTTGCTACAGTAAGT	1118
Qy	661	GAAATATTAAGGACGTGGGTATGAGAGTGGGTTTGGTGTGTAATTTTTTTTTAT	720
Db	1119	GAAATATTAAGGACGTGGGTATGAGAGTGGGTTTGGTGTGTAATTTTTTTTTAT	1178
Qy	721	TTTTACAGTTTGTGGTTTAAAGAAATTTGTATGTGATTTTTTAAAGGCTCGTCTC	780
Db	1179	TTTTACAGTTTGTGGTTTAAAGAAATTTGTATGTGATTTTTTAAAGGCTCGTCTC	1238
Qy	781	TGAACCTGAGCCTGAGCCCGACGAAACCGAGGCTTGCAAGACTTACCGCGCTCTTA	840
Db	1239	TGAACCTGAGCCTGAGCCCGACGAAACCGAGGCTTGCAAGACTTACCGCGCTCTTA	1298
Qy	841	AATGGCGCTGTATCTTGAGACGCCGCAATCACTGTGTCTAGAGAAATGCAATATGAG	900
Db	1299	AATGGCGCTGTATCTTGAGACGCCGCAATCACTGTGTCTAGAGAAATGCAATATGAG	1358
Qy	901	TACGAGTATGCTGTGACTCCGGTCTCTTACACACCTCTGAGATACACCCGGTGTCTC	960
Db	1359	TACGAGTATGCTGTGACTCCGGTCTCTTACACACCTCTGAGATACACCCGGTGTCTC	1418
Qy	961	GCTGTGCCCATTTAAACAGTTGCCGTGAGAGTTGTGTGGCGTGCACAGCCTGTGAATG	1020
Db	1419	GCTGTGCCCATTTAAACAGTTGCCGTGAGAGTTGTGTGGCGTGCACAGCCTGTGAATG	1478
Qy	1021	TATGAGGAGACTGTGTTAACGAGCCGGGCAACTTTGACTTGAACCTGTAACGCCCGAG	1080
Db	1479	TATGAGGAGACTGTGTTAACGAGCCGGGCAACTTTGACTTGAACCTGTAACGCCCGAG	1538
Qy	1081	GCCATTAAGGTAAACCTGTGATTCGTGTGTGTTAAACGCTTGTGTTGCTGAATGAT	1140

Db	1539	GCCATTAAGGTGTAACCTGTGATTCGGTGTGTGGTTAACCCCTTTGTTCGTGATGACT	1598
Qy	1141	TGAATGTAAGTTTATTAAGGAGGTGAGATAATGTTTAACCTTCATGCGCTGTTTAAATGGGCG	1200
Db	1599	TGATGTAAATTTAAATAAAGGCGTGAGTAATGTTTAACTTCGATGGCGGTGTTAAATGGGCGC	1658
Qy	1201	GGGGCTTAAAGGGTATTAATGCGCGCGTGGGCTTAATCTTGGTTACATCTGACCTCATGGA	1260
Db	1659	GGGGCTTAAAGGGGTATTAATGCGCGCGTGGGCTTAATCTTGGTTACATCTGACCTCATGGA	1718
Qy	1261	GGCTTGGAGTGTGTTGGAAATTTTTCTGCTGTGCGTAACTTGTGTGAGACAGAGCTTTAA	1320
Db	1719	GGCTTGGAGTGTGTTGGAAATTTTTCTGCTGTGCGTAACTTGTGTGAGACAGAGCTTTAA	1778
Qy	1321	CAGTAACTCTTGGTTTTGAGAGTTTTCTGTGGGCTCATCCGAGCAAAATTAGTCTGAG	1380
Db	1779	CAGTAACTCTTGGTTTTGAGAGTTTTCTGTGGGCTCATCCGAGCAAAATTAGTCTGAG	1838
Qy	1381	AATTAAGAGAGATTACAAAGGGGAATTTGAAGACTTTGAAATCCGTGGTGGCTGTT	1440
Db	1839	AATTAAGAGAGATTACAAAGGGGAATTTGAAGACTTTGAAATCCGTGGTGGCTGTT	1898
Qy	1441	TGATTTCTTTGAATCTGGGTCACAGAGCGCTTTTCCAAGAAAGTTCATCAAGCTTTTGA	1500
Db	1899	TGATTTCTTTGAATCTGGGTCACAGAGCGCTTTTCCAAGAAAGTTCATCAAGCTTTTGA	1958
Qy	1501	TTTTTCCACACCGGGGGCGCGCTGCGCTGTGCTTTTGAAGTTTAAAGGATTA	1560
Db	1959	TTTTTCCACACCGGGGGCGCGCTGCGCTGTGCTTTTGAAGTTTAAAGGATTA	2018
Qy	1561	ATGAGAGGAAAGAAACCCATCTGAGCGGGGGGTACCTGCTGAAATTTTCTGGCCATGACTCT	1620
Db	2019	ATGAGAGGAAAGAAACCCATCTGAGCGGGGGGTACCTGCTGAAATTTTCTGGCCATGACTCT	2078
Qy	1621	GTGAGAGCGGTTGTGAGACACAAGAAATCGCCCTGTCTATCTGTTGTCTTCGCTCGGCCCGGC	1680
Db	2079	GTGAGAGCGGTTGTGAGACACAAGAAATCGCCCTGTCTATCTGTTGTCTTCGCTCGGCCCGGC	2138
Qy	1681	GATTAATCCGACCGAGAGAGACAGACGACGACAGAGAGAAACCAAGCGCGCGCGCACGA	1740
Db	2139	GATTAATCCGACCGAGAGAGACAGACGACGACAGAGAGAAACCAAGCGCGCGCGCACGA	2198
Qy	1741	GCAGAGCCCATGGAACCCGAGAGCGCGGCTTGGAACCTCGGAAATGAATGTTGTACAGGTG	1800
Db	2199	GCAGAGCCCATGGAACCCGAGAGCGCGGCTTGGAACCTCGGAAATGAATGTTGTGTACAGGTG	2258
Qy	1801	GCTGAATCTGTAATCCAGAACCTGAGACGATTTTGACATTAACAGAGATGGGCAAGGGCTTA	1860
Db	2259	GCTGAATCTGTAATCCAGAACCTGAGACGATTTTGACATTAACAGAGATGGGCAAGGGCTTA	2318
Qy	1861	AAAGGGGTAAAGAGAGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT	1920
Db	2319	AAAGGGGTAAAGAGAGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT	2378
Qy	1921	TTTAAAGCTTAATGACACAGACCGGCTCGAGTGTATTACTTTTCAACAGATCAAGAGTAAT	1980
Db	2379	TTTAAAGCTTAATGACACAGACCGGCTCGAGTGTATTACTTTTCAACAGATCAAGAGTAAT	2438
Qy	1981	TGCGCTAATGAGCTTGAATCTGCTGTGCGCACAGAAATTCATATAGACAGCTGACCACTTAC	2040
Db	2439	TGCGCTAATGAGCTTGAATCTGCTGTGCGCACAGAAATTCATATAGACAGCTGACCACTTAC	2498
Qy	2041	TGCGTGCAGCCAGGGGATGATTTTGTAGAGAGCTTAATAGGGTATATGCAAAAGTGTGGCACTT	2100
Db	2499	TGCGTGCAGCCAGGGGATGATTTTGTAGAGAGCTTAATAGGGTATATGCAAAAGTGTGGCACTT	2558
Qy	2101	AGGCGCAATTTGCAAGTACAGATACAGAACTTGTAAATATCAAGAAATTTGTGTCTACATT	2160
Db	2559	AGGCGCAATTTGCAAGTACAGATACAGAACTTGTAAATATCAAGAAATTTGTGTCTACATT	2618
Qy	2161	TCTGGGAACGGGGCCGAGGTGTGAGATATGATACGAGAGATAGGTTGGCTTTTGAATGTAGC	2220
Db	2619	TCTGGGAACGGGGCCGAGGTGTGAGATATGATACGAGAGATAGGTTGGCTTTTGAATGTAGC	2678

QY 2221 ATGTAATAATATGCGCGGGGCTGCTTGCAATGACCGGGGTGTTATTATGATGTAAGG 2280
 Db 2679 ATGATTAATATGCGCGGGGCTGCTTGCAATGACCGGGGTGTTATTATGATGTAAGG 2738
 QY 2281 TTTACTGCGCCCAATTTTACCGGTAAGGTTTCTGCGCAATACCACTTTATCTTAC 2340
 Db 2739 TTTACTGCGCCCAATTTTACCGGTAAGGTTTCTGCGCAATACCACTTTATCTTAC 2798
 QY 2341 GGTGTAAGCTTCTATGCGGTTTAAACATACCTGTGTGGAAGGCTGACCGATGTAAGGTT 2400
 Db 2799 GGTGTAAGCTTCTATGCGGTTTAAACATACCTGTGTGGAAGGCTGACCGATGTAAGGTT 2858
 QY 2401 CGGCGCTGTGCTTTTAACTGTGTGTGGAAGGCGGTGTGTGTGCGCCCAAAAGAGGCT 2460
 Db 2859 CGGCGCTGTGCTTTTAACTGTGTGTGGAAGGCGGTGTGTGTGCGCCCAAAAGAGGCT 2918
 QY 2461 TCAATTAAAGAAATGCTTTTAAAGGTATCTTGGGTATCTGTCTGTAAGGTTACTCC 2520
 Db 2919 TCAATTAAAGAAATGCTTTTAAAGGTATCTTGGGTATCTGTCTGTAAGGTTACTCC 2978
 QY 2521 AGGGTGGCCCAATGTGCGCTCCGACTGTGTGCTTCAATGATGTAAGAAAGCGTGGCT 2580
 Db 2979 AGGGTGGCCCAATGTGCGCTCCGACTGTGTGCTTCAATGATGTAAGAAAGCGTGGCT 3038
 QY 2581 GTGATTAAGCAATACATGTAATGTGGCAATGCGAGGAGAGGCGCTCTCAGATGCTGACC 2640
 Db 3039 GTGATTAAGCAATACATGTAATGTGGCAATGCGAGGAGAGGCGCTCTCAGATGCTGACC 3098
 QY 2641 TGCTCGGACGGCAATCTGTCACTGTGTGAAGCAATTCACGTAGGCACTCTCGCAAG 2700
 Db 3099 TGCTCGGACGGCAATCTGTCACTGTGTGAAGCAATTCACGTAGGCACTCTCGCAAG 3158
 QY 2701 GCGTGGCCAGTGTGTGCAATACATGTAAGCACTGTGTGCTTCAATGATGTAAGAAAGCGTGGCT 2760
 Db 3159 GCGTGGCCAGTGTGTGCAATACATGTAAGCACTGTGTGCTTCAATGATGTAAGAAAGCGTGGCT 3218
 QY 2761 AGGGGGGTGTCTTCACTTACCAATGCAATTTAGTCACTAAGATATTGCTTGAAGCC 2820
 Db 3219 AGGGGGGTGTCTTCACTTACCAATGCAATTTAGTCACTAAGATATTGCTTGAAGCC 3278
 QY 2821 GAGAGCATGTTCAGAGGTGAACCTGAACGGGGTGTGTGACATGACATGAAATCTTGGAAG 2880
 Db 3279 GAGAGCATGTTCAGAGGTGAACCTGAACGGGGTGTGTGACATGACATGAAATCTTGGAAG 3338
 QY 2881 GTGTGAGTACATGTAAGACCGGACCAAGGTGAGAACCTCTGCAAGTGTGGGTAAACAT 2940
 Db 3339 GTGTGAGTACATGTAAGACCGGACCAAGGTGAGAACCTCTGCAAGTGTGGGTAAACAT 3398
 QY 2941 ATTAGAACCAAGCTGTGATGCTGATGTGAACCGAGAGCTGAAGCCCGATCACTGTGTG 3000
 Db 3399 ATTAGAACCAAGCTGTGATGCTGATGTGAACCGAGAGCTGAAGCCCGATCACTGTGTG 3458
 QY 3001 CTGCGCTGCAACCGCGCTGAAGTTGGCTTACGATGAAATACAGATTGAG 3052
 Db 3459 CTGCGCTGCAACCGCGCTGAAGTTGGCTTACGATGAAATACAGATTGAG 3510

RESULT 2
 US-08-735-609-1
 Sequence 1, Application US/08735609
 Patent No. 5994132

GENERAL INFORMATION:

APPLICANT: Chamberlain, Jeffrey S.
 Amalfitano, Andrea
 Hauser, Michael A.
 Kumar-Singh, Rajendra
 Hartigan-O'Connor, Dennis J.
 TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Medlen & Carroll, LLP
 STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco
 STATE: California
 COUNTRY: United States Of America
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/735,609
 FILING DATE: 23-Oct-1996
 CLASSIFICATION: <unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Ingolia, Diane E.
 REGISTRATION NUMBER: 40,027
 REFERENCE/DOCKET NUMBER: UM-02484
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35935 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-08-735-609-1

Query Match 100.0%; Score 3052; DB 2; Length 35935;

Best Local Similarity 100.0%; Pred. No. 0; Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTAGTATTTATACCGGGTAGTTCCTCAAGAGCCACTTGATGCGCAGCGAGT 60
 Db 459 CGGTAGTATTTATACCGGGTAGTTCCTCAAGAGCCACTTGATGCGCAGCGAGT 518
 QY 61 AGAGTTTCTCTCCGACCGCTCCGACACCGGAGCTGAATAATGACATATTATCTGCC 120
 Db 519 AGAGTTTCTCTCCGACCGCTCCGACACCGGAGCTGAATAATGACATATTATCTGCC 578
 QY 121 ACGAGGTGTATTATCCGAAGAAATGCGCGCACTCTTTTGGACGAGTGTGGAAGG 180
 Db 579 ACGAGGTGTATTATCCGAAGAAATGCGCGCACTCTTTTGGACGAGTGTGGAAGG 638
 QY 181 TACTGGCTGTAATCTTCCACTCTCTAGCACTTTTGAACCACTAACCTTACGAACTGT 240
 Db 639 TACTGGCTGTAATCTTCCACTCTCTAGCACTTTTGAACCACTAACCTTACGAACTGT 698
 QY 241 ATGATTTAGACGTACCGGCCCGGAGATCCCAAGAGAGCGGTTTCGACGATTTTTC 300
 Db 699 ATGATTTAGACGTACCGGCCCGGAGATCCCAAGAGAGCGGTTTCGACGATTTTTC 758
 QY 301 CCGACTCTGTAATGTGCGGTGTCAGAAAGGATTTGACTTACTCATCTTTCCGCGCGCC 360
 Db 759 CCGACTCTGTAATGTGCGGTGTCAGAAAGGATTTGACTTACTCATCTTTCCGCGCGCC 818
 QY 361 CCGGTTCTCGGAGCGCGCTCACCTTTCCCGGCGAGCCGAGCAGCGGAGAGAGGCT 420
 Db 819 CCGGTTCTCGGAGCGCGCTCACCTTTCCCGGCGAGCCGAGCAGCGGAGAGAGGCT 878
 QY 421 TGGGTCCGGTTTCTATGCAAACTTGTATCCGAGAGTGTGATCTTACTCTGCAAGG 480
 Db 879 TGGGTCCGGTTTCTATGCAAACTTGTATCCGAGAGTGTGATCTTACTCTGCAAGG 938
 QY 481 CTGCTTTTCCACCAAGTGAAGAGATGAAAGGAGTGTGATGATTTGTGTTAATTATG 540
 Db 939 CTGCTTTTCCACCAAGTGAAGAGATGAAAGGAGTGTGATGATTTGTGTTAATTATG 998
 QY 541 TGAGACACCGCGGAGCGGTTGACAGGCTTGTCAATTATCACCGAGAGAAACGGGGGACC 600

Db 999 TGAGACACCCGGGACGGTTGCAAGTCTTGTCATATCACCGAGAAATA CGGGGAGACC 1058
Qy 601 CAGATATTATATGTTTCGCTTTGCTATATGAGACCTGTGGCATGTGTTGTCTACAGTAAGT 660
Db 1059 CAGATATTATATGTTTCGCTTTGCTATATGAGACCTGTGGCATGTGTTGTCTACAGTAAGT 1118
Qy 661 GAAATTTATGGGCGATGGGTATAGATGTGTGGTTTGGTGTGAATTTTTTTTTTAAAT 720
Db 1119 GAAATTTATGGGCGATGGGTATAGATGTGTGGTTTGGTGTGAATTTTTTTTTTAAAT 1178
Qy 721 TTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATTGTGATTTTTTTTAAAGGTCCTGTGC 780
Db 1179 TTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATTGTGATTTTTTTTAAAGGTCCTGTGC 1238
Qy 781 TGAACCTGAGCTGACCCCGGACGAGAACCGGAGCTTGCAAGACTTACCCGCGCTCTAA 840
Db 1239 TGAACCTGAGCTGAGCCCGGACGAGAACCGGAGCTTGCAAGACTTACCCGCGCTCTAA 1298
Qy 841 AATGGCGCTGCTATCTCTGAGACGCGCCGACATCACTGTCTAGAGAAATGCAATAGTAG 900
Db 1299 AATGGCGCTGCTATCTCTGAGACGCGCCGACATCACTGTCTAGAGAAATGCAATAGTAG 1358
Qy 901 TACGATATAGCTGTGATCTCCGGTCTTCTTAAACAACCTTCTAGATACACCCGGTGTCCC 960
Db 1359 TACGATATAGCTGTGATCTCCGGTCTTCTTAAACAACCTTCTAGATACACCCGGTGTCCC 1418
Qy 961 GCTGCGCCCAATTAAACCAAGTTGCGGTGAGAGATTGTTGGGCGTCCGACGGCTGTGGAAATG 1020
Db 1419 GCTGCGCCCAATTAAACCAAGTTGCGGTGAGAGATTGTTGGGCGTCCGACGGCTGTGGAAATG 1478
Qy 1021 TATCGAGGACTTGTCTTAAACGAGCCTGGGCAACCTTTGGACTTGAAGCTTAAACGCCAG 1080
Db 1479 TATCGAGGACTTGTCTTAAACGAGCCTGGGCAACCTTTGGACTTGAAGCTTAAACGCCAG 1538
Qy 1081 GCCATTAAGTGTAAACCTGTGATTTGCTGTGTGTTAAACGCTTTGTTTGTGTGAATGAGT 1140
Db 1539 GCCATTAAGTGTAAACCTGTGATTTGCTGTGTGTTAAACGCTTTGTTTGTGTGAATGAGT 1598
Qy 1141 TGATGTAAGTTTAAATAAGGTTGAGATTAATGTTTAACTTGATGGCGGTAAATGGGGCC 1200
Db 1599 TGATGTAAGTTTAAATAAGGTTGAGATTAATGTTTAACTTGATGGCGGTAAATGGGGCC 1658
Qy 1201 GGGGCTTAAAGGTTATTAATATGCGCCGTGGCTAATCTTGGTTAACATCTGACCTCATGGA 1260
Db 1659 GGGGCTTAAAGGTTATTAATATGCGCCGTGGCTAATCTTGGTTAACATCTGACCTCATGGA 1718
Qy 1261 GGGTGGGAGTGTGTTGGAAGATTTTCTGTGTGCTAACTTGTGGAACAGAGCTCTAA 1320
Db 1719 GGGTGGGAGTGTGTTGGAAGATTTTCTGTGTGCTAACTTGTGGAACAGAGCTCTAA 1778
Qy 1321 CAGTACCTCTGTTTGGAGGTTTCTGTGGGGCTCAATCCGAGGCAAGTTAGTCTGAG 1380
Db 1779 CAGTACCTCTGTTTGGAGGTTTCTGTGGGGCTCAATCCGAGGCAAGTTAGTCTGAG 1838
Qy 1381 AATTAAAGAGATTAAACAAGTGGGAATTTGAAGAGCTTTTGAATCTGTGTGAGCTGTT 1440
Db 1839 AATTAAAGAGATTAAACAAGTGGGAATTTGAAGAGCTTTTGAATCTGTGTGAGCTGTT 1898
Qy 1441 TGATTTCTTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCAATCAAGACTTTGGA 1500
Db 1899 TGATTTCTTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCAATCAAGACTTTGGA 1958
Qy 1501 TTTTTCACACACCGGGGCGCGTGGCGGCTGCTTGTGCTTTTGAAGTTTAAAGGATTA 1560
Db 1959 TTTTTCACACACCGGGGCGCGTGGCGGCTGCTTGTGCTTTTGAAGTTTAAAGGATTA 2018
Qy 1561 ATGAGGCGAAGAAAACCAATCTGAGCGGGGGGTACCTGTGATTTTCTGSCCATGCAATCT 1620
Db 2019 ATGAGGCGAAGAAAACCAATCTGAGCGGGGGGTACCTGTGATTTTCTGSCCATGCAATCT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGTCTACTGTTGTCTCCGTCGCGCGGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGTCTACTGTTGTCTCCGTCGCGCGGC 2138

Qy 1681 GATAATACCGACGAGAGAGACGACGACGACGACGAGAGAAAGCCAGCGCGCGGACAGA 1740
Db 2139 GATAATACCGACGAGAGAGACGACGACGACGACGAGAGAAAGCCAGCGCGCGGACAGA 2198
Qy 1741 GCAGAGCCATGGAACCCGAGAGCGGCGCTGGAACCTCTGGGAATGAATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCATGGAACCCGAGAGCGGCGCTGGAACCTCTGGGAATGAATGTTGTACAGGTG 2258
Qy 1801 GCTGAACCTGATCCAGAACTGAGACGCAATTTTGACAAATTACAGAGATGGCGAGGGCTTA 1860
Db 2259 GCTGAACCTGATCCAGAACTGAGACGCAATTTTGACAAATTACAGAGATGGCGAGGGCTTA 2318
Qy 1861 AAGGGGGTAAAGAGAGGAGCGGGGGCTTTGAGGCTACAGAGAGGCTAGGAATCTACT 1920
Db 2319 AAGGGGGTAAAGAGAGGAGCGGGGGCTTTGAGGCTACAGAGAGGCTAGGAATCTACT 2378
Qy 1921 TTTAGCTTAAATGACACAGACCCGTCTGAGTGTATTACTTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAAATGACACAGACCCGTCTGAGTGTATTACTTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGGCTTATGAGCTTGATCTGTGGCGCAAGATTTTCATAGACAGCTGACCACTTAC 2040
Db 2439 TGGCTTATGAGCTTGATCTGTGGCGCAAGATTTTCATAGACAGCTGACCACTTAC 2498
Qy 2041 TGGCTGAGCGCAGGGGANTGATTTTGAAGAGCTATTAGGGATATTGCAAGGTCGACTT 2100
Db 2499 TGGCTGAGCGCAGGGGANTGATTTTGAAGAGCTATTAGGGATATTGCAAGGTCGACTT 2558
Qy 2101 AGGCGAATTTGCAAGTACAGAGTACAGAACTTGTAAATATCAGGAATGTTGTCTACAT 2160
Db 2559 AGGCGAATTTGCAAGTACAGAGTACAGAACTTGTAAATATCAGGAATGTTGTCTACAT 2618
Qy 2161 TCTGGAAACGGGCGCGAGGCTGAGATAGATACGAGATAGAGGTGGCTTTAGATGTAGC 2220
Db 2619 TCTGGAAACGGGCGCGAGGCTGAGATAGATACGAGATAGAGGTGGCTTTAGATGTAGC 2678
Qy 2221 ATGATTAATATGATGCGGGGGGTGCTTGCGATGGAACGGGGGTGTTAATATGAAATGTAAG 2280
Db 2679 ATGATTAATATGATGCGGGGGGTGCTTGCGATGGAACGGGGGTGTTAATATGAAATGTAAG 2738
Qy 2281 TTTACTGGCCCCAATTTTAAAGCGATTTCTGTGCGCAATACCAACTTATCTTACAC 2340
Db 2739 TTTACTGGCCCCAATTTTAAAGCGATTTCTGTGCGCAATACCAACTTATCTTACAC 2798
Qy 2341 GGTGTAAAGCTTCTATGGGTTTAAACAATACCTGTGTGGAAGCTTGAACGATTAAGGTT 2400
Db 2799 GGTGTAAAGCTTCTATGGGTTTAAACAATACCTGTGTGGAAGCTTGAACGATTAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGTGGGTGTGCCCCCAAAAGCAGGGCT 2460
Db 2859 CGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGTGGGTGTGCCCCCAAAAGCAGGGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTTGAAGAGTGAACCTTGGGTAATCTGTCTGAGGGTAATCTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTTGAAGAGTGAACCTTGGGTAATCTGTCTGAGGGTAATCTCC 2978
Qy 2521 AGGGTGGCCACAATGTGGGCTCCGACTGTGTGCTTCAATGCTAGTGAAGAAAGGTGGCT 2580
Db 2979 AGGGTGGCCACAATGTGGGCTCCGACTGTGTGCTTCAATGCTAGTGAAGAAAGGTGGCT 3038
Qy 2581 GTGATTAAGCAATAATGATGTGGAACCTGCGAGGACAGGGGCTCTCAGATCTGAC 2640
Db 3039 GTGATTAAGCAATAATGATGTGGAACCTGCGAGGACAGGGGCTCTCAGATCTGAC 3098
Qy 2641 TGCTCGAGCGCAACTGTCACTGTGTAAGACATTCACGTAAGCCAGCACTTCTGCAAG 2700
Db 3099 TGCTCGAGCGCAACTGTCACTGTGTAAGACATTCACGTAAGCCAGCACTTCTGCAAG 3158
Qy 2701 GCTTGGCAAGTGTGAGCAATACTGACCCGCTGTCTTGTGCAATTTGGGTTAACAGG 2760
Db 3159 GCTTGGCAAGTGTGAGCAATACTGACCCGCTGTCTTGTGCAATTTGGGTTAACAGG 3218

QY 2761 AGGGGGGTTCCTACCTTACCAATGCAATTTGAGTCACTAAGATTTGCTTGAGCCC 2820
DB 3219 AGGGGGGTTCCTACCTTACCAATGCAATTTGAGTCACTAAGATTTGCTTGAGCCC 3278
QY 2821 GAGAGCATGTCAGAGTGAACCTGAAAGGGGTGTTGATGATGACATGAAGATGAGAG 2880
DB 3279 GAGAGCATGTCAGAGTGAACCTGAAAGGGGTGTTGATGATGACATGAAGATGAGAG 3338
QY 2881 GTGCTGAGTACGATGAGACCCGACCAAGTGCAGACCTTGAGTGGCGTAAACAT 2940
DB 3339 GTGCTGAGTACGATGAGACCCGACCAAGTGCAGACCTTGAGTGGCGTAAACAT 3398
QY 2941 ATTAGGAACCAAGCTGTGATGCTGATGATGACCCAGAGAGCTGAGAGCCGATCACTTG 3000
DB 3399 ATTAGGAACCAAGCTGTGATGCTGATGATGACCCAGAGAGCTGAGAGCCGATCACTTG 3458
QY 3001 CTGGCCCTGCACCCGCGCTGATGATTTGGCTCTAGCGATGAATACGATTGAG 3052
DB 3459 CTGGCCCTGCACCCGCGCTGATGATTTGGCTCTAGCGATGAATACGATTGAG 3510

RESULT 3

US-08-379-452-43
Sequence 43. Application US/08379452
Patent No. 6040174
GENERAL INFORMATION:
APPLICANT: IMELER, Jean-Luc
APPLICANT: MEHTALI, Majid
APPLICANT: PAVRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,452
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00624
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 029395-002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-379-452-43

Query Match 100.0%; Score 3052; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTAGTATTTATACCGGATGATTCCTCAAGAGCCACTCTTGAGTCCAGCGAGT 60
|||||

DB 459 CGGTAGTATTTATATACCGGATGATTCCTCAAGAGCCACTCTTGAGTCCAGCGAGT 518
QY 61 AGAGTTTTCCTCCGAGCCGCTCCGACACCGGAGCTGAATAATGACATATATCTTGCC 120
DB 519 AGAGTTTTCCTCCGAGCCGCTCCGACACCGGAGCTGAATAATGACATATATCTTGCC 578
QY 121 ACGAGGTGTTATACCGAAGAAATGCGCGCATCTTTTGGACCACTGATTCGAAGAG 180
DB 579 ACGAGGTGTTATACCGAAGAAATGCGCGCATCTTTTGGACCACTGATTCGAAGAG 638
QY 181 TACTGCTGATTAATCTTCAACCTCTAGCCATTTTGAACCACTACCTTCACGAATCTGT 240
DB 639 TACTGCTGATTAATCTTCAACCTCTAGCCATTTTGAACCACTACCTTCACGAATCTGT 698
QY 241 ATGATTTAGAGTACGAGCCCGGAGAGATCCCAAGAGAGCGGTTTCGAGATTTTTC 300
DB 699 ATGATTTAGAGTACGAGCCCGGAGAGATCCCAAGAGAGCGGTTTCGAGATTTTTC 758
QY 301 CCGACTCTGTAATGTGGCGGTGACAGAGAGGATTTGACTTACTACTTTTCCGCGGCGC 360
DB 759 CCGACTCTGTAATGTGGCGGTGACAGAGAGGATTTGACTTACTACTTTTCCGCGGCGC 818
QY 361 CCGGTTCTCCGAGCCGCTCACCTTTCCGCGAGCCCGAGCAGCCGAGAGAGGCT 420
DB 819 CCGGTTCTCCGAGCCGCTCACCTTTCCGCGAGCCCGAGCAGCCGAGAGAGGCT 878
QY 421 TGGGTCCGTTTCTATGCAAACTTTGACCGAGGTGATGATCTTAACCTGCCAGAG 480
DB 879 TGGGTCCGTTTCTATGCAAACTTTGACCGAGGTGATGATCTTAACCTGCCAGAG 938
QY 481 CTGGCTTTCACCGAGTACGAGAGATGAAGGGTGGAGAGTTGTGTTAATTTATG 540
DB 939 CTGGCTTTCACCGAGTACGAGAGATGAAGGGTGGAGAGTTGTGTTAATTTATG 998
QY 541 TGGAGACCCCGGAGCGGTGACAGTCTTGTCAATTAACAACGAGAGATACGGGGAGCC 600
DB 999 TGGAGACCCCGGAGCGGTGACAGTCTTGTCAATTAACAACGAGAGATACGGGGAGCC 1058
QY 601 CAGATATTATGTGTTGCTTGTCTATATGAGACCTGAGCATTTGTCTACAGTAAGT 660
DB 1059 CAGATATTATGTGTTGCTTGTCTATATGAGACCTGAGCATTTGTCTACAGTAAGT 1118
QY 661 GAAATTTATGGGCGATGGGTATGAGTGTGGTTGGTGTGTTATTTTAT 720
DB 1119 GAAATTTATGGGCGATGGGTATGAGTGTGGTTGGTGTGTTATTTTAT 1178
QY 721 TTTTACGTTTGTGTTTAAAGAAATTTGATTTGATTTTAAAGGTCGTGTC 780
DB 1179 TTTTACGTTTGTGTTTAAAGAAATTTGATTTGATTTTAAAGGTCGTGTC 1238
QY 781 TGAACCTGAGCTGAGCCGAGCCAGAACCGAGCCTGCAAGACTACCGCGCTCTAA 840
DB 1239 TGAACCTGAGCTGAGCCGAGCCAGAACCGAGCCTGCAAGACTACCGCGCGCTCTAA 1298
QY 841 AATGGCGCTGCTATCTGAGAGCCCGGACATCACTGTGTCTGAAGATGATAGAG 900
DB 1299 AATGGCGCTGCTATCTGAGAGCCCGGACATCACTGTGTCTGAAGATGATAGAG 1358
QY 901 TAGGATAGCTGATCTCCGCTCTTCTTAAACACCTCTGAGATCAACCCGGTGTCC 960
DB 1359 TAGGATAGCTGATCTCCGCTCTTCTTAAACACCTCTGAGATCAACCCGGTGTCC 1418
QY 961 GCTGTGCCCATTTAAACAGTTGCGTGAAGATTGTTGGGCGTCCGAGGCTGTGAATG 1020
DB 1419 GCTGTGCCCATTTAAACAGTTGCGTGAAGATTGTTGGGCGTCCGAGGCTGTGAATG 1478
QY 1021 TATGAGAGCTTGCTTAAACAGCTGAGCACTTTTGAATGAGCTTAAACGCCCTAG 1080
DB 1479 TATGAGAGCTTGCTTAAACAGCTGAGCACTTTTGAATGAGCTTAAACGCCCTAG 1538
QY 1081 GCATTAAGTGTAAACGTGATTTGCGTGTGTTAAAGCCTTGTGTTGCTGATGAGT 1140
DB 1539 GCATTAAGTGTAAACGTGATTTGCGTGTGTTAAAGCCTTGTGTTGCTGATGAGT 1598

QY 1141 TGATGTAAGTTTAAATAAGGGGTGAGATTAATGTTTAACTTGATGCGCGGTAAATGGGGC 1200
Db 1599 TGATGTAAGTTTAAATAAGGGGTGAGATTAATGTTTAACTTGATGCGCGGTAAATGGGGC 1658
QY 1201 GGGGCTTAAAGGATTAATATGCGCGGTGATATCTTGTTATCATCTGATGATGGA 1260
Db 1659 GGGGCTTAAAGGATTAATATGCGCGGTGATATCTTGTTATCATCTGATGATGGA 1718
QY 1261 GGGCTTGGAGGTGTTGGAAAGTTTTTCTGCTGTGCTGATCTTGCTGGAACAGAGCTTAA 1320
Db 1719 GGGCTTGGAGGTGTTGGAAAGTTTTTCTGCTGTGCTGATCTTGCTGGAACAGAGCTTAA 1778
QY 1321 CAGTACCTCTTGTTGGAGGTCTGCTGGGGCTCAATCCGAGCAAGATTAAGTCTGAG 1380
Db 1779 CAGTACCTCTTGTTGGAGGTCTGCTGGGGCTCAATCCGAGCAAGATTAAGTCTGAG 1838
QY 1381 AATTAAAGAGGATTAACAAGTGGAAATTTGAAGAGCTTTGAAATCTGTGTGAGCTGTT 1440
Db 1839 AATTAAAGAGGATTAACAAGTGGAAATTTGAAGAGCTTTGAAATCTGTGTGAGCTGTT 1898
QY 1441 TGATTTCTTGAATCTGGGTCAACAGCGCTTTTCCAGAGAAAGTCATCAAGACTTTGGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACAGCGCTTTTCCAGAGAAAGTCATCAAGACTTTGGA 1958
QY 1501 TTTTTCACACCGGGGCGCGCTGCGGCTGCTGTTGCTTTTGAAGTTTAAAGAAATAA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGGCTGCTGTTGCTTTTGAAGTTTAAAGAAATAA 2018
QY 1561 ATGAGAGGAAAGAAACCCATCTGAAGCGGGGGTACCTGTGATTTTCTGGCCATGATCT 1620
Db 2019 ATGAGAGGAAAGAAACCCATCTGAAGCGGGGGTACCTGTGATTTTCTGGCCATGATCT 2078
QY 1621 GTGAGAGCGGTGTGAGACCAAGAAATCGCTGTCTGATCTGTTGTTCTCCGTCCGCGGC 1680
Db 2079 GTGAGAGCGGTGTGAGACCAAGAAATCGCTGTCTGATCTGTTGTTCTCCGTCCGCGGC 2138
QY 1681 GATTAATCCGACGAGAGAGCAGCAGCAGCAGAGAGAAACCGCGCGCGCGCAGGA 1740
Db 2139 GATTAATCCGACGAGAGAGCAGCAGCAGCAGCAGAGAGAAACCGCGCGCGCGCAGGA 2198
QY 1741 GCAGAGCCCATGAAACCCGAGAGCGCGCTGAGACCTTGAGAAATGAATGTTGAACAGGTG 1800
Db 2199 GCAGAGCCCATGAAACCCGAGAGCGCGCTGAGACCTTGAGAAATGAATGTTGAACAGGTG 2258
QY 1801 GCTGAATCTGATCCAGAACTGAGACGCAATTTGACATTAACAAGAGATGGCAGGGCTA 1860
Db 2259 GCTGAATCTGATCCAGAACTGAGACGCAATTTGACATTAACAAGAGATGGCAGGGCTA 2318
QY 1861 AAGGGGGTAAAGAGAGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTAGCT 1920
Db 2319 AAGGGGGTAAAGAGAGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTAGCT 2378
QY 1921 TTTAGCTTAATGACCAAGACCGTCTGAGTGAATTAATTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACCAAGACCGTCTGAGTGAATTAATTTTCAACAGATCAAGATTAAT 2438
QY 1981 TGCGCTAATGAGCTTGAATCTGCTGGCGCAAGAAATTTCCAAAGACAGCTGACCACTTAC 2040
Db 2439 TGCGCTAATGAGCTTGAATCTGCTGGCGCAAGAAATTTCCAAAGACAGCTGACCACTTAC 2498
QY 2041 TGCGTGCAGCCAGGGGATGATTTTGAAGAGCTATTAGGGTATTTGCAAAAGGTGGACATT 2100
Db 2499 TGCGTGCAGCCAGGGGATGATTTTGAAGAGCTATTAGGGTATTTGCAAAAGGTGGACATT 2558
QY 2101 AGGCGAAGTTGCAAGTACAGAGTACAGAACTTGTAAATATCAGGAATGTTGTCTACATT 2160
Db 2559 AGGCGAAGTTGCAAGTACAGAGTACAGAACTTGTAAATATCAGGAATGTTGTCTACATT 2618
QY 2161 TCTGGGAAACGGGGCGGAGGTGAGATAGATACGAGAGTAAAGGTGGCTTTAGATGTAAGC 2220
Db 2619 TCTGGGAAACGGGGCGGAGGTGAGATAGATACGAGAGTAAAGGTGGCTTTAGATGTAAGC 2678

QY 2221 ATGATAAATATGTCGCGGGGGTGTCTTGCCATGGAACGGGGGTGTTATTAATGATGTAAG 2280
Db 2679 ATGATAAATATGTCGCGGGGGTGTCTTGCCATGGAACGGGGGTGTTATTAATGATGTAAG 2738
QY 2281 TTTACTGGCCCAATTTTAAACCGGTACGGTTTTCTGCGCAATACCAACTTATCTTACAC 2340
Db 2739 TTTACTGGCCCAATTTTAAACCGGTACGGTTTTCTGCGCAATACCAACTTATCTTACAC 2798
QY 2341 GGTGTAGCTTCTATGAGGTTTAAACAATACCTGTGTGGAAGCTGTGAGACCGATGAAGGTT 2400
Db 2799 GGTGTAGCTTCTATGAGGTTTAAACAATACCTGTGTGGAAGCTGTGAGACCGATGAAGGTT 2858
QY 2401 CGGGGCTGTGCTTTTAACTGCTGCTGAGAAAGGGGTGTGTGTGCGCCCAAAAGAGGCT 2460
Db 2859 CGGGGCTGTGCTTTTAACTGCTGCTGAGAAAGGGGTGTGTGTGCGCCCAAAAGAGGCT 2918
QY 2461 TCAATTAAGAAATGCTCTTTGAAAGGTGAACCTTGGGTATCTGTCTGAGGGTAACTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTTGAAAGGTGAACCTTGGGTATCTGTCTGAGGGTAACTCC 2978
QY 2521 AGGGTGGCCCAATGTCGCTCGGACTGTGTGCTTCAATGCTAGTGAAGAAAGGTGCT 2580
Db 2979 AGGGTGGCCCAATGTCGCTCGGACTGTGTGCTTCAATGCTAGTGAAGAAAGGTGCT 3038
QY 2581 GTGATTAAGCATTAACATGATATGTCGCACTGCGAGGACAGGGGCTCTCAGATCTGACC 2640
Db 3039 GTGATTAAGCATTAACATGATATGTCGCACTGCGAGGACAGGGGCTCTCAGATCTGACC 3098
QY 2641 TGCTCGGACGGCAACTGTCACTGCTGGAAGCAATTCACGTAAGCCACTCTGCAAG 2700
Db 3099 TGCTCGGACGGCAACTGTCACTGCTGGAAGCAATTCACGTAAGCCACTCTGCAAG 3158
QY 2701 GCCCTGGCAAGTTTGAAGCAATACATCTGACCCGCGTCTCTTGCAATTTGGGGTAAACAG 2760
Db 3159 GCCCTGGCAAGTTTGAAGCAATACATCTGACCCGCGTCTCTTGCAATTTGGGGTAAACAG 3218
QY 2761 AGGGGGGTGTTCTCACTTCACTCAATGCAATGGAATGATGACACTAAGATTTGTTAGGCC 2820
Db 3219 AGGGGGGTGTTCTCACTTCACTCAATGCAATGGAATGATGACACTAAGATTTGTTAGGCC 3278
QY 2821 GAGAGCATGTCGAAGGTGAACCTGGAACCGGGGTGTTGAACATGACATGAAAGATCTGGAAG 2880
Db 3279 GAGAGCATGTCGAAGGTGAACCTGGAACCGGGGTGTTGAACATGACATGAAAGATCTGGAAG 3338
QY 2881 GTGCTGAGTACGATGAGTGAACCCGACAGGTGACGACCCGCGAGGTGGCGGTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGTGAACCCGACAGGTGACGACCCGCGAGGTGGCGGTAAACAT 3398
QY 2941 ATTAGAACCAGCTGTGATGCTGATGTGACCGAGAGCTGAGAGCCCGATCACTTGAGTG 3000
Db 3399 ATTAGAACCAGCTGTGATGCTGATGTGACCGAGAGCTGAGAGCCCGATCACTTGAGTG 3458
QY 3001 CTGGCTGCAACCGCGCTGAGTTTGCTCTGAGCGATGAAGATACAGATTGAG 3052
Db 3459 CTGGCTGCAACCGCGCTGAGTTTGCTCTGAGCGATGAAGATACAGATTGAG 3510

RESULT 4
US-09-315-372-1
Sequence 1, Application US/09315372
Patent No. 6057158
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Harigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco

QY 1 CGTGTAGTATTTATACCCGGTGAATTCCTCAAGAGCCACTCTTGAAGTCCAGCGAGT 60
Db 459 CGTGTAGTATTTATACCCGGTGAATTCCTCAAGAGCCACTCTTGAAGTCCAGCGAGT 518
QY 61 AGAGTTTCTCTCGAGCCGCTCCGACACCGGGGCTGAAATAGACATTTATCTGGCC 120
Db 519 AGAGTTTCTCTCGAGCCGCTCCGACACCGGGGCTGAAATAGACATTTATCTGGCC 578
QY 121 ACGGAGGTGTTATTAACGAAAGAAATGGCCGACGCTTTTGAACAGCTGATCGAAGAG 180
Db 579 ACGGAGGTGTTATTAACGAAAGAAATGGCCGACGCTTTTGAACAGCTGATCGAAGAG 638
QY 181 TACTGGCTGATATCTTCCACTCTCTAGCCATTTTGAACCACTTCTTCAAGACTGT 240
Db 639 TACTGGCTGATATCTTCCACTCTCTAGCCATTTTGAACCACTTCTTCAAGACTGT 698
QY 241 ATGATTTAGAGTACCGGCCCCCGAAGATCCCAACGAGGAGCGGTTTCGAGATTTTTC 300
Db 699 ATGATTTAGAGTACCGGCCCCCGAAGATCCCAACGAGGAGCGGTTTCGAGATTTTTC 758
QY 301 CCGACTCTGATATGTGGCGGTGACGAAAGGATTTGACTTACTACTTTTCCGCGGCGC 360
Db 759 CCGACTCTGATATGTGGCGGTGACGAAAGGATTTGACTTACTACTTTTCCGCGGCGC 818
QY 361 CCGGTTCTCCGAGCCGCTCACTCTTCCGCGACGCCGAGACCCGAGACAGAGCTT 420
Db 819 CCGGTTCTCCGAGCCGCTCACTCTTCCGCGACGCCGAGACCCGAGACAGAGCTT 878
QY 421 TGGTCCGGTTCTATGCGCAACCTTGAACGGAGGTGATGATCTTACCTGACCAAGAG 480
Db 879 TGGTCCGGTTCTATGCGCAACCTTGAACGGAGGTGATGATCTTACCTGACCAAGAG 938
QY 481 CTGGCTTTCCACCCAGTACGACGAGATGAAAGAGGTGAGAGATTTGTGTAGATTATG 540
Db 939 CTGGCTTTCCACCCAGTACGACGAGATGAAAGAGGTGAGAGATTTGTGTAGATTATG 998
QY 541 TGGAGACCCCGGGGACGGTTGACAGTCTTGTCAATTAACCGAGAGAAATCGGGGAGC 600
Db 999 TGGAGACCCCGGGGACGGTTGACAGTCTTGTCAATTAACCGAGAGAAATCGGGGAGC 1058
QY 601 CAGATTTATGTGTGCTTGTATATGAGACCTGTGAGCATTTTGTCTACAGTAAGT 660
Db 1059 CAGATTTATGTGTGCTTGTATATGAGACCTGTGAGCATTTTGTCTACAGTAAGT 1118
QY 661 GAAATTTATGGGCAAGGTGATAGAGTGTGGTTGTGTGTAATTTTATTTTAT 720
Db 1119 GAAATTTATGGGCAAGGTGATAGAGTGTGGTTGTGTGTAATTTTATTTTAT 1178
QY 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTGATTTTAAAGGTCTGTGTC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTGATTTTAAAGGTCTGTGTC 1238
QY 781 TGAACCTGAGCGCTGAGCCCGAGCAGAAACCGGAGCTGTGAAAGCTTCCCTTA 840
Db 1239 TGAACCTGAGCGCTGAGCCCGAGCAGAAACCGGAGCTGTGAAAGCTTCCCTTA 1298
QY 841 AATGGCCCTGTCTATCTCTGAGACGCCCGACATCACTGTGTCTAGAGAAATGCAATAG 900
Db 1299 AATGGCCCTGTCTATCTCTGAGACGCCCGACATCACTGTGTCTAGAGAAATGCAATAG 1358
QY 901 TACGGATAGCTGTGATCTCCGCTCTTCTAACACACTTCTGAGATPACAACCCGCTGTCC 960
Db 1359 TACGGATAGCTGTGATCTCCGCTCTTCTAACACACTTCTGAGATPACAACCCGCTGTCC 1418
QY 961 GCTGTGCCCATTTAAACAGTTGCGGTGAGAGTTGTGGGCTGTGCAAGGTGTGAGATG 1020
Db 1419 GCTGTGCCCATTTAAACAGTTGCGGTGAGAGTTGTGGGCTGTGCAAGGTGTGAGATG 1478
QY 1021 TATCGAGAGCTTGTCTTAACGAGCTGTGAGCACTTTTGAACCTTGTAAACGCCCTAG 1080
Db 1479 TATCGAGAGCTTGTCTTAACGAGCTGTGAGCACTTTTGAACCTTGTAAACGCCCTAG 1538

QY 1081 GCCATTAAGGTGTAAACCTGTGATTTGCTGTGTGTAAACGCTTTGTGTCTGATAGT 1140
Db 1539 GCCATTAAGGTGTAAACCTGTGATTTGCTGTGTGTAAACGCTTTGTGTCTGATAGT 1598
QY 1141 TGATGTAAAGTTTAAAGGGTGAGATTAAGTTTAACTGTGATGCGGCTTAAATGGGGC 1200
Db 1599 TGATGTAAAGTTTAAAGGGTGAGATTAAGTTTAACTGTGATGCGGCTTAAATGGGGC 1658
QY 1201 GGGGCTTAAAGGGTATTAATGCGCGGTGAGCTAATCTTGTGTTACATCTGACTATGTA 1260
Db 1659 GGGGCTTAAAGGGTATTAATGCGCGGTGAGCTAATCTTGTGTTACATCTGACTATGTA 1718
QY 1261 GGGCTTGAAGTGTGGAAGATTTTCTGCTGTGCTTAACTTGTGGAACAGAGCTCTAA 1320
Db 1719 GGGCTTGAAGTGTGGAAGATTTTCTGCTGTGCTTAACTTGTGGAACAGAGCTCTAA 1778
QY 1321 CAGTACCTCTTGTGTTGAGAGTTCTGTGGGGCTCATCCAGGCAAGTTAGTCTGAG 1380
Db 1779 CAGTACCTCTTGTGTTGAGAGTTCTGTGGGGCTCATCCAGGCAAGTTAGTCTGAG 1838
QY 1381 AATTAAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGGTGAAGTGT 1440
Db 1839 AATTAAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGGTGAAGTGT 1898
QY 1441 TGATTTCTTGAATCTGGGTCAACAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTGA 1958
QY 1501 TTTTTCACACCGGGGGGCGCTGCGGCTGTGCTTTTGTGTTTAAAGGATTA 1560
Db 1959 TTTTTCACACCGGGGGGCGCTGCGGCTGTGCTTTTGTGTTTAAAGGATTA 2018
QY 1561 ATGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGTGATTTTGTGGCATGATCT 1620
Db 2019 ATGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGTGATTTTGTGGCATGATCT 2078
QY 1621 GTGAGAGCGGTTGTGACACAAAGATCCGCTGTCTACTGTGTCTTCCGTCGCGCGC 1680
Db 2079 GTGAGAGCGGTTGTGACACAAAGATCCGCTGTCTACTGTGTCTTCCGTCGCGCGC 2138
QY 1681 GATTAATCCGACGGAGAGACGACGACGACGAGAGAAAGCCAGGGGGGGGCAAGA 1740
Db 2139 GATTAATCCGACGGAGAGACGACGACGACGAGAGAAAGCCAGGGGGGGGCAAGA 2198
QY 1741 GCAAGCCCATGAAACCCGAGCGGCTGTGACCTCTGAGATTAATGTTGTACAGGTG 1800
Db 2199 GCAAGCCCATGAAACCCGAGCGGCTGTGACCTCTGAGATTAATGTTGTACAGGTG 2258
QY 1801 GCTGAACCTGATCCGAACCTGAGACGCAATTTTGAATTAACAGAGATGGGCAAGGCTA 1860
Db 2259 GCTGAACCTGATCCGAACCTGAGACGCAATTTTGAATTAACAGAGATGGGCAAGGCTA 2318
QY 1861 AAGGGGTTAAAGGGGCGGGGGGCTTGTGAGGCTTCAAGAGAGGCTAGGAATCTAGCT 1920
Db 2319 AAGGGGTTAAAGGGGCGGGGGGCTTGTGAGGCTTCAAGAGAGGCTAGGAATCTAGCT 2378
QY 1921 TTTAGCTTAAATGACACACACCGCTCTGAGTATTACTTTTCAACAGATCAAGATAT 1980
Db 2379 TTTAGCTTAAATGACACACACCGCTCTGAGTATTACTTTTCAACAGATCAAGATAT 2438
QY 1981 TGGGCTAATGAGCTTGAATCTGTGGGCGAGAGATTTCCATAGACAGCTGACCACTTAC 2040
Db 2439 TGGGCTAATGAGCTTGAATCTGTGGGCGAGAGATTTCCATAGACAGCTGACCACTTAC 2498
QY 2041 TGGCTGACGACGAGGGATGATTTTGAAGAGGCTATTAGGGTATTAAGAAAGGTGCACTT 2100
Db 2499 TGGCTGACGACGAGGGATGATTTTGAAGAGGCTATTAGGGTATTAAGAAAGGTGCACTT 2558
QY 2101 AGGCGAAGATTGCAAGTACCAAGATCAGCAACTGTAAATATACAGAAATTTGTGTACATT 2160
Db 2559 AGGCGAAGATTGCAAGTACCAAGATCAGCAACTGTAAATATACAGAAATTTGTGTACATT 2618
QY 2161 TCTGGAGAACGGGGCCGAGGTGAGATTAACGAGATTAAGGTGCGCTTAAATGTAGC 2220

Db 2619 TCTGGGAACGGGGCCGAGGTGAGTACATACGAGGATAGAGGTGGCTTTAAGATGAGC 2678
Qy 2221 ATGATTAATATGTGCGCGGGGGTGTGGCATGACGGGGGTGTATTAATAAGTAAAG 2280
Db 2679 ATGATTAATAATGTGCGCGGGGGTGTGGCATGACGGGGGTGTATTAATAAGTAAAG 2738
Qy 2281 TTTACTGGCCCCCAATTTTAAAGCGGTATTCCTGGCCAAATACCAACTTATCTTAC 2340
Db 2739 TTTACTGGCCCCCAATTTTAAAGCGGTATTCCTGGCCAAATACCAACTTATCTTAC 2798
Qy 2341 GGTGTAAAGCTTCTATGTGGTTTAAACAATACCTGTGTGAAAGCGTGGACGATGAAAGGTT 2400
Db 2799 GGTGTAAAGCTTCTATGTGGTTTAAACAATACCTGTGTGAAAGCGTGGACGATGAAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGTGCTCCGCCAAAAGAGGGCT 2460
Db 2859 CGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGTGCTCCGCCAAAAGAGGGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTTGAAAAGGTGACCTTGGGTATCTGTGTAGAGGTAACTCC 2530
Db 2919 TCAATTAAGAAATGCTCTTTGAAAAGGTGACCTTGGGTATCTGTGTAGAGGTAACTCC 2978
Qy 2531 AGGGTGGCCCAAAATGTGGCTCCGACTGTGTGTCTTCAATGCTAAGTAAAGCGTGGCT 2580
Db 2979 AGGGTGGCCCAAAATGTGGCTCCGACTGTGTGTCTTCAATGCTAAGTAAAGCGTGGCT 3038
Qy 2581 GTGATTAAGCAATACATGTGTATGTGGCAATCGGACGACAGGGCTCTCAATCTGACC 2640
Db 3039 GTGATTAAGCAATACATGTGTATGTGGCAATCGGACGACAGGGCTCTCAATCTGACC 3098
Qy 2641 TGCTCGGACGGCAACTGTCACTGTGTAAGACCAATTCAGTAGCCAGCACTCTCGCAG 2700
Db 3099 TGCTCGGACGGCAACTGTCACTGTGTAAGACCAATTCAGTAGCCAGCACTCTCGCAG 3158
Qy 2701 GCCTGGCCAGTGTGTAGCAATACATGACCCGCTGTCTTTCATTTGGGTAAACAG 2760
Db 3159 GCCTGGCCAGTGTGTAGCAATACATGACCCGCTGTCTTTCATTTGGGTAAACAG 3218
Qy 2761 AGGGGGGTGTCTTCACTTACCAATGCAATTTAGTACACTAAGATTTTCTTGAAGCC 2820
Db 3219 AGGGGGGTGTCTTCACTTACCAATGCAATTTAGTACACTAAGATTTTCTTGAAGCC 3278
Qy 2821 GAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTTCATGATGACCATGAAGATCTGAAG 2880
Db 3279 GAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTTCATGATGACCATGAAGATCTGAAG 3338
Qy 2881 GTGCTGAGTACGATGAGACCCCGCACAGGTGACAGCCCTGCGAGTGTGGCGGTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGACCCCGCACAGGTGACAGCCCTGCGAGTGTGGCGGTAAACAT 3398
Qy 2941 ATTAGGAACCAAGCTGTATGCTGATGACCGAGAGAGTGAAGGCCCGGATCACTTGTGTG 3000
Db 3399 ATTAGGAACCAAGCTGTATGCTGATGACCGAGAGAGTGAAGGCCCGGATCACTTGTGTG 3458
Qy 3001 CTGGCTTCCACCGCGCTGATGTTGGCTCTTACGATGAAGATACAGATTGAG 3052
Db 3459 CTGGCTTCCACCGCGCTGATGTTGGCTCTTACGATGAAGATACAGATTGAG 3510

RESULT 6
US-09-245-497-1

Sequence 1, Application US/09245497
Patent No. 6083750
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/245,497
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
APPLICATION NUMBER: FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"

US-09-245-497-1

Query Match 100.0%; Score 3052; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTACTGATTAATTAACCCGGGTGAGTTCCTCAAGAGGCCACTTGTAGTCCGAGCGAGT 60
Db 459 CGTGTATGTAATTAATACCCGGGTGAGTTCCTCAAGAGGCCACTTGTAGTCCGAGCGAGT 518
Qy 61 AGATTTTCTCTCCGAGCGGCTCCGACACCGGACTGAATAATGACATATTAATCTGCC 120
Db 519 AGATTTTCTCTCCGAGCGGCTCCGACACCGGACTGAATAATGACATATTAATCTGCC 578
Qy 121 ACGGAGGTGTATTAACGAAGAAATGCGCCGACGTCTTTTGGACCAAGTATCGAAGAG 180
Db 579 ACGGAGGTGTATTAACGAAGAAATGCGCCGACGTCTTTTGGACCAAGTATCGAAGAG 638
Qy 181 TACTGGGTGTAATATCTTCCACTCTCTAGCAATTTTGAACCACTTACCAAGAACTGT 240
Db 639 TACTGGGTGTAATATCTTCCACTCTCTAGCAATTTTGAACCACTTACCAAGAACTGT 698
Qy 241 ATGATTTAGAGTGAACGGCCCGGAAGATCCCAAGAGAGCGGTTTCGAGATTTTTC 300
Db 699 ATGATTTAGAGTGAACGGCCCGGAAGATCCCAAGAGAGCGGTTTCGAGATTTTTC 758
Qy 301 CCGACTCTGTAATGTGGCGGTGAGGAAGGATTTGACTTCACTTTTCGCGCGCGC 360
Db 759 CCGACTCTGTAATGTGGCGGTGAGGAAGGATTTGACTTCACTTTTCGCGCGCGC 818
Qy 361 CCGGTTTCTCGGAGCGCCCTCACTTTCCCGGAGCCCGAGACCGGAGAGAGAGCT 420
Db 819 CCGGTTTCTCGGAGCGCCCTCACTTTCCCGGAGCCCGAGACCGGAGAGAGAGCT 878
Qy 421 TGGTCCGATTTCTATGCCAAACCTGTGACCGAGAGTATGATCTTAACCTGCCAGAG 480
Db 879 TGGTCCGATTTCTATGCCAAACCTGTGACCGAGAGTATGATCTTAACCTGCCAGAG 938
Qy 481 CTGGCTTTCACCGAGTGAACGAGAGTGAAGGGGTGAGAGATTGTGTTAATTATG 540

Dh 939 CTGGCTTTCCACCCAGTGACGACGAGATGAAGAGGATGTTGTTAGATTATG 998
Qy 541 TGGAGCACCCCGGGGACGGTTGCAAGTCTTGTCAATTATCACCGAGAAATACGGGGAGCC 600
Db 999 TGGAGCACCCCGGGGACGGTTGCAAGTCTTGTCAATTATCACCGAGAAATACGGGGAGCC 1058
Qy 601 CAGATATTAATGTTGCTTGTGCTATATAGAGACCTGAGGCACTGTTTCTACAGTAAGT 660
Db 1059 CAGATATTAATGTTGCTTGTGCTATATAGAGACCTGAGGCACTGTTTCTACAGTAAGT 1118
Qy 661 GAAATTAATGAGGAGTGGGTATAGAGTGTGGTTTGTGTGTAATTTTTTTTTTAAT 720
Db 1119 GAAATTAATGAGGAGTGGGTATAGAGTGTGGTTTGTGTGTAATTTTTTTTTTAAT 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGGTCCTGTGC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGGTCCTGTGC 1238
Qy 781 TGAACCTGAGCCTGAGCCGAGCCGAGACCGGAGCCTGCAAGACCTACCCGCGCTCTAA 840
Db 1239 TGAACCTGAGCCTGAGCCGAGCCGAGACCGGAGCCTGCAAGACCTACCCGCGCTCTAA 1298
Qy 841 AATGCGCCTGCTATCTCTGAGACGCGCCGACATCACTGTGCTAGAGAAATCAATAGTAG 900
Db 1299 AATGCGCCTGCTATCTCTGAGACGCGCCGACATCACTGTGCTAGAGAAATCAATAGTAG 1358
Qy 901 TAGGGATAGCTGTGATCTCGGTCCTTCTTAACAACCTCTGAGATACACCGGTGCTGCC 960
Db 1359 TAGGGATAGCTGTGATCTCGGTCCTTCTTAACAACCTCTGAGATACACCGGTGCTGCC 1418
Qy 961 GCTGTCGCCCATTAACACAGTTGCGGTGAGAGTTGGTGGGGGTGGCCAGGGCTGAGAAAG 1020
Db 1419 GCTGTCGCCCATTAACACAGTTGCGGTGAGAGTTGGTGGGGGTGGCCAGGGCTGAGAAAG 1478
Qy 1021 TATCGAGGACTTGTGCTTAACGAGCCTGGGCAACTTTGGACTTGAAGCTGTAAACGCCAG 1080
Db 1479 TATCGAGGACTTGTGCTTAACGAGCCTGGGCAACTTTGGACTTGAAGCTGTAAACGCCAG 1538
Qy 1081 GCCATTAAGTGTAAACCTGTGATTTGCGTGTGTTAAACGCTTTGTTTGTCTGAATGAGT 1140
Db 1539 GCCATTAAGTGTAAACCTGTGATTTGCGTGTGTTAAACGCTTTGTTTGTCTGAATGAGT 1598
Qy 1141 TGATGTAAATTAATTAAGGAGTGAATTAATGTTTAATCTGATGCGGTGTAATATGGGGC 1200
Db 1599 TGATGTAAATTAATTAAGGAGTGAATTAATGTTTAATCTGATGCGGTGTAATATGGGGC 1658
Qy 1201 GGGGCTTAAGGAGTATATATGCGCGGTGGCTAATCTTGGTATCATCTGACTCATGGA 1260
Db 1659 GGGGCTTAAGGAGTATATATGCGCGGTGGCTAATCTTGGTATCATCTGACTCATGGA 1718
Qy 1261 GGGCTTGAAGTGTGGAAGATTTTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTCTAA 1320
Db 1719 GGGCTTGAAGTGTGGAAGATTTTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTCTAA 1778
Qy 1321 CAGTAACTCTGTTGTTTGAAGGTTTCTGTGGGGCTCAATCCAGGCAAAAGTAAAGTCTGAG 1380
Db 1779 CAGTAACTCTGTTTGAAGGTTTCTGTGGGGCTCAATCCAGGCAAAAGTAAAGTCTGAG 1838
Qy 1381 AATTAAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1440
Db 1839 AATTAAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1898
Qy 1441 TGATTTCTTTGAATCTGGGTCAACAGGGCTTTTCCAAAGAAAGTCAATCAAGACTTTGGA 1500
Db 1899 TGATTTCTTTGAATCTGGGTCAACAGGGCTTTTCCAAAGAAAGTCAATCAAGACTTTGGA 1958
Qy 1501 TTTTTCACACCGGGGGGCGCTGGGGCTGCTGTTTGTGTTTGAAGTTTAAAGGATTA 1560
Db 1959 TTTTTCACACCGGGGGGCGCTGGGGCTGCTGTTTGTGTTTGAAGTTTAAAGGATTA 2018
Qy 1561 ATGAGAGGAAGAAACCAATCTGAGCGGGGGGTACCTGTGATTTTCTGAGCATGACATCT 1620
Db 2019 ATGAGAGGAAGAAACCAATCTGAGCGGGGGGTACCTGTGATTTTCTGAGCATGACATCT 2078

Qy 1621 GTGAGAGCGGTTGTGAGACCAAGAATCGCTGCTACTGTGTTCTTCCGTCGCCCGGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACCAAGAATCGCTGCTACTGTGTTCTTCCGTCGCCCGGC 2138
Qy 1681 GATTAATCCGAGGAGGAGCAGCAGCAGCAGCAGAGAGGAAACCGAGCGCGCGGCAAGA 1740
Db 2139 GATTAATCCGAGGAGGAGCAGCAGCAGCAGCAGAGAGGAAACCGAGCGCGCGGCAAGA 2198
Qy 1741 GCAGAGCCATGGAACCCGAGAGCGGCTGGAACCTTCGAGAAATGAATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCATGGAACCCGAGAGCGGCTGGAACCTTCGAGAAATGAATGTTGTACAGGTG 2258
Qy 1801 GCTGAACGTATCCAGAACTGAGACGCAATTTTGAACAATTAACAAGATGGCAGGGCTA 1860
Db 2259 GCTGAACGTATCCAGAACTGAGACGCAATTTTGAACAATTAACAAGATGGCAGGGCTA 2318
Qy 1861 AAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGGAGGCTAAGGAATCTAGCT 1920
Db 2319 AAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGGAGGCTAAGGAATCTAGCT 2378
Qy 1921 TTTAGCTTAATGACACAGACCGTCTGAGTGTATTACTTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACACAGACCGTCTGAGTGTATTACTTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGGCCTAATGACTTGAATCTGTGCGCGCAAGATTAATTCATAGACAGCTGACCACTTAC 2040
Db 2439 TGGCCTAATGACTTGAATCTGTGCGCGCAAGATTAATTCATAGACAGCTGACCACTTAC 2498
Qy 2041 TGGCTGACGACGAGGGAGTAAATTTTGAAGAGGCTATTGAGGATATGCAAAAGTGGCACTT 2100
Db 2499 TGGCTGACGACGAGGGAGTAAATTTTGAAGAGGCTATTGAGGATATGCAAAAGTGGCACTT 2558
Qy 2101 AGGCGAATGTCAGATCAAGATCAGCAAACTTGTAAATATCAGAAATTTGTTGCTACATT 2160
Db 2559 AGGCGAATGTCAGATCAAGATCAGCAAACTTGTAAATATCAGAAATTTGTTGCTACATT 2618
Qy 2161 TCTGGGAAACGGGGCCGAGAGTGAATAGATACGAGAGTAAAGGTGGCCTTTAAGTATGAG 2220
Db 2619 TCTGGGAAACGGGGCCGAGAGTGAATAGATACGAGAGTAAAGGTGGCCTTTAAGTATGAG 2678
Qy 2221 ATGATTAATATGTGCGGGGGGTGCTTGGCATGGAACGGGGGTGTTATTAAGATGAAG 2280
Db 2679 ATGATTAATATGTGCGGGGGGTGCTTGGCATGGAACGGGGGTGTTATTAAGATGAAG 2738
Qy 2281 TTTACTGGCCCAATTTTAAAGCGTACCGTTTTCTGTGCAATACCAACTTATCTTACAC 2340
Db 2739 TTTACTGGCCCAATTTTAAAGCGTACCGTTTTCTGTGCAATACCAACTTATCTTACAC 2798
Qy 2341 GGTGTAAAGCTTTATGAGGTTTAAACAATACCTGTGTGAAGCTGAGCCGATGAAGGTT 2400
Db 2799 GGTGTAAAGCTTTATGAGGTTTAAACAATACCTGTGTGAAGCTGAGCCGATGAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTAACTGTGCTGGAAGGGGGGTGTGTGCGCCCAAAAGAGGGCT 2460
Db 2859 CGGGGCTGTGCTTTTAACTGTGCTGGAAGGGGGGTGTGTGCGCCCAAAAGAGGGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTTTGAAGGTTGTAACCTTGGGTATCTGTGTGAGGTTAACTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTTTGAAGGTTGTAACCTTGGGTATCTGTGTGAGGTTAACTCC 2978
Qy 2521 AGGGTGGCCCAATGTGGCTCCGACTGTGTGTTGCTTCAATGTATGAAAAGCGTGGCT 2580
Db 2979 AGGGTGGCCCAATGTGGCTCCGACTGTGTGTTGCTTCAATGTATGAAAAGCGTGGCT 3038
Qy 2581 GTGATTAAGCAATTAACATGTATGTGCAACTGCGAGGACAGGGGCTCTCAAGATCTGACC 2640
Db 3039 GTGATTAAGCAATTAACATGTATGTGCAACTGCGAGGACAGGGGCTCTCAAGATCTGACC 3098
Qy 2641 TGCTGGAGCGGCAACTGTCACTGTGTAAGAACATTCACGTAGGCAACACTCTGCGAAG 2700
Db 3099 TGCTGGAGCGGCAACTGTCACTGTGTAAGAACATTCACGTAGGCAACACTCTGCGAAG 3158

QY	2701	GCCCTGGCCAGTGTTTGAGCAATTAATCTGACCCGCGTGTCTTGCAATTTGGGTAACAGG	2760
Db	3159	GCCCTGGCCAGTGTTTGAGCAATTAATCTGACCCGCGTGTCTTGCAATTTGGGTAACAGG	3218
QY	2761	AGGGGGGTGTTCCTACCTTAACCAATGCATATTTGAGTCACTAAGATATTGCTTGAGCCC	2820
Db	3219	AGGGGGGTGTTCCTACCTTAACCAATGCATATTTGAGTCACTAAGATATTGCTTGAGCCC	3278
QY	2821	GAGAGCATGTGTCCAGAGTGAACTTAACGGGGGTGTTTGATCATGACATGAAGATCTGGAG	2880
Db	3279	GAGAGCATGTGTCCAGAGTGAACTTAACGGGGGTGTTTGATCATGACATGAAGATCTGGAG	3338
QY	2881	GTGCTGAGGTTCGATGAGACCCCGCACCAAGTGTGCAGACCTTCGAGTGTGGCGGTAAACAT	2940
Db	3339	GTGCTGAGGTTCGATGAGACCCCGCACCAAGTGTGTGCAGACCTTCGAGTGTGGCGGTAAACAT	3398
QY	2941	ATTAGGAACCAAGCCTGTGATCTGATATGTGACCAAGAGATGAGAGCCCGATCATCTTGGTG	3000
Db	3399	ATTAGGAACCAAGCCTGTGATCTGATATGTGACCAAGAGATGAGAGCCCGATCATCTTGGTG	3458
QY	3001	CTGGCCTTGCAACCCCGCGCTGAGATTGGGCTCTTAAGCGATTAAGTAAACAGATTGAG	3052
Db	3459	CTGGCCTTGCAACCCCGCGCTGAGATTGGGCTCTTAAGCGATTAAGTAAACAGATTGAG	3510

Db 1479 TATGAGGACTTGCCTTAACGAGCCCTGGCAACCTTTGAGACTTGAAGCTTAAACGCCCCAG 1538
Qy 1081 GCCATTAAGCTTAAACCTGTGATTCGCTGTGTGTGAACCGCTTTGTTGCTGAATAGT 1140
Db 1539 GCCATTAAGCTTAAACCTGTGATTCGCTGTGTGTGAACCGCTTTGTTGCTGAATAGT 1598
Qy 1141 TGATGTAACTTAATTAAGGCTGAGATTAATGTTTAACTTGCATGCGCTGTTAAATGGGCG 1200
Db 1599 TGAATTAAGTTTAATTAAGGCTGAGATTAATGTTTAACTTGCATGCGCTGTTAAATGGGCG 1658
Qy 1201 GGGGCTTAAGGCTTAATTAATGCGCGCTGAGCTTAATCTTGTGATCATCTGACCTCATGGA 1260
Db 1659 GGGGCTTAAGGCTTAATTAATGCGCGCTGAGCTTAATCTTGTGATCATCTGACCTCATGGA 1718
Qy 1261 GGGCTGGAGAGTGTGGAGAGATTTTCTGCTGTGTGTAACCTGCTGAAACAGAGCTCTAA 1320
Db 1719 GGGCTGGAGAGTGTGGAGAGATTTTCTGCTGTGTGTAACCTGCTGAAACAGAGCTCTAA 1778
Qy 1321 CAGTAACCTTGGCTTTTGGAGAGTTTCTGTGGGGCTCATCCGAGCAAGTTAGTCTGAG 1380
Db 1779 CAGTAACCTTGGCTTTTGGAGAGTTTCTGTGGGGCTCATCCGAGCAAGTTAGTCTGAG 1838
Qy 1381 AATTAAAGAGGATTAACAAGTGGAAATTTGAAGAGCTTTGAAATCCTGTGGTGAAGTCT 1440
Db 1839 AATTAAAGAGGATTAACAAGTGGAAATTTGAAGAGCTTTGAAATCCTGTGGTGAAGTCT 1898
Qy 1441 TGATTTCTTGAATCTGGGTCAACAGCGCTTTTCCAGAGAGAGTCAATCAAGCTTTTGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACAGCGCTTTTCCAGAGAGAGTCAATCAAGCTTTTGA 1958
Qy 1501 TTTTTCACACCGGGGGCGCGCTGCGCTGCTGCTTTTGAAGTTTAAAGATTA 1560
Db 1959 TTTTTCACACCGGGGGCGCGCTGCGCTGCTGCTTTTGAAGTTTAAAGATTA 2018
Qy 1561 ATGAGAGCAAGAAACCCATCTGAGCGGGGGGTACCTGTGATTTTCTGGCATGCAATCT 1620
Db 2019 ATGAGAGCAAGAAACCCATCTGAGCGGGGGGTACCTGTGATTTTCTGGCATGCAATCT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGTCTATCTGTGTCTTCCGCTCCGCGCC 1680
Db 2079 GTGAGAGCGGTTGTGAGACCAAGAAATCGCTGTCTATCTGTGTCTTCCGCTCCGCGCC 2138
Qy 1681 GATTAATCCGACGAG 1740
Db 2139 GATTAATCCGACGAG 2198
Qy 1741 GCAGAGCCATGGAACCCGAGAGCGGCGTGGACCTTCGGGAATGAATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCATGGAACCCGAGAGCGGCGTGGACCTTCGGGAATGAATGTTGTACAGGTG 2258
Qy 1801 GCTGAATCTGTATCCAGAACTGAGACGCAATTTTGAATTAACAGAGATGGGCAAGGCTTA 1860
Db 2259 GCTGAATCTGTATCCAGAACTGAGACGCAATTTTGAATTAACAGAGATGGGCAAGGCTTA 2318
Qy 1861 AAGGGGTTAAAGAGGAGCGGGGGGCTTTGTAGGCTTACAGAGAGGCTTAGAATCTTAGCT 1920
Db 2319 AAGGGGTTAAAGAGGAGCGGGGGGCTTTGTAGGCTTACAGAGAGGCTTAGAATCTTAGCT 2378
Qy 1921 TTTAGCTTAATGACCAACACCGCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACCAACACCGCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGGCTTAATGAGCTTGAATCTGCTGCGCAGAAATTAATCAATAGAGAGCTGACCACTTAC 2040
Db 2439 TGGCTTAATGAGCTTGAATCTGCTGCGCAGAAATTAATCAATAGAGAGCTGACCACTTAC 2498
Qy 2041 TGGCTGAGCGGAGGAGTGAATTTTGAAGAGCTTAATTAAGGTTAATGCAAAAGTGGCACTT 2100
Db 2499 TGGCTGAGCGGAGGAGTGAATTTTGAAGAGCTTAATTAAGGTTAATGCAAAAGTGGCACTT 2558
Qy 2101 AGGCGAATTTGCAAGTCAAGATCAGCAAACTTGAATTAATCAAGATTTGTTGCTAATTT 2160

Db 2559 AGGCGAATTTGCAAGTCAAGATCAGCAAACTTGAATTAATCAAGATTTGTTGCTAATTT 2618
Qy 2161 TCTGGGAAACGGGGCCGAGAGTGAAGATTAATCGAGAGATTAAGGCTTGAATGATAGC 2220
Db 2619 TCTGGGAAACGGGGCCGAGAGTGAAGATTAATCGAGAGATTAAGGCTTGAATGATAGC 2678
Qy 2221 ATGATTAATATGTGGCCGGGGGCTTGTGCAATGGAACGGGCTGATTAATGAATGAAG 2280
Db 2679 ATGATTAATATGTGGCCGGGGGCTTGTGCAATGGAACGGGCTGATTAATGAATGAAG 2738
Qy 2281 TTTACTGAGCCCAATTTTAAGAGGATTTTCTGTGCAATACCAACTTAATCTTAC 2340
Db 2739 TTTACTGAGCCCAATTTTAAGAGGATTTTCTGTGCAATACCAACTTAATCTTAC 2798
Qy 2341 GGTGTAAGCTTCTAATGGGTTTAAACATACCTGTGTGGAAGCTTGAACCGATGAAGGTT 2400
Db 2799 GGTGTAAGCTTCTAATGGGTTTAAACATACCTGTGTGGAAGCTTGAACCGATGAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTACTGTCTGTGGAAGGGGCTGTGTGTGCGCCCAAAAGAGGGCT 2460
Db 2859 CGGGGCTGTGCTTTTACTGTCTGTGGAAGGGGCTGTGTGTGCGCCCAAAAGAGGGCT 2918
Qy 2461 TCAATTAAGAAATGCGCTTTTGAAGGTTAATCTTGGGTTATCCTGTGAGGGTTAATCC 2520
Db 2919 TCAATTAAGAAATGCGCTTTTGAAGGTTAATCTTGGGTTATCCTGTGAGGGTTAATCC 2978
Qy 2521 AGGGTGGCCCAATGTGGCTCCGACTGTGTGTTCTTCAATGTAGTGAAGAGGCTGCT 2580
Db 2979 AGGGTGGCCCAATGTGGCTCCGACTGTGTGTTCTTCAATGTAGTGAAGAGGCTGCT 3038
Qy 2581 GTGATTAAGCAATTAATGTATGTGCAATCTGAGAGAGAGGCTTCTAGATGCTGACC 2640
Db 3039 GTGATTAAGCAATTAATGTATGTGCAATCTGAGAGAGAGGCTTCTAGATGCTGACC 3098
Qy 2641 TGTCTGGAGCGGCAATCTGTCACTGTGGAAGACATTAAGTGAAGCCACTCTCGAAG 2700
Db 3099 TGTCTGGAGCGGCAATCTGTCACTGTGGAAGACATTAAGTGAAGCCACTCTCGAAG 3158
Qy 2701 GCTTGGCAGTGTGTTGAGCAATTAATTAATGACCGGCTGTTCTTGTGATTTGGGTAAACAG 2760
Db 3159 GCTTGGCAGTGTGTTGAGCAATTAATTAATGACCGGCTGTTCTTGTGATTTGGGTAAACAG 3218
Qy 2761 AGGGGGGTGTTCTTCACTTCAATGCAATGCAATTTGATGATCACTAAGATTTGCTTGAAGCC 2820
Db 3219 AGGGGGGTGTTCTTCACTTCAATGCAATGCAATTTGATGATCACTAAGATTTGCTTGAAGCC 3278
Qy 2821 GAGAGCATGTCCAAGGTAACCTGAACGGGGTGTGTAACATGAACCAATGAAGATCTGAG 2880
Db 3279 GAGAGCATGTCCAAGGTAACCTGAACGGGGTGTGTAACATGAACCAATGAAGATCTGAG 3338
Qy 2881 GTGCTGAGTACGATGAGAGCCCGCACAGGTGAGACCTTGCAGAGTGTGGCGTTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGAGCCCGCACAGGTGAGACCTTGCAGAGTGTGGCGTTAAACAT 3398
Qy 2941 ATTAAGAACCAAGCTGTGATGTGATGTGAACGAGAGAGTGAAGGCCGATCACTTGGTG 3000
Db 3399 ATTAAGAACCAAGCTGTGATGTGATGTGAACGAGAGAGTGAAGGCCGATCACTTGGTG 3458
Qy 3001 CTGGGCTGACCGGCGCTGAGTTTGGCTTAAGGATGAAGATCAAGTTAG 3052
Db 3459 CTGGGCTGACCGGCGCTGAGTTTGGCTTAAGGATGAAGATCAAGTTAG 3510

RESULT 8
US-09-562-919-1
; Sequence 1, Application US/09562919
; Patent No. 6451596
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; Amalfitano, Andrea
; Hauser, Michael A.
; Kumar-Singh, Rajendra
; Hartigan-O'Connor, Dennis J.

TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/562,919
FILING DATE: 02-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-562-919-1
Query Match 100.0%; Score 3052; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGTAGTATTAATACCGGCTGAGTTCCTCAAGAGGCACTGTTAGTCCGACGAGT 60
DB CGGTAGTATTAATACCGGCTGAGTTCCTCAAGAGGCACTGTTAGTCCGACGAGT 518
QY 61 AGAGTTTCTCTCCGAGCGGCTCCGACACCGGAGCTGAAATGACATATTAATCTGCC 120
DB AGAGTTTCTCTCCGAGCGGCTCCGACACCGGAGCTGAAATGACATATTAATCTGCC 578
QY 121 ACGAGGCTTATTAACGAGAAATGCGCCGACGCTTTTGGACCAAGTGAAGAG 180
DB ACGAGGCTTATTAACGAGAAATGCGCCGACGCTTTTGGACCAAGTGAAGAG 638
QY 579 ACGAGGCTTATTAACGAGAAATGCGCCGACGCTTTTGGACCAAGTGAAGAG 638
DB 181 TACTGGCGATTAATCTCACTCTAGCCATTTTGAACACCACTTACACCTTACAGACGT 240
QY 639 TACTGGCGATTAATCTCACTCTAGCCATTTTGAACACCACTTACACCTTACAGACGT 698
DB 241 ATGATTTAGACGTACGCGCCCGCAAGATCCCAAGAGAGCGGTTTCGAGATTTTTC 300
QY 699 ATGATTTAGACGTACGCGCCCGCAAGATCCCAAGAGAGCGGTTTCGAGATTTTTC 758
DB 301 CCGAGCTCTGTAATGTGGCGGTGCAAGAGGATTTGACTTACTCATTTTCCGCGGCGC 360
QY 759 CCGAGCTCTGTAATGTGGCGGTGCAAGAGGATTTGACTTACTCATTTTCCGCGGCGC 818
DB 361 CCGGTTCTCCGAGCGCGCTCACCTTTCCGGGACCGCGAGACCGGAGAGAGAGCT 420
QY 819 CCGGTTCTCCGAGCGCGCTCACCTTTCCGGGACCGCGAGACCGGAGAGAGAGCT 878
QY 421 TGGGTCCGTTTCTATGCAAACTTGTACCGGAGGTGATGATCTTAACCTGCCACGAG 480

DB 879 TGGGTCCGTTTCTATGCAAACTTGTACCGGAGGTGATGATCTTAACCTGCCACGAG 938
QY 481 CTGGCTTTCCACCCAGTGAAGAGATGAAGAGGTGAGAGTTGTGTAACTATATG 540
DB CTGGCTTTCCACCCAGTGAAGAGATGAAGAGGTGAGAGTTGTGTAACTATATG 998
QY 541 TGGAGCACCCCGGAGCACTGTGAGGCTTGTCAATTAACCCGAGGAAATACGGGGAGC 600
DB TGGAGCACCCCGGAGCACTGTGAGGCTTGTCAATTAACCCGAGGAAATACGGGGAGC 1058
QY 601 CAGATATTAATGTGTTGCTTGTATATGAGACCTGTGACATTTGTCTACAGTAAGT 660
DB CAGATATTAATGTGTTGCTTGTATATGAGACCTGTGACATTTGTCTACAGTAAGT 1158
QY 661 GAAATTAATGCGCAGTGGGTGATGAGTGTGGTTGTGTGTATATTTTATTTTAT 720
DB GAAATTAATGCGCAGTGGGTGATGAGTGTGGTTGTGTGTATATTTTATTTTAT 1178
QY 721 TTTTACAGTTTGTGTTTAAAGATTTGTATGATTTTAAAGGTCCTGTGTC 780
DB TTTTACAGTTTGTGTTTAAAGATTTGTATTTGTATTTTAAAGGTCCTGTGTC 1238
QY 781 TGAACCTGACCTGAGCCCGAGCCAGAACCGAGCTGCAAGACTACCCGCTCTTAA 840
DB TGAACCTGACCTGAGCCCGAGCCAGAACCGAGCTGCAAGACTACCCGCTCTTAA 1298
QY 841 AATGCGCCCTGCTATCTCTGAGAGCCCGACATCACTGTGTCTTGAAGATTAAGTAG 900
DB AATGCGCCCTGCTATCTCTGAGAGCCCGACATCACTGTGTCTTGAAGATTAAGTAG 1358
QY 901 TACGATAGCTGTGACTCCGAGCTCTTCTAACAACCTCTGAGATACACCGGTGTCCC 960
DB TACGATAGCTGTGACTCCGAGCTCTTCTAACAACCTCTGAGATACACCGGTGTCCC 1418
QY 1359 TACGATAGCTGTGACTCCGAGCTCTTCTAACAACCTCTGAGATACACCGGTGTCCC 1418
DB 961 GCTGTGCCCCATTAAACCACTGTGAGAGTTGTGGGCTGTGCCAGGCTGTGAATG 1020
QY 1419 GCTGTGCCCCATTAAACCACTGTGAGAGTTGTGGGCTGTGCCAGGCTGTGAATG 1478
DB 1021 TATCGAGACTTGTCTTAAACGAGCTGTGGCAACCTTTTGAACCTTGAACCTTGAACGCCCCAG 1080
QY 1479 TATCGAGACTTGTCTTAAACGAGCTGTGGCAACCTTTTGAACCTTGAACCTTGAACGCCCCAG 1538
DB 1081 GCCATAAGGTGTAACCTGTGATTTGCGTGTGTTAACCCCTTTTGTCTGAATAGT 1140
QY 1539 GCCATAAGGTGTAACCTGTGATTTGCGTGTGTTAACCCCTTTTGTCTGAATAGT 1598
DB 1141 TGATGTAAGTTTAAATAAAGGTGAGATATGTTTAACTTGCATGCGGTAAATGAGGCGC 1200
QY 1599 TGATGTAAGTTTAAATAAAGGTGAGATATGTTTAACTTGCATGCGGTAAATGAGGCGC 1658
DB 1201 GGGGCTTAAAGGCTATTAATGCGCGGTGGCTTAACTTGTGTTACATCTGACCTCATGGA 1260
QY 1659 GGGGCTTAAAGGCTATTAATGCGCGGTGGCTTAACTTGTGTTACATCTGACCTCATGGA 1718
DB 1261 GGGCTTGAAGATTTTGTGAGAAATTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTCTAA 1320
QY 1719 GGGCTTGAAGATTTTGTGAGAAATTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTCTAA 1778
DB 1321 CAGTACCTTGTGTTTGAAGGTTTCTGTGGGCTCATCCGAGCAAAATTAATGTGCGAG 1380
QY 1779 CAGTACCTTGTGTTTGAAGGTTTCTGTGGGCTCATCCGAGCAAAATTAATGTGCGAG 1838
DB 1381 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGACTTTTGAATCCCTGTGTGAGCTGT 1440
QY 1839 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGACTTTTGAATCCCTGTGTGAGCTGT 1898
DB 1441 TGAATCTTGAATCTGGGTCAACGAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTTGA 1500
QY 1899 TGAATCTTGAATCTGGGTCAACGAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTTGA 1958
QY 1501 TTTTTCACACCGGGGCGCGCTGCGGCTGTGTTCTTTTGAAGTTTAAAGATTA 1560
DB 1959 TTTTTCACACCGGGGCGCGCTGCGGCTGTGTTCTTTTGAAGTTTAAAGATTA 2018

1561 ATGAGCGAAGAAACCCATCTGAGCGGGGGGTACTGCTGGAATTTTCTGGCCATGCACT 1620
2019 ATGAGCGAAGAAACCCATCTGAGCGGGGGGTACTGCTGGAATTTTCTGGCCATGCACT 2078
1621 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGCTACTGTGTTCTTCGTCGCGCGGC 1680
2079 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGCTACTGTGTTCTTCGTCGCGCGGC 2138
1681 GATTAATACCGAGGAGAGCAGCAGCAGCAGCAGAGAGAGAGCCAGGCGCGCGCAGAGA 1740
2139 GATTAATACCGAGGAGAGCAGCAGCAGCAGCAGAGAGAGAGCCAGGCGCGCGCAGAGA 2198
1741 GCAGAGCCCATGGAACCCGAGAGCGCGCTGAGACCTTGGGAAATGAATTTGTACAGTGT 1800
2199 GCAGAGCCCATGGAACCCGAGAGCGCGCTGAGACCTTGGGAAATGAATTTGTACAGTGT 2258
1801 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGGATGGGCAAGGCTA 1860
2259 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGGATGGGCAAGGCTA 2318
1861 AAGGGGGTAAAGAGGAGCGGGGGGCTTTGTAGGCTACAGAGAGGCTAAGGATCTAGCT 1920
2319 AAGGGGGTAAAGAGGAGCGGGGGGCTTTGTAGGCTACAGAGAGGCTAAGGATCTAGCT 2378
1921 TTTAGCTTAATGACCAACACACCCGCTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
2379 TTTAGCTTAATGACCAACACCCGCTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
1981 TGCGCTAATGAGCTTGTATCTGCTGGCGAGAAATTCATATAGAGCAGCTAGCCACTTAC 2040
2439 TGCGCTAATGAGCTTGTATCTGCTGGCGAGAAATTCATATAGAGCAGCTAGCCACTTAC 2498
2041 TGCGTGAGCCAGGGGATGATTTTGAAGAGGCTATTAGGGTATATGCAAGGTGGCACTT 2100
2499 TGCGTGAGCCAGGGGATGATTTTGAAGAGGCTATTAGGGTATATGCAAGGTGGCACTT 2558
2101 AGGCGCAATTTGCAAGTACAGATCAGCAAACTTTGAAATATCAGAAATTTGTTGCTACATT 2160
2559 AGGCGCAATTTGCAAGTACAGATCAGCAAACTTTGAAATATCAGAAATTTGTTGCTACATT 2618
2161 TCTGGAGAACGGGGCCGAGAGTGAATAGATACGAGAGATAGAGGTGGCTTTAGATGTAAGC 2220
2619 TCTGGAGAACGGGGCCGAGAGTGAATAGATACGAGAGATAGAGGTGGCTTTAGATGTAAGC 2678
2221 ATGATAAATATGTGCGCGGGGGTCTTGGCATGAGACGGGGTGTATTATATGATGTAAGG 2280
2679 ATGATAAATATGTGCGCGGGGGTCTTGGCATGAGACGGGGTGTATTATATGATGTAAGG 2738
2281 TTTTACTGGCCCCAATTTTATAGCGGTATTCCTGGCCAAATACCAACCTTATCTTACAC 2340
2739 TTTTACTGGCCCCAATTTTATAGCGGTATTCCTGGCCAAATACCAACCTTATCTTACAC 2798
2341 GGTTAGTACCTTCTATGAGGTTTAAACAATCCTGTGTGAAGGCTGGAACCGATGAAGGTT 2400
2799 GGTTAGTACCTTCTATGAGGTTTAAACAATCCTGTGTGAAGGCTGGAACCGATGAAGGTT 2858
2401 CGGGGCTGTGCTTTTACTGCTGTGAAGGGGGTGTGTGTGCGCCCAAAAAGAGGAGCT 2460
2859 CGGGGCTGTGCTTTTACTGCTGTGAAGGGGGTGTGTGTGCGCCCAAAAAGAGGAGCT 2918
2461 TCAATTTAAGAAATGCTCTTTTGAAGGTTTAAACAATCCTGTGTGAAGGTTTAAACAAT 2520
2919 TCAATTTAAGAAATGCTCTTTTGAAGGTTTAAACAATCCTGTGTGAAGGTTTAAACAAT 2978
2521 AGGGTGGCCCAATGAGGCTCCGAGCTGTGTTGCTTCAATAGTGAAGAAAGGAGGCT 2580
2979 AGGGTGGCCCAATGAGGCTCCGAGCTGTGTTGCTTCAATAGTGAAGAAAGGAGGCT 3038
2581 GTGATTTAAGCAATATGATGATGTGCAACTGCGAGAGCAAGGAGGCTCTCAATGCTGAC 2640
3039 GTGATTTAAGCAATATGATGATGTGCAACTGCGAGAGCAAGGAGGCTCTCAATGCTGAC 3098

2641 TGCTCGAGCGGCAATCTGACCTGCTGAAGACATTCAGCTAGCCAGCACTCTCGCAG 2700
3099 TGCTCGAGCGGCAATCTGACCTGCTGAAGACATTCAGCTAGCCAGCACTCTCGCAG 3158
2701 GCCTGGCCAGTGTGTGAGCAATACATACCTGACCGCTGTCTTCTTGCATTTGGTAAACAG 2760
3159 GCCTGGCCAGTGTGTGAGCAATACATACCTGACCGCTGTCTTCTTGCATTTGGTAAACAG 3218
2761 AGGGGGGTGTTCTTCACTTACCTTACCAATGCAATTTAGTCACTAAGATATTTGAGGCC 2820
3219 AGGGGGGTGTTCTTCACTTACCTTACCAATGCAATTTAGTCACTAAGATATTTGAGGCC 3278
2821 GAGAGCATGCTCAAGTGAACCTTGAACCGGGTGTGTTGACATGACATTAATATCTGAG 2880
3279 GAGAGCATGCTCAAGTGAACCTTGAACCGGGTGTGTTGACATGACATTAATATCTGAG 3338
2881 GTGCTGAGTACATGAGACCCGACCAAGGAGACCCCTGAGTGTGGGTTAAACAT 2940
3339 GTGCTGAGTACATGAGACCCGACCAAGGAGACCCCTGAGTGTGGGTTAAACAT 3398
2941 ATTAGAAACAGCCTGTGATGCTGATGTGAACCGAGAGCTGAGGCCGATCACTTGGTG 3000
3399 ATTAGAAACAGCCTGTGATGCTGATGTGAACCGAGAGCTGAGGCCGATCACTTGGTG 3458
3001 CTGGCTGCAACCGCGCTGAGTTGGCTGTACGATGAAGATTAAGATTGAG 3052
3459 CTGGCTGCAACCGCGCTGAGTTGGCTGTACGATGAAGATTAAGATTGAG 3510

RESULT 9
US-09-956-335-1
; Sequence 1, Application US/09956335

; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly
; APPLICANT: KUPPASHAMI, Mohan
; APPLICANT: DORONIN, Konstantin
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
; FILE REFERENCE: 16153-8394
; CURRENT APPLICATION NUMBER: US/09/956,335
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 35978
; TYPE: DNA
; ORGANISM: Adenovirus
US-09-956-335-1

Query Match 100.0%; Score 3052; DB 4; Length 35978;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGTGTAGTATTTTAAACCGGTGAGTTCTCAAGAGGCCACTTGTAGTCCAGCGAGT 60
459 CGTGTAGTATTTTAAACCGGTGAGTTCTCAAGAGGCCACTTGTAGTCCAGCGAGT 518
61 AGATTTTCTCCCGAGCGGCTCCGACACCGGGACCTGAAATATGACATTTATCTGCC 120
519 AGATTTTCTCCCGAGCGGCTCCGACACCGGGACCTGAAATATGACATTTATCTGCC 578
121 ACGGAGGTGTTATTAACGAAATATGCGCCAGCTTTTGTGACAGTGAATGCAAGAG 180
579 ACGGAGGTGTTATTAACGAAATATGCGCCAGCTTTTGTGACAGTGAATGCAAGAG 638
181 TACTGGCTGATATCTTCCACCTCTTACCATTTTGAACCACTTACCTTCAAGAACTGT 240
639 TACTGGCTGATATCTTCCACCTCTTACCATTTTGAACCACTTACCTTCAAGAACTGT 698
241 ATGATTTAAGAGTGAACCGGCCCGGAGATCCCAAGAGAGGAGGTTTGGCAGATTTTTC 300

D	b	699	ATGATTTTAGACGTACGGCCCCCGCAAGATCCCAACGAGAGGCGGTTTCGACATTTTTC	758
Q	y	301	CCGACTCTGTATATGTGTGGCGGTGACGAGAGGGAATTGACTTACTCTTTTCCGCGGCGC	360
D	b	759	CCGACTCTGTATATGTGTGGCGGTGACGAGAGGGAATTGACTTACTCTTTTCCGCGGCGC	818
Q	y	361	CCGGTTCTCCGGAGACCGGCTCACTTTTCCCGGACAGCCCGAGCAGCCGAGCAGAGAGCT	420
D	b	819	CCGGTTCTCCGGAGACCGGCTCACTTTTCCCGGACAGCCCGAGCAGCCGAGCAGAGAGCT	878
Q	y	421	TGGGTCGGGTTTCTATGCAAACTGTACCGGAGGATGATGACTTACCTGACCAAGG	480
D	b	879	TGGGTCGGGTTTCTATGCAAACTGTACCGGAGGATGATGACTTACCTGACCAAGG	938
Q	y	481	CTGGCTTTCACCCAGTACACGACGAGATGAAGAAGGTGAGAGATTGTGTATGATTATG	540
D	b	939	CTGGCTTTCACCCAGTACACGACGAGATGAAGAAGGTGAGAGATTGTGTATGATTATG	998
Q	y	541	TGAGACACCCCGGGGACCGGTTGCAGGTTTGTCAATTACCCGAGGAAATACGGGGGACC	600
D	b	999	TGAGACACCCCGGGGACCGGTTGCAGGTTTGTCAATTACCCGAGGAAATACGGGGGACC	1058
Q	y	601	CAGATATTATGTTGGCTTGGCTATATAGAGAACCTGGGGCATGTTTGTCTACAGTAAT	660
D	b	1059	CAGATATTATGTTGGCTTGGCTATATAGAGAACCTGGGGCATGTTTGTCTACAGTAAT	1118
Q	y	661	GAAATATTAGGACAGTGGTGATAGAGTGATGGGTTGGTGGTAAATTTTTTTTTTAAT	720
D	b	1119	GAAATATTAGGACAGTGGTGATAGAGTGATGGGTTGGTGGTAAATTTTTTTTTTAAT	1178
Q	y	721	TTTTACAGTTTGTGGTTTAAAGAAATTTTGTAATTGTGATTTTTTTTAAAGGTCGTGTC	780
D	b	1179	TTTTACAGTTTGTGGTTTAAAGAAATTTTGTAATTGTGATTTTTTTTAAAGGTCGTGTC	1238
Q	y	781	TGAACCTGAGCGCTAGCCCGGACCAAGAACCGGAGCCTGCAAGACTACCCGCGTCTTA	840
D	b	1239	TGAACCTGAGCGCTAGCCCGGACCAAGAACCGGAGCCTGCAAGACTACCCGCGTCTTA	1298
Q	y	841	AATGGCGCTCTATCTCTGAGACGCCGCCACATCACTGTGTCTAGAGAAATGCATATAG	900
D	b	1289	AATGGCGCTCTATCTCTGAGACGCCGCCACATCACTGTGTCTAGAGAAATGCATATAG	1358
Q	y	901	TACGGATAGCTGTGACTCCGGTCTTCTTAACAACCTCTGAGATPACCCCGGTGTC	960
D	b	1359	TACGGATAGCTGTGACTCCGGTCTTCTTAACAACCTCTGAGATPACCCCGGTGTC	1418
Q	y	961	GCTGCCCCCACTTAAACAAGTTGCCGTGAGAGTTGGGGGTGCCAGCGTGGGAATG	1020
D	b	1419	GCTGCCCCCACTTAAACAAGTTGCCGTGAGAGTTGGGGGTGCCAGCGTGGGAATG	1478
Q	y	1021	TATCAGAGACTTGTCTTAAACGAGCCTGGGCAACTTTGGACTTGTAGCTGTAAACGCCAG	1080
D	b	1479	TATCAGAGACTTGTCTTAAACGAGCCTGGGCAACTTTGGACTTGTAGCTGTAAACGCCAG	1538
Q	y	1081	GCCATAGGTGTAAACCTGTGATTTGCGTGTGGTTAAACGCTTTGTTTGTGTAATAGT	1140
D	b	1539	GCCATAGGTGTAAACCTGTGATTTGCGTGTGGTTAAACGCTTTGTTTGTGTAATAGT	1598
Q	y	1141	TGATCTAAGTTTAAATAAAGGGTGAATATCTTTTAACTTGAATGCGGTAAATGGGGC	1200
D	b	1599	TGATCTAAGTTTAAATAAAGGGTGAATATCTTTTAACTTGAATGCGGTAAATGGGGC	1658
Q	y	1201	GGGGCTTAAAGGTTATATATGCGCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA	1260
D	b	1659	GGGGCTTAAAGGTTATATATGCGCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA	1718
Q	y	1261	GGCTTGGGAGTGTGTGAAGAATTTTCTGCTGTGCGTAACCTTGTGGAACAGACTTAA	1320
D	b	1719	GGCTTGGGAGTGTGTGAAGAATTTTCTGCTGTGCGTAACCTTGTGGAACAGACTTAA	1778
Q	y	1321	CAGTACCTCTTGTGTTTGGAGTTTCTGTGGGGCTACATCCAGGCAAAAGTTAGTCTGAG	1380
D	b	1779	CAGTACCTCTTGTGTTTGGAGTTTCTGTGGGGCTACATCCAGGCAAAAGTTAGTCTGAG	1838

QY	1381	AATTAAGAGGATTTACAAGTGGGAAATTGAAGCTTTGAAATCTGTGCTGACTGTT	1440
Db	1839	AATTAAGAGGAGATTACAGTGGGAAATTGGAAGCTTTTGAATCTGTGGGACTGTT	1898
QY	1441	TGATTCCTTTGAATCTGGGATCACAGGCGCTTTCCAGAGGAAGATCAACAAGCTTTGGA	1500
Db	1899	TGATTCCTTTGAATCTGGGATCACAGGCGCTTTCCAGAGGAAGATCAACAAGCTTTGGA	1958
QY	1501	TTTTCACACCGGGGCGGCTGCGGCTGCTGCTTTTGAAGTTTATTAAGATTA	1560
Db	1959	TTTTTCACACCGGGGCGGCTGCGGCTGCTGCTTTTGAAGTTTATTAAGATTA	2018
QY	1561	ATGAGAGGAAAGAAACCATCTGAGCGGGGGTAACTGCTGATTTTCTGGCCATGCACTT	1620
Db	2019	ATGAGAGGAAAGAAACCATCTGAGCGGGGGTAACTGCTGATTTTCTGGCCATGCACTT	2078
QY	1621	GTCGAGAGCGGTTGTGAGACAAAGATCGCGTCACTGTGTCTTCGTCGCGCGGCG	1680
Db	2079	GTCGAGAGCGGTTGTGAGACAAAGATCGCGTCACTGTGTCTTCGTCGCGCGGCG	2138
QY	1681	GATTAATACCGACGAGAGACAGACAGCAGCAGAGAGAACCGCAGCGCGCACAGA	1740
Db	2139	GATTAATACCGACGAGAGACAGACAGCAGCAGAGAGAACCGCAGCGCGCACAGA	2198
QY	1741	GCAAGGCCAATGGAACCCGAGAGCGGCGCTGGAACCTTGGGAAATGATGTGTACAGGTG	1800
Db	2199	GCAAGGCCAATGGAACCCGAGAGCGGCGCTGGAACCTTGGGAAATGATGTGTACAGGTG	2258
QY	1801	GCATGAATGTATTCAGAACTGAGACGCAATTTGACAAATTAACAGAGAGTGGCAGGGGCTA	1860
Db	2259	GCATGAATGTATTCAGAACTGAGACGCAATTTGACAAATTAACAGAGAGTGGCAGGGGCTA	2318
QY	1861	AAGGGGGTAAAGAGGAGCGGGGGGCTTGTGAGGCTACAGAGAGGCTTAGAATTTAGCT	1920
Db	2319	AAGGGGGTAAAGAGGAGCGGGGGGCTTGTGAGGCTACAGAGAGGCTTAGAATTTAGCT	2378
QY	1921	TTTAGCTTAATGACACAGACACCGTCCGTAGTATTAATCTTTCAACAGATCAAGATTAAT	1980
Db	2379	TTTAGCTTAATGACACAGACACCGTCCGTAGTATTAATCTTTCAACAGATCAAGATTAAT	2438
QY	1981	TGGGCTTAATGAGTTATCTGCTGGGCGCAAGATTTCCATGACACACTGACCACTTAC	2040
Db	2439	TGGGCTTAATGAGTTATCTGCTGGGCGCAAGATTTCCATGACACACTGACCACTTAC	2498
QY	2041	TGGCTGACGACAGGGGATGATTTTGTGAGAGGCTATTAAGGTTATGCAAAAGGTGACATT	2100
Db	2499	TGGCTGACGACAGGGGATGATTTTGTGAGAGGCTATTAAGGTTATGCAAAAGGTGACATT	2558
QY	2101	AGGCGCAAGTTGCAAGTACAAAGATCAGCAAACTTGTAAATATCAGGAATTTGTGCTACATT	2160
Db	2559	AGGCGCAAGTTGCAAGTACAAAGATCAGCAAACTTGTAAATATCAGGAATTTGTGCTACATT	2618
QY	2161	TCGTGGGAACGGGGGCGAGGTGAGATGATTAACGAGAGATAGGGTGGCCCTTTAGATGTAGC	2220
Db	2619	TCGTGGGAACGGGGGCGAGGTGAGATGATTAACGAGAGATAGGGTGGCCCTTTAGATGTAGC	2678
QY	2221	ATGATTAATATGTGAGCGGGGGGCTGTGGCATGAGACGGGGTGGTTATTAATGAAATGTAAGG	2280
Db	2679	ATGATTAATATGTGAGCGGGGGGCTGTGGCATGAGACGGGGTGGTTATTAATGAAATGTAAGG	2738
QY	2281	TTTACTGGCCCCAATTTTAGCGGTACGGTTTTTCTGGCCAAATACCAACCTTATCTTACAC	2340
Db	2739	TTTACTGGCCCCAATTTTAGCGGTACGGTTTTTCTGGCCAAATACCAACCTTATCTTACAC	2798
QY	2341	GGTGTAAAGCTTCTATGGGTTTAAACAATACCTGTGTGGAAGGCTTGAACGATGTAAAGGTT	2400
Db	2799	GGTGTAAAGCTTCTATGGGTTTAAACAATACCTGTGTGGAAGGCTTGAACGATGTAAAGGTT	2858
QY	2401	CGGGGCGTGCCCTTTTACGTGCTGTGGAAGGGGGGTGTGTGTGCCCCAAAAGCAGGGCT	2460
Db	2859	CGGGGCGTGCCCTTTTACGTGCTGTGGAAGGGGGGTGTGTGTGCCCCAAAAGCAGGGCT	2918

Qy	2461	CCATTTAAGAAATGCTCTTTGAAAGGTATCTTTGGTATCTCTGTGAGGGTAACTCC	2520
Db	2919	TCAATTAAAGAAATCCTCTTTGAAAGGTATCTTTGGTATCTCTGTGAGGGTAACTCC	2978
Qy	2521	AGGGTGCACCAATGTGGGCTCCGACCTGTGGTCTTACATGCTAGTAAAGGCGTGGCT	2580
Db	2979	AGGGTGCACCAATGTGGGCTCCGACCTGTGGTCTTACATGCTAGTAAAGGCGTGGCT	3038
Qy	2581	GTGATTAAGCATTAATGTGATGTGGCAACTGGAGGACAGAGGCTCTCAGATCTGACC	2640
Db	3039	GTGATTAAGCATTAATGTGATGTGGCAACTGGAGGACAGAGGCTCTCAGATCTGACC	3098
Qy	2641	TGCTCCGACGGGCAACTGTCACTCTGTGAAGACATTCACGTAGGACGCACTCTCGCAG	2700
Db	3099	TGCTCCGACGGGCAACTGTCACTCTGTGAAGACATTCACGTAGGACGCACTCTCGCAG	3158
Qy	2701	GCCCTGGCCAGTGTGAGCATTAATACTAGACCCGCTGTCTTGCATTTGGGTTAACAG	2760
Db	3159	GCCCTGGCCAGTGTGAGCATTAATACTAGACCCGCTGTCTTGCATTTGGGTTAACAG	3218
Qy	2761	AGGGGGGTGTCTTCTTACCTTACCAATGCATTTGAGTCACTAAGATATTTGCTGAGCC	2820
Db	3219	AGGGGGGTGTCTTCTTACCTTACCAATGCATTTGAGTCACTAAGATATTTGCTGAGCC	3278
Qy	2821	GAGAGCATGTCCAAAGGTGAACTCTGAACGGGGTGTGATCATGACATGAAGATCTGAG	2880
Db	3279	GAGAGCATGTCCAAAGGTGAACTCTGAACGGGGTGTGATCATGACATGAAGATCTGAG	3338
Qy	2881	GTGCTGAGGTATGATGAGACCCGACCCAGGTGCAACCTTGCAGTGTGGCGGTAAACAT	2940
Db	3339	GTGCTGAGGTATGATGAGACCCGACCCAGGTGCAACCTTGCAGTGTGGCGGTAAACAT	3398
Qy	2941	ATTAGGAACCAAGCCTGTGATGCTGATGTGATCCAGAGAGCTGAGGCCCGATCACTTGGT	3000
Db	3399	ATTAGGAACCAAGCCTGTGATGCTGATGTGATCCAGAGAGCTGAGGCCCGATCACTTGGT	3458
Qy	3001	CTGGCCTTGCAACCCGCGCTGAGTGTGGCTCTTAGCATGAATACAGATTGAG	3052
Db	3459	CTGGCCTTGCAACCCGCGCTGAGTGTGGCTCTTAGCATGAATACAGATTGAG	3510
RESULT 10			
US-09-714-550-18			
Sequence 18, Application US/09714550			
Patent No. 6558948			
GENERAL INFORMATION:			
APPLICANT: Kochanek, Stefan			
TITLE OF INVENTION: Permanent amniocytic cell line, its			
TITLE OF INVENTION: production and use for the production of gene transfer			
FILE REFERENCE: 50125/007002			
CURRENT APPLICATION NUMBER: US/09/714,550			
CURRENT FILING DATE: 2000-11-16			
PRIOR APPLICATION NUMBER: US 60/167,439			
PRIOR FILING DATE: 1999-11-23			
NUMBER OF SEQ ID NOS: 18			
SOFTWARE: Faesteq for Windows Version 4.0			
SEQ ID NO 18			
LENGTH: 7090			
TYPE: DNA			
ORGANISM: Plasmid STK146			
US-09-714-550-18			

Query Match	98.5%	Score 3005.8;	DB 4	Length 7090;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 3008; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 43 TCTGATGCCAGGAGTAGTTTCTCCCTCGAGCGCTCCGACACCGGAGATGAAAA 102
2749 TATGAGAGCCAGCAGTAGATTTTCTCTCCAGCGCTCCACACCGGAGATGAAAA 2808
103 TGAACATATTATCTGCCAGGAGTGTTATTACCGAAGAAATGGCCGCAAGTCTTTGG 162

Db	2809	TTGACACATTAATATTCGCCACGGAGGTGTATTAATACCGAAGAAATGCGCCACGTCTTTTGG	2868
OY	163	ACCAAGCTGATGGAAGAGGATCTGGCTGATAATCTTCAACCTCTAGCCCATTTTGAACAC	222
Db	2869	ACCAAGCTGATGGAAGAGGATCTGGCTGATAATCTTCAACCTCTAGCCCATTTTGAACAC	2928
OY	223	CTACCTTTACGAACTGTATGATTTTAAAGCTGACGGCCCCCGAAGATCCACAGAGAGG	282
Db	2929	CTACCTTTACGAACTGTATGATTTTAAAGCTGACGGCCCCCGAAGATCCACAGAGAGG	2988
OY	283	CGGTTTGGCAATTTTTTCCGACCTCTGTAAATGTTGGCGGTGACAGAAAGGATTTGACTTAC	342
Db	2989	CGGTTTGGCAATTTTTTCCGACCTCTGTAAATGTTGGCGGTGACAGAAAGGATTTGACTTAC	3048
OY	343	TCACCTTTCCGCGCGCGCGGCTTCTCGGAGCGCGCTCACTTTCCCGGACGCCGAGC	402
Db	3049	TCACCTTTCCGCGCGCGCGGCTTCTCGGAGCGCGCTCACTTTCCCGGACGCCGAGC	3108
OY	403	AGCCGAGACAGAGACCTTGGGTCCGGTTCTATGCAAACTTTGACCGAGGTGATCG	462
Db	3109	AGCCGAGACAGAGACCTTGGGTCCGGTTCTATGCAAACTTTGACCGAGGTGATCG	3168
OY	463	ATCTTACCTGCGACAGAGCTGGCTTTTCCACCACTGACGACGAGAGATGAAGAGGTGAG	522
Db	3169	ATCTTACCTGCGACAGAGCTGGCTTTTCCACCACTGACGACGAGAGATGAAGAGGTGAG	3228
OY	523	AGTTTGTGTTAGATTATGTGGAGACCCCGGGACCGTTGCAAGGTCTTGTCAATATAC	582
Db	3229	AGTTTGTGTTAGATTATGTGGAGACCCCGGGACCGTTGCAAGGTCTTGTCAATATAC	3288
OY	583	GGAGGAATACGGGGGAGCCAGATTTATGTTGCTTGTCTATATGATGAGACCTGTGGCA	642
Db	3289	GGAGGAATACGGGGGAGCCAGATTTATGTTGCTTGTCTATATGATGAGACCTGTGGCA	3348
OY	643	TGTTTGTCTACATGATGAAAAATTATGGCAGTGGGTGATGAGTGTGGTGTGTGT	702
Db	3349	TGTTTGTCTACATGATGAAAAATTATGGCAGTGGGTGATGAGTGTGGTGTGTGT	3408
OY	703	GGTAATTTTTTTTTTAAATTTTAAAGTTTGTGTTTAAAGAAATTTGTATTTGATTTT	762
Db	3409	GGTAATTTTTTTTTTAAATTTTAAAGTTTGTGTTTAAAGAAATTTGTATTTGATTTT	3468
OY	763	TTTAAAGAGTCTGTCTGTGAACCTGTAGCCGTGAGCCCGACAGAACCGGAGCTGTCAAG	822
Db	3469	TTTAAAGAGTCTGTCTGTGAACCTGTAGCCGTGAGCCCGACAGAACCGGAGCTGTCAAG	3528
OY	823	ACCTAACCCGCGCTTAAATGGCGCCTGTATCTTGAGACGCCGACATCACTGTGTCT	882
Db	3529	ACCTAACCCGCGCTTAAATGGCGCCTGTATCTTGAGACGCCGACATCACTGTGTCT	3588
OY	883	TAGGAATTCGCAATGTATGTATGATAGATAGCTGTGATCCGGTCTTCTTAAACACACTCTCTGA	942
Db	3589	TAGGAATTCGCAATGTATGTATGATAGATAGCTGTGATCCGGTCTTCTTAAACACACTCTCTGA	3648
OY	943	GATACACCCGCGTGTCCCGCTGTGCCCCCATTTAAACAGTTGCCGTGAGTGGTGGCG	1002
Db	3649	GATACACCCGCGTGTGTCCCGCTGTGCCCCCATTTAAACAGTTGCCGTGAGTGGTGGCG	3708
OY	1003	TCGCGCAGGCTGTGGAATGTATCGAGGACTTGTAAAGACCTGGGCAACTTTTGACTT	1062
Db	3709	TCGCGCAGGCTGTGGAATGTATCGAGGACTTGTAAAGACCTGGGCAACTTTTGACTT	3768
OY	1063	GAGCTGTAAACGCCCGCAGGCGCTAAAGGTGTAAACCTGTGATTTGGGTGTGTAAACGCC	1122
Db	3769	GAGCTGTAAACGCCCGCAGGCGCTAAAGGTGTAAACCTGTGATTTGGGTGTGTAAACGCC	3828
OY	1123	TTTGTGTTGCGAATGAGTTGATGTATGATTTTAAATGAAGGGGAGATATGTTTAACTTGA	1182
Db	3829	TTTGTGTTGCGAATGAGTTGATGTATGATTTTAAATGAAGGGGAGATATGTTTAACTTGA	3888
OY	1183	TGGGTGTGTTAAATGGGCGGGGCTTTAAAGGTTATATATCGCGCTGGGCTAAATCTTGGT	1242

Db 3829 TTTTGTTCGATGAGTTATGTAAATTAAAGGGAGAGTAAATGTTAACTTGCA 3888
 QY 1183 TGCGCTGTTAAATGGGCGGAGCTTAAAGGGTATATATATCGCGCTGGGCTAAATCTTGCT 1242

Db 3889 TGCGGTGTTAAATGCGCGGCGCTTAAAGGGTATATAATGCGCCGCTAGCTACTTGGT 3948
Qy 1243 TACATCTGACCTCATGAGAGCTTTGGAGAGTCTTTTGGAGATTTTTCTGCTGCGCTAACTT 1302
Db 3949 TACATCTGACCTCATGAGAGCTTTGGAGAGTCTTTTGGAGATTTTTCTGCTGCGCTAACTT 4008
Qy 1303 GCTGGAACAGAGCTCTAACACATACCTCTTGGTTTTGGAGTTTTCTGCGGAGCTATCCCA 1362
Db 4009 GCTGGAACAGAGCTCTAACACATACCTCTTGGTTTTGGAGTTTTCTGCGGAGCTATCCCA 4068
Qy 1363 GCGAAAGTTAGTCTGACAGATTTAAAGAGAGATTACAGTGGGAATTTGAAGACTTTTGA 1422
Db 4069 GCGAAAGTTAGTCTGACAGATTTAAAGAGAGATTACAGTGGGAATTTGAAGACTTTTGA 4128
Qy 1423 ATCTGTGAGTGAAGCTGTTTGAATCTTTGAATCTGGGTACACAGGCGCTTTTCCAAAGAA 1482
Db 4129 ATCTGTGAGTGAAGCTGTTTGAATCTTTGAATCTGGGTACACAGGCGCTTTTCCAAAGAA 4188
Qy 1483 GGTGATCAAGACTTTGGATTTTTCCACACCGGGGCGCTCGGCTGCTGTTGCTTTTTT 1542
Db 4189 GGTGATCAAGACTTTGGATTTTTCCACACCGGGGCGCTCGGCTGCTGTTGCTTTTTT 4248
Qy 1543 GAGTTTTATAAAGATTAATGAGAGAAACCCTATCTGAGCGGGGGTACCTGCTGGA 1602
Db 4249 GAGTTTTATAAAGATTAATGAGAGAAACCCTATCTGAGCGGGGGTACCTGCTGGA 4308
Qy 1603 TTTTCTGGCCATGATCTGTGTGAGAGCGGTGTGTGAGACAAAGATCCCTGCTACTGTT 1662
Db 4309 TTTTCTGGCCATGATCTGTGTGAGAGCGGTGTGTGAGACAAAGATCCCTGCTACTGTT 4368
Qy 1663 GTCTTCGCTCCGCGCGGATTAATCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1722
Db 4369 GTCTTCGCTCCGCGCGGATTAATCCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4428
Qy 1723 CAGCGCGGCGGAG 1782
Db 4429 CAGCGCGGCGGAG 4488
Qy 1783 ATGAATGTGTACAGAGTGGCTGAACTGTATCCAGAACCTGAAACCGATTTTGAACAATTA 1842
Db 4489 ATGAATGTGTACAGAGTGGCTGAACTGTATCCAGAACCTGAAACCGATTTTGAACAATTA 4548
Qy 1843 GAGAGTGGCGAGGGGCTTAAAGGGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1902
Db 4549 GAGAGTGGCGAGGGGCTTAAAGGGGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4608
Qy 1903 GAGGCTAGAGATCTAGCTTTTGTAGCTTAAATGACACAGACACCGTCTGAGTGTATTA 1962
Db 4609 GAGGCTAGAGATCTAGCTTTTGTAGCTTAAATGACACAGACACCGTCTGAGTGTATTA 4668
Qy 1963 CAACAGATCAAGAGATTAATTTGGGCTAAATGAGCTGATCTGCTGGCGCAAGATTTCCATA 2022
Db 4669 CAACAGATCAAGAGATTAATTTGGGCTAAATGAGCTGATCTGCTGGCGCAAGATTTCCATA 4728
Qy 2023 GAGGAGCTGACCACTTATGCTGCTGAGCGAGGAGATTTTGAAGAGAGCTATTAGGGTA 2082
Db 4729 GAGGAGCTGACCACTTATGCTGCTGAGCGAGGAGATTTTGAAGAGAGCTATTAGGGTA 4788
Qy 2083 TATGCAAAAGTGGACCTTAGCGCCAGATTTGCAAGTACAGCAAACTTTGAATATTC 2142
Db 4789 TATGCAAAAGTGGACCTTAGCGCCAGATTTGCAAGTACAGCAAACTTTGAATATTC 4848
Qy 2143 AGGAATTTGCTCTACATTTCTGGGAAAGGGGCGAGAGTGGAGATGAGACGAGAGATGG 2202
Db 4849 AGGAATTTGCTCTACATTTCTGGGAAAGGGGCGAGAGTGGAGATGAGACGAGAGATGG 4908
Qy 2203 GTGGCCCTTTAGATGAGCATGATAAATATGTGCGCGGGGCTGCTTGAGATGAGACGGGTTG 2262
Db 4909 GTGGCCCTTTAGATGAGCATGATAAATATGTGCGCGGGGCTGCTTGAGATGAGACGGGTTG 4968
Qy 2263 GTTATTTATGAATGTGAAGTTTATCTGGCCCAATTTTACCGGTAACGGTTTCTGCGCAAT 2322
Db 4969 GTTATTTATGAATGTGAAGTTTATCTGGCCCAATTTTACCGGTAACGGTTTCTGCGCAAT 5028

Qy 2323 ACCAACCTTATCCACAGCGGATGAAGCTTCTATGGGTTTAAACAATACCTGTGTGAAGCC 2382
Db 5029 ACCAACCTTATCCACAGCGGATGAAGCTTCTATGGGTTTAAACAATACCTGTGTGAAGCC 5088
Qy 2383 TGAACCGATGTAAGGGTTTCGGGGCTGTGCTTTTACTGCTGTGAAGGGGGTGTGT 2442
Db 5089 TGAACCGATGTAAGGGTTTCGGGGCTGTGCTTTTACTGCTGTGAAGGGGGTGTGTGT 5148
Qy 2443 CGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATCCTTGGGTATC 2502
Db 5149 CGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATCCTTGGGTATC 5208
Qy 2503 CTGTCTGAGGGTAACTCCAGGGTGCAGCAATGTGACTCCGACTGAGTTGCTTCATG 2562
Db 5209 CTGTCTGAGGGTAACTCCAGGGTGCAGCAATGTGACTCCGACTGAGTTGCTTCATG 5268
Qy 2563 CTAGTAAAAAGCGTGTGTGATTAAGCATTAACATGATGTGCAACTGCGAGACAGG 2622
Db 5269 CTAGTAAAAAGCGTGTGTGATTAAGCATTAACATGATGTGCAACTGCGAGACAGG 5328
Qy 2623 GCTCTCAATGCTGACCTGTGTGAGAGGCACTGTCACTGCTGAAAGACATTCAGTA 2682
Db 5329 GCTCTCAATGCTGACCTGTGTGAGAGGCACTGTCACTGCTGAAAGACATTCAGTA 5388
Qy 2683 GCCAGCCACTCTGCAAGAGCTGGCCAGTGTGAGCATTAACATGACTGACCCGCTGTTCC 2742
Db 5389 GCCAGCCACTCTGCAAGAGCTGGCCAGTGTGAGCATTAACATGACTGACCCGCTGTTCC 5448
Qy 2743 TTGCAATTTGGGTAAACAGAGGGGGGTGTTCTTACTTAACCAATGCAATTTGATGACACT 2802
Db 5449 TTGCAATTTGGGTAAACAGAGGGGGGTGTTCTTACTTAACCAATGCAATTTGATGACACT 5508
Qy 2803 AAGATATTGCTTGAAGCCGAGAGATGTCCAAGTGAACCTGAAACGGGGCTTTGACATG 2862
Db 5509 AAGATATTGCTTGAAGCCGAGAGATGTCCAAGTGAACCTGAAACGGGGCTTTGACATG 5568
Qy 2863 ACCATGAAGATCTGGAAGTGTGAGGTAGATGATGAGACCCGACAGAGTGAAGACCTGTC 2922
Db 5569 ACCATGAAGATCTGGAAGTGTGAGGTAGATGATGAGACCCGACAGAGTGAAGACCTGTC 5628
Qy 2923 GAGTGTGGCGGTAAACATATTATTAAGAACCAAGCTGTGTGATGTGACCGAGAGCTG 2982
Db 5629 GAGTGTGGCGGTAAACATATTATTAAGAACCAAGCTGTGTGATGTGACCGAGAGCTG 5688
Qy 2983 AGGCCCATCACTTGTGTGTGCTGTGACCCCGCTGAGTTTGGCTTAAGGATGAAGAT 3042
Db 5689 AGGCCCATCACTTGTGTGTGCTGTGACCCCGCTGAGTTTGGCTTAAGGATGAAGAT 5748
Qy 3043 ACAGATTGAG 3052
Db 5749 ACAGATTGAG 5758

RESULT 11
US-09-956-335-2
; Sequence 2, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly
; APPLICANT: KUPPASMAM, Mohan
; APPLICANT: DORONIN, Konstantin
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
; FILE REFERENCE: 16153-8394
; CURRENT APPLICATION NUMBER: US/09/956,335
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 35871
; TYPE: DNA

i ORGANISM: Adenovirus									
US-09-956-335-2									
Query Match 92.5%; Score 2822; DB 4; Length 35871;									
Best Local Similarity 96.6%; Pred. No. 0;									
Matches 2947, Conservative 0; Mismatches 0; Indels 105; Gaps 2;									
Qy	1	CGGTAGTATATTTATACCGCGTGAAGTTCTTCMAAGAGCCACTCTTGAGTGCACGAGT	60						
Db	459	CGTGTAGTATATTTATACCGCGTGAAGTTCTTCMAAGAGCCACTCTTGAGTGCACGAGT	518						
Qy	61	AGAGTTTCTCTCCGAGCGGCTCGACACCGGGAGCTGAATGAGACATATTAATCGCC	120						
Db	519	AGAGTTTCTCTCCGAGCGGCTCGACACCGGGAGCTGAATGAGACATATTAATCGCC	568						
Qy	121	ACGGAGGTATTAACCGAAGAAATGGCCGCGAGTCTTTTGAACCAAGCTGATCGAAGAG	180						
Db	569	-----GAGG	572						
Qy	181	TACTGCGTGAATATCTTCCACTCTAGCCATTTTGAAACCACTTACCTTACGAACTGT	240						
Db	573	TACTGCGTGAATATCTTCCACTCTAGCCATTTTGAAACCACTTACCTTACGAACTGT	632						
Qy	241	ATGATTTAGACGTACGCGCCCGGAAAGATCCCAACGAGAGCGGTTTCGAGATTTTTC	300						
Db	633	ATGATTTAGACGTACGCGCCCGGAAAGATCCCAACGAGAGCGGTTTCGAGATTTTTC	692						
Qy	301	CCGACTCTGATATGTGGCGGTGACAGAAAGGATTTGACTCACTTTTCGCGCGGCG	360						
Db	693	CCGACTCTGATATGTGGCGGTGACAGAAAGGATTTGACTCACTTTTCGCGCGGCG	752						
Qy	361	CCGCTTCTCCGAGCGGCTCACTTTTCGCGAGCCCGAGAGCCGAGACAGAGAGCTT	420						
Db	753	CCGCTTCTCCGAGCGGCTCACTTTTCGCGAGCCCGAGAGCCGAGACAGAGAGCTT	812						
Qy	421	TGGTCCGCTTCTATGCGCAACCTTGAACGAGAGTATGATCTTACCTTGACAGAGG	480						
Db	813	TGGTCCGCTT-----TGCCAGAGG	833						
Qy	481	CTGCGCTTCCACCGAGTACGACAGAGTGAAGAGGTGAGAGATTGTGTTAATATG	540						
Db	834	CTGCGCTTCCACCGAGTACGACAGAGTGAAGAGGTGAGAGATTGTGTTAATATG	893						
Qy	541	TGAGACACCCCGGCGACGCTTGCAGGTCTTGTCAATACCCGAGAAATCCGGGGACC	600						
Db	894	TGAGACACCCCGGCGACGCTTGCAGGTCTTGTCAATACCCGAGAAATCCGGGGACC	953						
Qy	601	CAGATATTAATGTGCTTGTGCTATATAGAGACCTGTGGCATGTTGTCTACAGTATG	660						
Db	954	CAGATATTAATGTGCTTGTGCTATATAGAGACCTGTGGCATGTTGTGTACAGTATG	1013						
Qy	661	GAATATTAATGAGGAGTGTGATAGAGTGTGGTTTGTGTGTAATTTTTTTTTTAT	720						
Db	1014	GAATATTAATGAGGAGTGTGATAGAGTGTGGTTTGTGTGTAATTTTTTTTTTAT	1073						
Qy	721	TTTTACAGTTTGTGCTTAAAGATTTTGTATTTGTATTTTTTTTAAAGGTCTGTGTC	780						
Db	1074	TTTTACAGTTTGTGCTTAAAGATTTTGTATTTGTATTTTTTTTAAAGGTCTGTGTC	1133						
Qy	781	TGAACCTGAGCGCTGAGCCGAGCGAAGCCGAGAGCTGCAAGACCTTACCGCGCTTAA	840						
Db	1134	TGAACCTGAGCGCTGAGCCGAGCGAAGCCGAGAGCTGCAAGACCTTACCGCGCTTAA	1193						
Qy	841	AATGGCGCTGCTATCTCTGAGACGCGCGACATCACTGTGTCTAGAGATGCAATAGTAG	900						
Db	1194	AATGGCGCTGCTATCTCTGAGACGCGCGACATCACTGTGTCTAGAGATGCAATAGTAG	1253						
Qy	901	TACGATAGCTGTGACTCCGCTCTTCAACACACTCTCTGAGATACACCCGGTGTGCC	960						
Db	1254	TACGATAGCTGTGACTCCGCTCTTCAACACACTCTCTGAGATACACCCGGTGTGCC	1313						
Qy	961	GCTGTGCCCATTAACAGTTGCGGTGAGAGTGTGGGCGTGCAGGCTGTGGAATG	1020						

Db	1314	GCTGTGCCCATTAACAGTTGCGGTGAGAGTGTGGGCGTGCAGGCTGTGGAATG	1373						
Qy	1021	TATGAGAGACTTGTCTTAACGAGCTGAGCAACTTTGAGCTTGAAGCTTAACGCCCCAG	1080						
Db	1374	TATGAGAGACTTGTCTTAACGAGCTGAGCAACTTTGAGCTTGAAGCTTAACGCCCCAG	1433						
Qy	1081	GCCATAGCTTAACCTGTGATTTGCGTGTGTAAACGCTTGTGTTGCTGATATGAT	1140						
Db	1434	GCCATAGCTTAACCTGTGATTTGCGTGTGTAAACGCTTGTGTTGCTGATATGAT	1493						
Qy	1141	TGATGATGTTAATTAAGGAGTGAATATGTTAACTTGATGCGGTGAATAAGGGC	1200						
Db	1494	TGATGATGTTAATTAAGGAGTGAATATGTTAACTTGATGCGGTGAATAAGGGC	1553						
Qy	1201	GGGCTTAAGGATATATATGCGCGCTGATCTTGTGTTAATCTGATGACTTATGGA	1260						
Db	1554	GGGCTTAAGGATATATATGCGCGCTGATCTTGTGTTAATCTGATGACTTATGGA	1613						
Qy	1261	GGCTTGGAGATGTTGAAGAATTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTTAA	1320						
Db	1614	GGCTTGGAGATGTTGAAGAATTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTTAA	1673						
Qy	1321	CAGTACCTCTTGTGTTGAGAGTTCTGTGGGCTCAATCCAGGCAAGTTAGTTCAG	1380						
Db	1674	CAGTACCTCTTGTGTTGAGAGTTCTGTGGGCTCAATCCAGGCAAGTTAGTTCAG	1733						
Qy	1381	AATTAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTAGACTGTT	1440						
Db	1734	AATTAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTAGACTGTT	1793						
Qy	1441	TGATTTCTTGAATCTGGGTCCAGCGGCTTTCCAGAGAAAGGTCAACAACCTTGA	1500						
Db	1794	TGATTTCTTGAATCTGGGTCCAGCGGCTTTCCAGAGAAAGGTCAACAACCTTGA	1853						
Qy	1501	TTTTTCCACACGGGAGCGCTGCGCTGTGTCTTTTGAAGTTTAAAGATTA	1560						
Db	1854	TTTTTCCACACGGGAGCGCTGCGCTGTGTCTTTTGAAGTTTAAAGATTA	1913						
Qy	1561	ATGAGCGAAGAAACCAATCTGAGCGGGGGTACCTGTGATTTTCTGCAATGATCT	1620						
Db	1914	ATGAGCGAAGAAACCAATCTGAGCGGGGGTACCTGTGATTTTCTGCAATGATCT	1973						
Qy	1621	GTGAGAGCGGTGTGAGACCAAGAATCGCTGTCTGTGTCTTCCGCGCGCGG	1680						
Db	1974	GTGAGAGCGGTGTGAGACCAAGAATCGCTGTCTGTGTCTTCCGCGCGCGG	2033						
Qy	1681	GATATACCGACGAGAGACAGACAGACAGACAGAGAAACAGCGCGCGAGAGA	1740						
Db	2034	GATATACCGACGAGAGACAGACAGACAGACAGAGAAACAGCGCGCGAGAGA	2093						
Qy	1741	GCAGAGCCCATGAAACCGAGAGCCGCGCTGAGCCCTCGGGAATGATGTTGTAAGGTG	1800						
Db	2094	GCAGAGCCCATGAAACCGAGAGCCGCGCTGAGCCCTCGGGAATGATGTTGTAAGGTG	2153						
Qy	1801	GCTGAATCTGATCCAGAACGTGAGACGATTTTGCAATTAAGAGGANTGGGCGGGGCTA	1860						
Db	2154	GCTGAATCTGATCCAGAACGTGAGACGATTTTGCAATTAAGAGGANTGGGCGGGGCTA	2213						
Qy	1861	AAGGGGTTAAAGAGAGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTTAACTTAACT	1920						
Db	2214	AAGGGGTTAAAGAGAGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTTAACTTAACT	2273						
Qy	1921	TTTACCTTAATGACACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT	1980						
Db	2274	TTTACCTTAATGACACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT	2333						
Qy	1981	TGGGCTATGAGCTTGAATCTGTGCGAGAGAAATTCATATAGAGAGCTGACCACTTAC	2040						
Db	2334	TGGGCTATGAGCTTGAATCTGTGCGAGAGAAATTCATATAGAGAGCTGACCACTTAC	2393						
Qy	2041	TGGCTGACCGCAGGAGATGATTTTGAAGAGCTTAAAGGTATATGCAAGGTGGCACTT	2100						
Db	2394	TGGCTGACCGCAGGAGATGATTTTGAAGAGCTTAAAGGTATATGCAAGGTGGCACTT	2453						

2101 AGGCCAGATTGCAAGTACAGATCAGCAACTTGTAAATATCAGGAATTGTTGCTACATT 2160
2454 AGGCCAGATTGCAAGTACAGATCAGCAACTTGTAAATATCAGGAATTGTTGCTACATT 2513
2161 TCTGGGAAACGGGGCCGAGAGTGAAGTAGATAACGAGATAGAGGTGGCTTTAGATGAGC 2220
2514 TCTGGGAAACGGGGCCGAGAGTGAAGTAGATAACGAGATAGAGGTGGCTTTAGATGAGC 2573
2221 ATGATTAATATGATGCGCGGGGGTGTGGCATGACCGGGGTGTTATTAATGATGTAAGG 2280
2574 ATGATTAATATGATGCGCGGGGGTGTGGCATGACCGGGGTGTTATTAATGATGTAAGG 2633
2281 TTTACTGGCCCCCAATTTTAAAGCGGTACGGTTTCTCGGCCAATACCAACTTACTACAC 2340
2634 TTTACTGGCCCCCAATTTTAAAGCGGTACGGTTTCTCGGCCAATACCAACTTACTACAC 2693
2341 GGTGTAAAGCTTCTATGGGTTTAAACAATACCTGTGTGAAAGCCTGGAACGATGTAAAGGTT 2400
2694 GGTGTAAAGCTTCTATGGGTTTAAACAATACCTGTGTGAAAGCCTGGAACGATGTAAAGGTT 2753
2401 CGGGGCTGTGCTTTTAACTGCTGCGAAGGGGGTGTGTCTGCCCCCAAAAGCAGGGCT 2460
2754 CGGGGCTGTGCTTTTAACTGCTGCGAAGGGGGTGTGTCTGCCCCCAAAAGCAGGGCT 2813
2461 TCAATTAAGAAATGCTCTTGAAGAGGTACCTTGGGTATCTGTCTGAGGGTAACTCC 2520
2814 TCAATTAAGAAATGCTCTTGAAGAGGTACCTTGGGTATCTGTCTGAGGGTAACTCC 2873
2521 AGGGTGCAGCAATATGTCCTCCGACTGTGTGCTTCAATGATGAAAAAGCTGTGCT 2580
2874 AGGGTGCAGCAATATGTCCTCCGACTGTGTGCTTCAATGATGAAAAAGCTGTGCT 2933
2581 GTGATTAAGCAATAATGATGATGTCGCACTGCGAAGCAGGGGCTCTCAATGCTGACC 2640
2934 GTGATTAAGCAATAATGATGATGTCGCACTGCGAAGCAGGGGCTCTCAATGCTGACC 2993
2641 TGCTCGGACGGCAACTGCTCACTGCTGGAAGCAATTCAGTAGCCAGCCACTCTCGCAG 2700
2994 TGCTCGGACGGCAACTGCTCACTGCTGGAAGCAATTCAGTAGCCAGCCACTCTCGCAG 3053
2701 GCTGCGCAAGTGTGTCGATTAACAATGTAACCCGCTGCTCTTGACATTTGGGTAAACAG 2760
3054 GCTGCGCAAGTGTGTCGATTAACAATGTAACCCGCTGCTCTTGACATTTGGGTAAACAG 3113
2761 AGGGGGGGTGTCCATCACTTAACAATGTAACCTTGAAGTCACTTAAGATTTGCTTGAAGCC 2820
3114 AGGGGGGGTGTCCATCACTTAACAATGTAACCTTGAAGTCACTTAAGATTTGCTTGAAGCC 3173
2821 GAGAGCAATGTCAGAGTGAACCTGAAACGGGGTGTGTCATGATGATCAATGAATCTGGAAG 2880
3174 GAGAGCAATGTCAGAGTGAACCTGAAACGGGGTGTGTCATGATGATCAATGAATCTGGAAG 3233
2881 GTGCTGAGTACGATGAGAACCCGCAACAGGTGCAAGCCCTGCGAGTGTGGCGGTAAACAT 2940
3234 GTGCTGAGTACGATGAGAACCCGCAACAGGTGCAAGCCCTGCGAGTGTGGCGGTAAACAT 3293
2941 ATTAGGAACCAAGCTGTGATGCTGATGTCGAGAGGCTGAGGCCCGGATCACTTGCTG 3000
3294 ATTAGGAACCAAGCTGTGATGCTGATGTCGAGAGGCTGAGGCCCGGATCACTTGCTG 3353
3001 CTGAGCTGCAACCCGCGCTGAGTTTGGCTCTAGCGATGAGATTAAGATTGAG 3052
3354 CTGAGCTGCAACCCGCGCTGAGTTTGGCTCTAGCGATGAGATTAAGATTGAG 3405

RESULT 12
US-08-735-609-4

; Sequence 4, Application US/08735609

; Patent No. 5955360

; GENERAL INFORMATION:

; APPLICANT: Chamberlain, Jeffrey S.

; APPLICANT: Amalfitano, Andrea

APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-735-609-4

Query Match 70.8%; Score 2161; DB 2; Length 34303;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 892 CAATAGTAGTACGGATAGCTGTGACTCCGGTCTTCTTAACACACCTCTGAGATACACC 951
DB 2853 CAATAGTAGTACGGATAGCTGTGACTCCGGTCTTCTTAACACACCTCTGAGATACACC 2912
QY 952 GGTGTCCCGCTGTGCCCCCATTAACCAAGTTGCCGTGAGAGTTGTGTGGCGTCCGACAGGC 1011
DB 2913 GGTGTCCCGCTGTGCCCCCATTAACCAAGTTGCCGTGAGAGTTGTGTGGCGTCCGACAGGC 2972
QY 1012 TGTGAATGTATGAGAGACTTGTGCTTAACGAGCCGTGGCAACCTTGGACTTGAAGCTGTAA 1071
DB 2973 TGTGAATGTATGAGAGACTTGTGCTTAACGAGCCGTGGCAACCTTGGACTTGAAGCTGTAA 3072
QY 1072 ACGCCCCAGGCCAATGAAGGTGAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTTTGC 1131
DB 3033 ACGCCCCAGGCCAATGAAGGTGAACCTGTGATTCGCTGTGTGTTAAACGCTTTGTTTGC 3092
QY 1132 TGAATGACTTGAATGATTAATTAAGGGGTGAGATATATGTTTAACTTGCATGGCGTGT 1191
DB 3093 TGAATGACTTGAATGATTAATTAAGGGGTGAGATATATGTTTAACTTGCATGGCGTGT 3152
QY 1192 AAATGGGGCGGGGCTTAAGGGTATTAATGCGCGGAGGCTAATCTTGGTTACATCTGA 1251
DB 3153 AAATGGGGCGGGGCTTAAGGGTATTAATGCGCGGAGGCTAATCTTGGTTACATCTGA 3212
QY 1252 CTTGATGAGAGCTTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCGTAACTTGTGGAACA 1311
DB 3213 CTTGATGAGAGCTTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCGTAACTTGTGGAACA 3272
QY 1312 GAGCTTAACAGTACTCTTGTGTTTGAAGGTTTCTGTGGGCTCATCCAGGCAAAATT 1371
DB 3273 GAGCTTAACAGTACTCTTGTGTTTGAAGGTTTCTGTGGGCTCATCCAGGCAAAATT 3332

```

QY 1372 AGTCTGCAAGATTAAAGAGATTACAACTGGGAATTTGAAGCTTTTGAATCTCTGG 1431
Db AGTCTGCAAGATTAAAGAGATTACAACTGGGAATTTGAAGCTTTTGAATCTCTGG 3392
QY 1432 TGACCTGTTGATCTTTGAATCTGGGTCAACGAGCGCTTTCCAGAGAGTCAATCA 1491
Db TGACCTGTTGATCTTTGAATCTGGGTCAACGAGCGCTTTCCAGAGAGTCAATCA 3452
QY 1492 GACTTTGATTTTTCACACCGGGCGCGCTGGCTGCTGTGTTTTTGAATTTAT 1551
Db GACTTTGATTTTTCACACCGGGCGCGCTGGCTGCTGTGTTTTTGAATTTAT 3512
QY 1552 AAAGAGTAAATGAGCGGAGAAACCACTGAAGCGGGGGTACTGCTGATTTTCTGGC 1611
Db AAAGAGTAAATGAGCGGAGAAACCACTGAAGCGGGGGTACTGCTGATTTTCTGGC 3572
QY 1612 CATCATCTGTGAGAGCGGTGTGAGACACAGAAATGCGCTGCTACTGTGCTTCCGT 1671
Db CATCATCTGTGAGAGCGGTGTGAGACACAGAAATGCGCTGCTACTGTGCTTCCGT 3632
QY 1672 CCGCGCGCGATTAATACCGAGCGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1731
Db CCGCGCGCGATTAATACCGAGCGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 3692
QY 1732 GCGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1791
Db GCGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3752
QY 1792 GTACAGGTGCTGAAGTGTATCCAGAACTGAGAGCATTTTGAACAATTAGAGAGATGG 1851
Db GTACAGGTGCTGAAGTGTATCCAGAACTGAGAGCATTTTGAACAATTAGAGAGATGG 3812
QY 1852 CAGGGGCTAAAGGGGGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1911
Db CAGGGGCTAAAGGGGGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3872
QY 1912 AATTAGCTTTTACTGTTAATGACCAAGACCGTCTGAGTGTATTTCAACAGATC 1971
Db AATTAGCTTTTACTGTTAATGACCAAGACCGTCTGAGTGTATTTCAACAGATC 3932
QY 1972 AAGGATTAATGCGGTAATGAGCTTGATGCTGGGCGAGAAATTCATAGAGAGCTG 2031
Db AAGGATTAATGCGGTAATGAGCTTGATGCTGGGCGAGAAATTCATAGAGAGCTG 3992
QY 2032 ACCACTTACTGCTGACGACGAGGGATGATTTTGAAGAGCTAATAGGATATGCAAG 2091
Db ACCACTTACTGCTGACGACGAGGGATGATTTTGAAGAGCTAATAGGATATGCAAG 4052
QY 2092 GTGGCACTTGAAGCGAGTGTCAAGTCAAGATCAAGCAACTTTGTAATATCAGAGATGT 2151
Db GTGGCACTTGAAGCGAGTGTCAAGTCAAGATCAAGCAACTTTGTAATATCAGAGATGT 4112
QY 2152 TGCTACATTTCTGGGAAACGGGGCGAGGTGAGATAGTACGAGAGATAGGGTCCCTT 2211
Db TGCTACATTTCTGGGAAACGGGGCGAGGTGAGATAGTACGAGAGATAGGGTCCCTT 4172
QY 2212 AGATGTAGCATGATTAATATGTGCGCGGGGTGCTTGGCATGACGAGGTGTTATATG 2271
Db AGATGTAGCATGATTAATATGTGCGCGGGGTGCTTGGCATGACGAGGTGTTATATG 4232
QY 2272 AATGTAAAGTTTACTGGCCCCCAATTTTACCGGTACCGTTTTCTGGCCAAATCAACCTT 2331
Db AATGTAAAGTTTACTGGCCCCCAATTTTACCGGTACCGTTTTCTGGCCAAATCAACCTT 4292
QY 2332 ATCTTACACGAGTGAAGCTTATAGGGTTTAAACAATCTGTGAGAGAGAGAGAGAGAG 2391
Db ATCTTACACGAGTGAAGCTTATAGGGTTTAAACAATCTGTGAGAGAGAGAGAGAGAG 4352
QY 2392 GTAAAGGTTTCGGGGCTGTGCTTTTACTGCTGTGAGAGAGAGAGAGAGAGAGAGAG 2451
Db GTAAAGGTTTCGGGGCTGTGCTTTTACTGCTGTGAGAGAGAGAGAGAGAGAGAGAG 4412

```

```

QY 2452 AGCAGGGCTTCAATTAGAAATGCTCTTTGAAGGTGATCCTGGGATCTGCTGAG 2511
Db AGCAGGGCTTCAATTAGAAATGCTCTTTGAAGGTGATCCTGGGATCTGCTGAG 4472
QY 2512 GGTAACTTCAGAGGGTCCGCAATAGTGGCTCCGACTGTGTTCTTCAATGATGAAA 2571
Db GGTAACTTCAGAGGGTCCGCAATAGTGGCTCCGACTGTGTTCTTCAATGATGAAA 4532
QY 2572 AGCGTGTGTGATTAAGCATTAATGATGTGTGCAACTGCGAGAGAGAGAGAGAGAG 2631
Db AGCGTGTGTGATTAAGCATTAATGATGTGTGCAACTGCGAGAGAGAGAGAGAGAG 4592
QY 2632 ATGCTGACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2691
Db ATGCTGACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4652
QY 2692 TCTGCAAGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2751
Db TCTGCAAGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4712
QY 2752 GGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2811
Db GGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4772
QY 2812 CTTGAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2871
Db CTTGAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4832
QY 2872 ATCTGAAAGGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2931
Db ATCTGAAAGGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4892
QY 2932 GGTAAACATATTAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2991
Db GGTAAACATATTAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4952
QY 2992 CACTTGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3051
Db CACTTGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5012
QY 3052 G 3052
Db 5013 G 5013

RESULT 13
US-08-735-609-4
; Sequence 4, Application US/08735609
; Patent No. 5994132
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; Inventor: Amalfitano, Andrea
; Hauser, Michael A.
; Kumar-Singh, Rajendra
; Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,609
; FILING DATE: 23-Oct-1996
; CLASSIFICATION: <Unknown>

```

ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-735-609-4
Query Match 70.8%; Score 2161; DB 2; Length 34303;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 892 CAATAGTATGACGATAGCTGTGACTCCGCTCTTCTAACAACACCTCTGAGATACACC 951
DB 2853 CAATAGTATGACGATAGCTGTGACTCCGCTCTTCTAACAACACCTCTGAGATACACC 2912
QY 952 GGTGTCCTCCGCTGTCGCCCATTAACACAGTTCGCGTGAAGATGGTGGCGTCGCCAGGC 1011
DB 2913 GGTGTCCTCCGCTGTCGCCCATTAACACAGTTCGCGTGAAGATGGTGGCGTCGCCAGGC 2972
QY 1012 TGTGGAATGTATCGAGACCTTGCTTAACAGACCTGGGCAACCTTGGACTTGAGCTGTAA 1071
DB 2973 TGTGGAATGTATCGAGACCTTGCTTAACAGACCTGGGCAACCTTGGACTTGAGCTGTAA 3032
QY 1072 AGCCCCAGGCCATAGGTGTAAACCTGTATTCGTGTGTGTAAACGCTTGTGTTC 1131
DB 3033 AGCCCCAGGCCATAGGTGTAAACCTGTATTCGTGTGTGTAAACGCTTGTGTTC 3092
QY 1132 TGAATGAGTATGATTAATTAATAGGGTGAATATGTTTAACTTGCANGGCGTGT 1191
DB 3093 TGAATGAGTATGATTAATTAATAGGGTGAATATGTTTAACTTGCANGGCGTGT 3152
QY 1192 AAATGGGCGGGGCTTAAAGGGTATATATGCGCGGTGGCTAACTTGTGTAACTCTGA 1251
DB 3153 AAATGGGCGGGGCTTAAAGGGTATATATGCGCGGTGGCTAACTTGTGTAACTCTGA 3212
QY 1252 CCTCATGAGAGCTTGGAGTGTGGAAAGATTTTCTGCTGTGGTAACTTGTCTGGAACA 1311
DB 3213 CCTCATGAGAGCTTGGAGTGTGGAAAGATTTTCTGCTGTGGTAACTTGTCTGGAACA 3272
QY 1312 GAGCTCTAAGATCTCTGTGGTTTGAAGTTCTGTGGGGCTCATCCAGGCAAGTT 1371
DB 3273 GAGCTCTAAGATCTCTGTGGTTTGAAGTTCTGTGGGGCTCATCCAGGCAAGTT 3332
QY 1372 AGCTGTCAGAAATTAAGAGATTAACAAGTGGAAATTTGAGATCTTCTGTG 1431
DB 3333 AGCTGTCAGAAATTAAGAGATTAACAAGTGGAAATTTGAGATCTTCTGTG 3392
QY 1432 TGAGCTGTTTGAATCTTGAATCTGGGTCAACAGCGCTTTCCAAAGAAAGTTCATAA 1491
DB 3393 TGAGCTGTTTGAATCTTGAATCTGGGTCAACAGCGCTTTCCAAAGAAAGTTCATAA 3452
QY 1492 GACTTTGGAATTTTCCACACGGGGGCGGCTGCGGCTGTGTGTTTGAAGTTTAT 1551
DB 3453 GACTTTGGAATTTTCCACACGGGGGCGGCTGCGGCTGTGTGTTTGAAGTTTAT 3512
QY 1552 AAAGATTAATGAGACGAAAGAAACCATCTGAGCGGGGGTAACTTGTGAATTTCTGGC 1611
DB 3513 AAAGATTAATGAGACGAAAGAAACCATCTGAGCGGGGGTAACTTGTGAATTTCTGGC 3572
QY 1612 CATGATCTGTGAGAGCGGTTGTGAGACAAAGAAATGCTGCTGATCTGTGTCTTCCGT 1671
DB 3573 CATGATCTGTGAGAGCGGTTGTGAGACAAAGAAATGCTGCTGATCTGTGTCTTCCGT 3632

QY 1672 CCGCCCGGCGATATATACGACGGAGAGACAGACAGACAGAGAGAAAGCCAGCGCG 1731
DB 3633 CCGCCCGGCGATATATACGACGGAGAGACAGACAGACAGAGAGAGAGAGCCAGCGCG 3692
QY 1732 GCGGACAGAGACAGACCATATGAACCCGAGAGCCGCGCTGAGCCCTCGGAATGATGT 1791
DB 3693 GCGGACAGAGACAGACCATATGAACCCGAGAGCCGCGCTGAGCCCTCGGAATGATGT 3752
QY 1792 GTACAGGTGCTGAATCTGTATCCGAACCTGAGAGCATTTTGAACAATTAACAGAGATGG 1851
DB 3753 GTACAGGTGCTGAATCTGTATCCGAACCTGAGAGCATTTTGAACAATTAACAGAGATGG 3812
QY 1852 CAGGGGCTAAAGGGGGTAAAGAGGAGACGGGGGCTTGTGAGGCTACAGAGAGGCTAGG 1911
DB 3813 CAGGGGCTAAAGGGGGTAAAGAGGAGACGGGGGCTTGTGAGGCTACAGAGAGGCTAGG 3872
QY 1912 AATCTAGCTTTTACCTTAATGACACAGACACCGTCTGATGTATTAATTTCAACAGATC 1971
DB 3873 AATCTAGCTTTTACCTTAATGACACAGACACCGTCTGATGTATTAATTTCAACAGATC 3932
QY 1972 AAGATTAATTCGCTAATGAGCTTGTATCTGTGCGCAGAAATTTCCATAGACAGCTG 2031
DB 3933 AAGATTAATTCGCTAATGAGCTTGTATCTGTGCGCAGAAATTTCCATAGACAGCTG 3992
QY 2032 ACCACTTACTGCGCTGACAGCGGAGATGATTTTGAAGAGGCTAATTAAGGATATGCAAG 2091
DB 3993 ACCACTTACTGCGCTGACAGCGGAGATGATTTTGAAGAGGCTAATTAAGGATATGCAAG 4052
QY 2092 GTGGCACTTAGGCCAGATTTGCAATGACAGATCAGCAAACTTGTAAATATCAGGAATGT 2151
DB 4053 GTGGCACTTAGGCCAGATTTGCAATGACAGATCAGCAAACTTGTAAATATCAGGAATGT 4112
QY 2152 TGTCAATTTCTGGGAACGGGGCCGAGGTGAGATTAATAGAGAGATAGGTTGGCTTT 2211
DB 4113 TGTCAATTTCTGGGAACGGGGCCGAGGTGAGATTAATAGAGAGATAGGTTGGCTTT 4172
QY 2212 AGATGTAGCATTAATTAATGATGCGCGGGGTGCTTGGCATGACGCGGGTGTATTATG 2271
DB 4173 AGATGTAGCATTAATTAATGATGCGCGGGGTGCTTGGCATGACGCGGGTGTATTATG 4232
QY 2272 AATGTAAGTTTACTGCGCCCAATTTTACGCGTACGCGTTCCTGCGCAATACCAACTT 2331
DB 4233 AATGTAAGTTTACTGCGCCCAATTTTACGCGTACGCGTTCCTGCGCAATACCAACTT 4292
QY 2332 ATCTTAACAGGTGTAACCTTCTATAGGTTTAAACAATCTGTGTGGAAGCTTGAACGAT 2391
DB 4293 ATCTTAACAGGTGTAACCTTCTATAGGTTTAAACAATCTGTGTGGAAGCTTGAACGAT 4352
QY 2392 GTAAGGGTTGGGGCTGTGCTTTTACTGCTGTGAAAGGGGGTGTGTGCGCCCAA 2451
DB 4353 GTAAGGGTTGGGGCTGTGCTTTTACTGCTGTGAAAGGGGGTGTGTGCGCCCAA 4412
QY 2452 AGCAGGCTTCAATTAAGAAATGCTCTTGTGAAGAGTATCTTGGGTATCTGTCTGAG 2511
DB 4413 AGCAGGCTTCAATTAAGAAATGCTCTTGTGAAGAGTATCTTGGGTATCTGTCTGAG 4472
QY 2512 GGTAACTCCAGGGTGGCCCAATGTGGCCCTCCGACATGTGTTCCTCAATCTGATGAA 2571
DB 4473 GGTAACTCCAGGGTGGCCCAATGTGGCCCTCCGACATGTGTTCCTCAATCTGATGAA 4532
QY 2572 AGCTGCTGTGATTTAAGCATTAACATGTATGTGGCAACTGCGAGACAGGGGCTTCTAG 2631
DB 4533 AGCTGCTGTGATTTAAGCATTAACATGTATGTGGCAACTGCGAGACAGGGGCTTCTAG 4592
QY 2632 ATGCTGACTGTCTGGAACGGCAACTGTCACTGTGAAGACATTAACGAGCCAC 2691
DB 4593 ATGCTGACTGTCTGGAACGGCAACTGTCACTGTGAAGACATTAACGAGCCAC 4652
QY 2692 TCTGCAAGGCTGGCCAGTGTGAGATTAACAATACATGACCCGCTGTCTTGCATTTG 2751
DB 4653 TCTGCAAGGCTGGCCAGTGTGAGATTAACAATACATGACCCGCTGTCTTGCATTTG 4712

QY 2752 GGTAAACGAGAGGGGGTTCCTACCTTAACCAATGCAATTTGAGTCACACTAATATATG 2811
 DB 4713 GGTAAACGAGAGGGGGTTCCTACCTTAACCAATGCAATTTGAGTCACACTAATATATG 4772
 QY 2812 CTTAGACCCGAGAGCACTGTCCAAAGTGAACCTGAAACGGGGTGTGTGACATGACCATGAG 2871
 DB 4773 CTTAGACCCGAGAGCACTGTCCAAAGTGAACCTGAAACGGGGTGTGTGACATGACCATGAG 4832
 QY 2872 ATCTGGAAGGTGCTGAGGTACGATGAGACCCGCAACAGGTGACAGACCTGCGAGTGTGGC 2931
 DB 4833 ATCTGGAAGGTGCTGAGGTACGATGAGACCCGCAACAGGTGACAGACCTGCGAGTGTGGC 4892
 QY 2932 GGTAAACATATTTAGAACCAACCTGTGTATGCTGATGTGACCGAGAGCTGAGCCCGAT 2991
 DB 4893 GGTAAACATATTTAGAACCAACCTGTGTATGCTGATGTGACCGAGAGCTGAGCCCGAT 4952
 QY 2992 CACTTGGTGTGCTGAGGTGACCGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3051
 DB 4953 CACTTGGTGTGCTGAGGTGACCGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 5012
 QY 3052 G 3052
 DB 5013 G 5013

RESULT 14
 US-09-315-372-4
 : Sequence 4, Application US/09315372
 : Patent No. 6057158
 : GENERAL INFORMATION:
 : APPLICANT: Chamberlain, Jeffrey S.
 : APPLICANT: Amalfitano, Andrea
 : APPLICANT: Hauber, Michael A.
 : APPLICANT: Kumar-Singh, Rajendra
 : APPLICANT: Hartigan-O'Connor, Dennis J.
 : TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
 : NUMBER OF SEQUENCES: 15
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Medlen & Carroll, LLP
 : STREET: 220 Montgomery Street, Suite 2200
 : CITY: San Francisco
 : STATE: California
 : COUNTRY: United States Of America
 : ZIP: 94104
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/315,372
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/735,609
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Ingolia, Diane E.
 : REGISTRATION NUMBER: 40,027
 : REFERENCE/DOCKET NUMBER: UM-02484
 : TELEPHONE: (415) 705-8410
 : TELEFAX: (415) 397-8338
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 34303 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: other nucleic acid
 : DESCRIPTION: /desc = "DNA"
 : US-09-315-372-4

Query Match 70.8%; Score 2161; DB 3; Length 34303;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 892 CAATAGTAGTACGGATGAGTGTGATCTCGGCTCTTCAACACACTCCTGAGATACACCC 951
 DB 2853 CAATAGTAGTACGGATGAGTGTGATCTCGGCTCTTCAACACACTCCTGAGATACACCC 2912
 QY 952 GGTGTGCTCCGCTGTGCTCCCATTTAAACAGTTGCCGTGAGAGTTGTGGCGCTGCCAGGC 1011
 DB 2913 GGTGTGCTCCGCTGTGCTCCCATTTAAACAGTTGCCGTGAGAGTTGTGGCGCTGCCAGGC 2972
 QY 1012 TGTGGAATGTATGAGAGACTTGTCTTAAACGAGCTGTGGCAACTTTGACATTGACCTGTA 1071
 DB 2973 TGTGGAATGTATGAGAGACTTGTCTTAAACGAGCTGTGGCAACTTTGACATTGACCTGTA 3032
 QY 1072 ACGCCCAAGGCGCATPAAGGTGTAACCTGTGATGTCGTGTGTGTTAAACGCTTTGTTTGC 1131
 DB 3033 ACGCCCAAGGCGCATPAAGGTGTAACCTGTGATGTCGTGTGTGTTAAACGCTTTGTTTGC 3092
 QY 1132 TGAATGAGTGTATGATTAATTAATTAAGGTGAGATATGTTTAACCTTGCATGCGGTGT 1191
 DB 3093 TGAATGAGTGTATGATTAATTAATTAAGGTGAGATATGTTTAACCTTGCATGCGGTGT 3152
 QY 1192 AAATGGGGCGGGGCTTTAAAGGCTATTAATGCGCGGTGGCTAATCTTGGTTACATCTGA 1251
 DB 3153 AAATGGGGCGGGGCTTTAAAGGCTATTAATGCGCGGTGGCTAATCTTGGTTACATCTGA 3212
 QY 1252 CCTCATGAGAGCTTGGAGAGTGTGTAAGATTTTCTGCTGTGCTGTAACCTGTGAAACA 1311
 DB 3213 CCTCATGAGAGCTTGGAGAGTGTGTAAGATTTTCTGCTGTGCTGTAACCTGTGAAACA 3272
 QY 1312 GAGCTTAACAGTACCTCTTGTGTTTGAAGTTCGTGTGGGCTCATCCAGGCAAAATT 1371
 DB 3273 GAGCTTAACAGTACCTCTTGTGTTTGAAGTTCGTGTGGGCTCATCCAGGCAAAATT 3332
 QY 1372 AGTGTGAGAAATTAAGAGAGTTCAGAGTGGAAATTTGAAGACTTTTGAATCTGTGG 1431
 DB 3333 AGTGTGAGAAATTAAGAGAGTTCAGAGTGGAAATTTGAAGACTTTTGAATCTGTGG 3392
 QY 1432 TGAGCTGTTGATCTTGTGATCTGGGTACACAGGCGCTTTCCAGAGAAAGTCATCA 1491
 DB 3393 TGAGCTGTTGATCTTGTGATCTGGGTACACAGGCGCTTTCCAGAGAAAGTCATCA 3452
 QY 1492 GACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGCTGTTTGAAGTTTAT 1551
 DB 3453 GACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGCTGTTTGAAGTTTAT 3512
 QY 1552 AAAGATTAATGAGAGCAAAACCCATCTGAGCGGGGGTACTGCTGCAATTTTCTGGC 1611
 DB 3513 AAAGATTAATGAGAGCAAAACCCATCTGAGCGGGGGTACTGCTGCAATTTTCTGGC 3572
 QY 1612 CATGATCTGTGAGAGCGGTTGTGAGACCAAGATCGCCTGTAAGTTTCTGCGT 1671
 DB 3573 CATGATCTGTGAGAGCGGTTGTGAGACCAAGATCGCCTGTAAGTTTCTGCGT 3632
 QY 1672 CCGCCCGGCGATTAATACCGAGAGAGCAGCAGCAGCAGAGAGAGAGAGCAGCGCG 1731
 DB 3633 CCGCCCGGCGATTAATACCGAGAGAGCAGCAGCAGCAGAGAGAGAGAGCAGCGCG 3692
 QY 1732 GCGGCAAGAGCAGAGCCCATGGAACCCGAGAGCGGCTGGAACCTTGGGAAATGAATGT 1791
 DB 3693 GCGGCAAGAGCAGAGCCCATGGAACCCGAGAGCGGCTGGAACCTTGGGAAATGAATGT 3752
 QY 1792 GTACAGGTGCTGAATCTGTATCCAGACTGAGACGATTTTGAATTAACAGAGATGG 1851
 DB 3753 GTACAGGTGCTGAATCTGTATCCAGACTGAGACGATTTTGAATTAACAGAGATGG 3812
 QY 1852 CAGGGCTTAAAGGGGTTAAAGAGAGCGGGGCTTGTAGGCTTACAGAGAGCTTAA 1911
 DB 3813 CAGGGCTTAAAGGGGTTAAAGAGAGCGGGGCTTGTAGGCTTACAGAGAGCTTAA 3872
 QY 1912 AATCTAGCTTTAGCTTAATGACAGACACCGTCTGAGTATTAATCTTTCAACAGATC 1971

Db 3873 AATCAGTTTATGCTTAATGACGACACCGTCTGATGATTAATCTTTCAACAGATC 3992
Qy 1972 AAGGATTAATTCGGCTTAATGACCTGATCTGCTGGGCGCAAGATATTCATGAGACGCTG 2031
Db 3933 AAGGATTAATTCGGCTTAATGACCTGATCTGCTGGGCGCAAGATATTCATGAGACGCTG 3992
Qy 2032 ACCACTTACTGGCTGACGACCGAGGATGATTTTGAAGAGGCTAATTAAGGATATGCAAG 2091
Db 3993 ACCACTTACTGGCTGACGACCGAGGATGATTTTGAAGAGGCTAATTAAGGATATGCAAG 4052
Qy 2092 GTGGCACTTAAGGCGCAGATTTGCAAGATCAGCAAACTTGTAAATATCAGGAATTTGT 2151
Db 4053 GTGGCACTTAAGGCGCAGATTTGCAAGATCAGCAAACTTGTAAATATCAGGAATTTGT 4112
Qy 2152 TGCTAACATTTCTGGGAAAGGGGGCCGAGGTGAGATGATTAAGGAGATAGGGTGGCTTT 2211
Db 4113 TGCTAACATTTCTGGGAAAGGGGGCCGAGGTGAGATGATTAAGGAGATAGGGTGGCTTT 4172
Qy 2212 AGATGTAGCATGATTAATATATGTCGCGGGGTGCTTGGCATGACGCGGGTGGTTATTATG 2271
Db 4173 AGATGTAGCATGATTAATATATGTCGCGGGGTGCTTGGCATGACGCGGGTGGTTATTATG 4232
Qy 2272 AATGTAAAGTTTAACTGGCCCAATTTAGCGGTACGATTTTCTGGCCCAATACCAACTT 2331
Db 4233 AATGTAAAGTTTAACTGGCCCAATTTAGCGGTACGATTTTCTGGCCCAATACCAACTT 4292
Qy 2332 ATCTTACACCGGTAAAGCTTAAATGAGGTTTAAACATACCTGTGTGGAAGCCTGACCGAT 2391
Db 4293 ATCTTACACCGGTAAAGCTTAAATGAGGTTTAAACATACCTGTGTGGAAGCCTGACCGAT 4352
Qy 2392 GTAAGGGTTCGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGGTGTGTGCGCCCAA 2451
Db 4353 GTAAGGGTTCGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGGTGTGTGCGCCCAA 4412
Qy 2452 AGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGATCCTTGATCTGTAG 2511
Db 4413 AGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGATCCTTGATCTGTAG 4472
Qy 2512 GGTAATCTCCAGGGTGGCCCAATGTCGCTCCGATGTGTGTTCTTCAATCTGATGAA 2571
Db 4473 GGTAATCTCCAGGGTGGCCCAATGTCGCTCCGATGTGTGTTCTTCAATCTGATGAA 4532
Qy 2572 AGCGTGGCTGTGATTAAGCATATGATGTGGAACCTGCGAGACAGGGCTCTGAG 2631
Db 4533 AGCGTGGCTGTGATTAAGCATATGATGTGGAACCTGCGAGACAGGGCTCTGAG 4592
Qy 2632 ATGCTGACCTGCTCGACCGGCACTGTCACTGCTGAAAGCAATTCAGTACCAAGCCAC 2691
Db 4593 ATGCTGACCTGCTCGACCGGCACTGTCACTGCTGAAAGCAATTCAGTACCAAGCCAC 4652
Qy 2692 TCTGGCAAGGGCTGGCCAGTGTGAGATTAACATACGACCCGCTGTTCTTGATTTG 2751
Db 4653 TCTGGCAAGGGCTGGCCAGTGTGAGATTAACATACGACCCGCTGTTCTTGATTTG 4712
Qy 2752 GGTAACAGAGAGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCACTAAGATATTTG 2811
Db 4713 GGTAACAGAGAGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCACTAAGATATTTG 4772
Qy 2812 CTGAGCCCGAGAGCATGTCGAAGTGAACTGAAAGGGGTGTTTGAATGACATGACATGAAG 2871
Db 4773 CTGAGCCCGAGAGCATGTCGAAGTGAACTGAAAGGGGTGTTTGAATGACATGACATGAAG 4832
Qy 2872 ATCTGGAAGGTGCTGAGGTAGATGAGACCGGCAACGAGGTGCAACCTGTGAGGTGGC 2931
Db 4833 ATCTGGAAGGTGCTGAGGTAGATGAGACCGGCAACGAGGTGCAACCTGTGAGGTGGC 4892
Qy 2932 GGTAACATATTTAGGAACCAAGCTGTGATGCTGATGATGACCGAGAGCTAGAGCCGAT 2991
Db 4893 GGTAACATATTTAGGAACCAAGCTGTGATGCTGATGATGACCGAGAGCTAGAGCCGAT 4952
Qy 2992 CACTTGGTGTGCGCTGACCCGCGCTGAGTTTGGCTTACGATGAAGATACAGATTGA 3051

Db 4953 CACTTGGTGTGCGCTGACCCGCGCTGATGATTTGGCTTACGATGAAGATACAGATTGA 5012
Qy 3052 G 3052
Db 5013 G 5013

RESULT 15
US-09-244-752-4
; Sequence 4, Application US/09244752
; Patent No. 6063622
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Amalfitano, Andrea
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/244,752
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/735,609
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; US-09-244-752-4

Query Match 70.8%; Score 2161; DB 3; Length 34303;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3033 ACGCCGACGACATTAAGGCTTAACCTGTGATGCGGTGTGCTTAAGCCCTTGTTCG 3092
Qy 1132 TGAATGAGTTGATGTAAGTTTAATTAAGGGGTGAGATAATGTTTAACTTGCACTGCGCTTT 1191
Db 3093 TGAATGAGTTGATGTAAGTTTAATTAAGGGGTGAGATAATGTTTAACTTGCACTGCGCTTT 3152
Qy 1192 AAATGGGGCGGGGCTTAAGGGGTATATATATGCGCGGTGGGCTTAATCTTGATTAATCTGGA 1251
Db 3153 AAATGGGGCGGGGCTTAAGGGGTATATATATGCGCGGTGGGCTTAATCTTGATTAATCTGGA 3212
Qy 1252 CCTCATGAGGCTTGAGAGTGTGGAAGATTTTCTGCTGTGCTAACTTGCTGGAACA 1311
Db 3213 CCTCATGAGGCTTGAGAGTGTGGAAGATTTTCTGCTGTGCTAACTTGCTGGAACA 3272
Qy 1312 GAGCTTAAACGTAACCTCTTGCTTTTGAAGGTTTCTGTGGGGCTCATCCAGGCAAGTT 1371
Db 3273 GAGCTTAAACGTAACCTCTTGCTTTTGAAGGTTTCTGTGGGGCTCATCCAGGCAAGTT 3332
Qy 1372 AGTCTGCAAGTAAAGAGATTAACAGTGGGAATTTGAAGGCTTTGAAATCCTGTGG 1431
Db 3333 AGTCTGCAAGTAAAGAGATTAACAGTGGGAATTTGAAGGCTTTGAAATCCTGTGG 3392
Qy 1432 TGAGCTGTTGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAAGAAAGTCAATCA 1491
Db 3393 TGAGCTGTTGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAAGAAAGTCAATCA 3452
Qy 1492 GACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGCTGTGCTTTTGAAGTTTAT 1551
Db 3453 GACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGCTGTGCTTTTGAAGTTTAT 3512
Qy 1552 AAAGGATTAATGAGCGAAGAAACCATCTGAGCGGGGGGTAACTGCTGGAATTTCTGGC 1611
Db 3513 AAAGGATTAATGAGCGAAGAAACCATCTGAGCGGGGGGTAACTGCTGGAATTTCTGGC 3572
Qy 1612 CATCATCTGTGAGAGCGGTTGTGAGACACAGAAATGCTGCTAATGTTTCTTCCGT 1671
Db 3573 CATCATCTGTGAGAGCGGTTGTGAGACACAGAAATGCTGCTAATGTTTCTTCCGT 3632
Qy 1672 CCGCGCCGCGATTAATCCGACGAGAGACAGACAGACAGACAGAGAGAGAGAGAGAGAGAG 1731
Db 3633 CCGCGCCGCGATTAATCCGACGAGAGACAGACAGACAGACAGAGAGAGAGAGAGAGAGAG 3692
Qy 1732 GCGGCGAG 1791
Db 3693 GCGGCGAG 3752
Qy 1792 GTACAGGTGCTGAATCTGTATCCAGAACTGAGACGATTTTGAACAATTAACAGAGATGG 1851
Db 3753 GTACAGGTGCTGAATCTGTATCCAGAACTGAGACGATTTTGAACAATTAACAGAGATGG 3812
Qy 1852 CAGGGGCTAAAGGGGGTAAAG 1911
Db 3813 CAGGGGCTAAAGGGGGTAAAG 3872
Qy 1912 AATCTAGCTTTTAACTTAATGACACAGACAGCTGCTGATGATTAATCTTTCAACAGATC 1971
Db 3873 AATCTAGCTTTTAACTTAATGACACAGACAGCTGCTGATGATTAATCTTTCAACAGATC 3932
Qy 1972 AAGGATTAATGCGCTAAATGAGCTTGTCTGGCGCAGAAATTTCCATAGAGACAGCTG 2031
Db 3933 AAGGATTAATGCGCTAAATGAGCTTGTCTGGCGCAGAAATTTCCATAGAGACAGCTG 3992
Qy 2032 ACCACTTACTGGCTGACGCCAGGGGATGATTTTGAAGAGGCTATTAAGGATTAATGCAAG 2091
Db 3993 ACCACTTACTGGCTGACGCCAGGGGATGATTTTGAAGAGGCTATTAAGGATTAATGCAAG 4052
Qy 2092 GTGCACTTAAGCCAGATGCAAGTACAGATCAAGTAACTTTGAAATATCAAGAAATGT 2151
Db 4053 GTGCACTTAAGCCAGATGCAAGTACAGATCAAGTAACTTTGAAATATCAAGAAATGT 4112
Qy 2152 TGCTTACATTTCTGGGAACGGGGCCGAGGTGAGATAGATACGAGAGATAGGGTGGCTTT 2211
Db 4113 TGCTTACATTTCTGGGAACGGGGCCGAGGTGAGATAGATACGAGAGATAGGGTGGCTTT 4172

Qy 2212 AGATGTAAGTAAATATATATGCGCGGGGTGCTTGCGATGACGCGGGGTATTAATG 2271
Db 4173 AGATGTAAGTAAATATATATGCGCGGGGTGCTTGCGATGACGCGGGGTATTAATG 4232
Qy 2272 AATGTAAGTAACTTGCGGCCCAATTTTAAAGGGTACCGGTTTCTCGGCCAATTAACCACTT 2331
Db 4233 AATGTAAGTAACTTGCGGCCCAATTTTAAAGGGTACCGGTTTCTCGGCCAATTAACCACTT 4292
Qy 2332 ATCTTACACGAGTAAAGCTTATAGGTTTAAACAATCTGTGTGAAAGCTTGACCGAT 2391
Db 4293 ATCTTACACGAGTAAAGCTTATAGGTTTAAACAATCTGTGTGAAAGCTTGACCGAT 4352
Qy 2392 GTAAAGGTTTGGGGGTGCTGCTTTTAACTGCTGCTGGAAGGGGGGTGTGTGCGCCCAA 2451
Db 4353 GTAAAGGTTTGGGGGTGCTGCTTTTAACTGCTGCTGGAAGGGGGGTGTGTGCGCCCAA 4412
Qy 2452 AGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGGGATCTGTGAG 2511
Db 4413 AGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGGGATCTGTGAG 4472
Qy 2512 GGTAACTTCAAGGGTGCAGCAATGTGCTCCGACTGTGTGCTTCACTAGTAA 2571
Db 4473 GGTAACTTCAAGGGTGCAGCAATGTGCTCCGACTGTGTGCTTCACTAGTAA 4532
Qy 2572 AGCGTGTGCTGATTAAGCATTAATGTGATGTGCAATCTGCAAGAGACAGGCTCTGAG 2631
Db 4533 AGCGTGTGCTGATTAAGCATTAATGTGATGTGCAATCTGCAAGAGACAGGCTCTGAG 4592
Qy 2632 ATGCTGACCTGTGCTGAGAGCGGCACTGTGCTGAAAGCATTAACAGTAAAGCGCAC 2691
Db 4593 ATGCTGACCTGTGCTGAGAGCGGCACTGTGCTGAAAGCATTAACAGTAAAGCGCAC 4652
Qy 2692 TCTGCAAGGCTGCGCAAGTGTGAGCATTAACATCTGACCCGCTGTTCCCTGATTTG 2751
Db 4653 TCTGCAAGGCTGCGCAAGTGTGAGCATTAACATCTGACCCGCTGTTCCCTGATTTG 4712
Qy 2752 GGTAAACGAGAGGGGGGTGCTTCACTTAACATGCAATTTGAGTCACTAAGATATG 2811
Db 4713 GGTAAACGAGAGGGGGGTGCTTCACTTAACATGCAATTTGAGTCACTAAGATATG 4772
Qy 2812 CTTGAGCCCGAGACATGTCCAAAGTGAACCTGAACGGGGGTGTTGACATGACATGAAG 2871
Db 4773 CTTGAGCCCGAGACATGTCCAAAGTGAACCTGAACGGGGGTGTTGACATGACATGAAG 4832
Qy 2872 ATCTGAAAGGTCTGAGATGATGAGACCCGCAACAGTGCAGACCTGCGAGTGTGC 2931
Db 4833 ATCTGAAAGGTCTGAGATGATGAGACCCGCAACAGTGCAGACCTGCGAGTGTGC 4892
Qy 2932 GGTAAACATTAATTAAGAAACAGCTGTGATGCTGATGATGACCGAGAGCTGAGCCGAT 2991
Db 4893 GGTAAACATTAATTAAGAAACAGCTGTGATGCTGATGATGACCGAGAGCTGAGCCGAT 4952
Qy 2992 CACTTGTGCTGCTGCAACCGCGCTGAGTGTGCTCTGACGATGAAGATTAAGATTGA 3051
Db 4953 CACTTGTGCTGCTGCAACCGCGCTGAGTGTGCTCTGACGATGAAGATTAAGATTGA 5012

Search completed: October 28, 2005, 09:05:32
Job time : 528 secs

this page blank (uspto)

Matches 3052: Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	CGTGTAGTATATTTATACCCGGTGAATTCTCTAAGAGCCACTCTTAGTCCGACGAGT	60	
Db	1	CGTGTAGTATATTTATACCCGGTGAATTCTCTAAGAGCCACTCTTAGTCCGACGAGT	60	
Qy	61	AGATTTTCTCTCCGAGCGGCTCCGACACGGGAGCTGAATAAGACATATTATCTGCC	120	
Db	61	AGATTTTCTCTCCGAGCGGCTCCGACACGGGAGCTGAATAAGACATATTATCTGCC	120	
Qy	121	ACGAGGTGTTATTAACGAAATAATGCGCGCAGTCTTTTGACAGCTGATTCGAAGAG	180	
Db	121	ACGAGGTGTTATTAACGAAATAATGCGCGCAGTCTTTTGACAGCTGATTCGAAGAG	180	
Qy	181	TACTGGCTGATTAATCTTCCACTCTAGCCATTTTGAACCACTACCTTACGAACTGT	240	
Db	181	TACTGGCTGATTAATCTTCCACTCTAGCCATTTTGAACCACTACCTTACGAACTGT	240	
Qy	241	ATGATTTAGAGTACGAGCGGCCCCGGAAGATCCCAACGAGGAGCGGTTCCGAGATTTTTC	300	
Db	241	ATGATTTAGAGTACGAGCGGCCCCGGAAGATCCCAACGAGGAGCGGTTCCGAGATTTTTC	300	
Qy	301	CCGACTCTGTAATGTGGCGGTGACAGAAAGGATTTGACTTACTCATCTTTCGCGCGCGC	360	
Db	301	CCGACTCTGTAATGTGGCGGTGACAGAAAGGATTTGACTTACTCATCTTTCGCGCGCGC	360	
Qy	361	CCGGTTCTCCGAGCGGCTCACTTTTCCGGCAGCCCGAGCAGCCGAGCAGAGAGCT	420	
Db	361	CCGGTTCTCCGAGCGGCTCACTTTTCCGGCAGCCCGAGCAGCCGAGCAGAGAGCT	420	
Qy	421	TGGTCCGGTTTCTATGCGCAACCTTGTAACGAGGTGATGATCTTACCTTGCCACGAG	480	
Db	421	TGGTCCGGTTTCTATGCGCAACCTTGTAACGAGGTGATGATCTTACCTTGCCACGAG	480	
Qy	481	CTGCTTTTCCACCGAGTACGACGAGTGAAGAAGGTGAGAGATTTGTAGATTATG	540	
Db	481	CTGCTTTTCCACCGAGTACGACGAGTGAAGAAGGTGAGAGATTTGTAGATTATG	540	
Qy	541	TGGAGCACCCCGGGCAGGTTGCAAGTCTTGTCAATACCCGAGGAATCCGGGGAGCC	600	
Db	541	TGGAGCACCCCGGGCAGGTTGCAAGTCTTGTCAATACCCGAGGAATCCGGGGAGCC	600	
Qy	601	CAGATTTATGTGTGCTTGTCTATATAGAGACCTGTGGCATGTTGTCTACAGTAAGT	660	
Db	601	CAGATTTATGTGTGCTTGTCTATATAGAGACCTGTGGCATGTTGTCTACAGTAAGT	660	
Qy	661	GAATAATATGAGGAGTGGGTATAGAGTGTGGTTGGTGTGTAATTTTTTTTTTAT	720	
Db	661	GAATAATATGAGGAGTGGGTATAGAGTGTGGTTGGTGTGTAATTTTTTTTTTAT	720	
Qy	721	TTTTTACAGTTTGTGTTTAAAGAAATTTTGTATTTGATTTTTTTTAAAGTCCGTGTC	780	
Db	721	TTTTTACAGTTTGTGTTTAAAGAAATTTTGTATTTGATTTTTTTTAAAGTCCGTGTC	780	
Qy	781	TGAACCTGAGCTGAGCCGAGCAGAAACCGAGCCTGCAAGACTACCCCGCTCTAA	840	
Db	781	TGAACCTGAGCTGAGCCGAGCAGAAACCGAGCCTGCAAGACTACCCCGCTCTAA	840	
Qy	841	AATGAGCGCTGTCTATCTGAGACGCGCCGACATCACTGTGTCTAGAGATGCAATAGTAG	900	
Db	841	AATGAGCGCTGTCTATCTGAGACGCGCCGACATCACTGTGTCTAGAGATGCAATAGTAG	900	
Qy	901	TACGAGTATGCTGATCTCCGCTCTTTCTTAACAACCTTCTGAGATACACCCGGTGTGCC	960	
Db	901	TACGAGTATGCTGATCTCCGCTCTTTCTTAACAACCTTCTGAGATACACCCGGTGTGCC	960	
Qy	961	GCTGTGCCCCATTAAACAGATGCGGTGAGATTTGTGTGGCTGCGCAGGCTGTGGAATG	1020	
Db	961	GCTGTGCCCCATTAAACAGATGCGGTGAGATTTGTGTGGCTGCGCAGGCTGTGGAATG	1020	
Qy	1021	TATGAGAGACTTGTCTTAAAGAGCCTGGGCAACTTTTGACTTGAAGCTGTAAACGCCCGAG	1080	
Db	1021	TATGAGAGACTTGTCTTAAAGAGCCTGGGCAACTTTTGACTTGAAGCTGTAAACGCCCGAG	1080	

Qy	1081	GCCATTAAAGGTGTAACCTGTGATTTGCTGTGTGTTAACCCCTTTGTTTGTCTGAATGAGT	1140	
Db	1081	GCCATTAAAGGTGTAACCTGTGATTTGCTGTGTGTTAACCCCTTTGTTTGTCTGAATGAGT	1140	
Qy	1141	TGATGTAAAGTTTAAATAAGGTGAGATTAATGTTTAACTTGCAATGGCGTGTAAATGGGGC	1200	
Db	1141	TGATGTAAAGTTTAAATAAGGTGAGATTAATGTTTAACTTGCAATGGCGTGTAAATGGGGC	1200	
Qy	1201	GAGGCTTAAAGGTATTAATGCGCGCTGAGCTTAATCTTGTTACATCTGACTCATGGA	1260	
Db	1201	GAGGCTTAAAGGTATTAATGCGCGCTGAGCTTAATCTTGTTACATCTGACTCATGGA	1260	
Qy	1261	GCGTTGGGAGCTTTTGAAGATTTTCTGCTGCCGTAATCTGTGTGAACAGAGCTCTAA	1320	
Db	1261	GCGTTGGGAGCTTTTGAAGATTTTCTGCTGCCGTAATCTGTGTGAACAGAGCTCTAA	1320	
Qy	1321	CAGTACCTCTTGTGTTTGAAGATTTTCTGTGGGCTCATCCAGGCAAGTTAGCTGACG	1380	
Db	1321	CAGTACCTCTTGTGTTTGAAGATTTTCTGTGGGCTCATCCAGGCAAGTTAGCTGACG	1380	
Qy	1381	AATTAAGAGAGATTTACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT	1440	
Db	1381	AATTAAGAGAGATTTACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT	1440	
Qy	1441	TGATTTCTTTGAATCTGGGTCAACAGCGGCTTTCCAGAGAGGTCAATCAAGACTTTGGA	1500	
Db	1441	TGATTTCTTTGAATCTGGGTCAACAGCGGCTTTCCAGAGAGGTCAATCAAGACTTTGGA	1500	
Qy	1501	TTTTTCCACACCGGGGCGCGCTGCGCTGCTGTTTCTTTTGAAGTTTAAAGATTA	1560	
Db	1501	TTTTTCCACACCGGGGCGCGCTGCGCTGCTGTTTCTTTTGAAGTTTAAAGATTA	1560	
Qy	1561	ATGAGCGGAAGAAACCATCTGAGCGGGGGTACCTGCTGATTTTCTGGCCTATGCATCT	1620	
Db	1561	ATGAGCGGAAGAAACCATCTGAGCGGGGGTACCTGCTGATTTTCTGGCCTATGCATCT	1620	
Qy	1621	GTTGAGAGCGGTTGTGAGACAAAGAAATCGCTGCTGCTGTTTCCGTCGCGCGCGGC	1680	
Db	1621	GTTGAGAGCGGTTGTGAGACAAAGAAATCGCTGCTGCTGTTTCCGTCGCGCGCGGC	1680	
Qy	1681	GATTAATCCGACCGGAGGAGCAGCAGCAGCAGAGAGAAACGAGCGCGCGCGCAGGA	1740	
Db	1681	GATTAATCCGACCGGAGGAGCAGCAGCAGCAGAGAGAAACGAGCGCGCGCGCAGGA	1740	
Qy	1741	GCAGAGCCCATGGAACCCGAGAGCCGCGCTGGAACCTTCGGGAATGAAATGTTGTACAGGTG	1800	
Db	1741	GCAGAGCCCATGGAACCCGAGAGCCGCGCTGGAACCTTCGGGAATGAAATGTTGTACAGGTG	1800	
Qy	1801	GCTGAACGTATCCAGAACTGAGACGCAATTTTGAATTAACAGAGATGGGCAGGGGCTA	1860	
Db	1801	GCTGAACGTATCCAGAACTGAGACGCAATTTTGAATTAACAGAGATGGGCAGGGGCTA	1860	
Qy	1861	AAGGGGTAAAGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTAGCT	1920	
Db	1861	AAGGGGTAAAGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTAGCT	1920	
Qy	1921	TTTAGCTTAAATGACCAACACCGTCTGAGTGTATTAATTTTCAACAGATTAAGATTAAT	1980	
Db	1921	TTTAGCTTAAATGACCAACACCGTCTGAGTGTATTAATTTTCAACAGATTAAGATTAAT	1980	
Qy	1981	TGGGCTAATGAGCTGATCTGCTGGGAGAGAAATTCATATAGAGCAGCTGACCACTTAC	2040	
Db	1981	TGGGCTAATGAGCTGATCTGCTGGGAGAGAAATTCATATAGAGCAGCTGACCACTTAC	2040	
Qy	2041	TGGCTGAGCAGGAGGATTAATTTTGAAGAGCTAATTAAGGTATATGCAAAAGGTGGCACTT	2100	
Db	2041	TGGCTGAGCAGGAGGATTAATTTTGAAGAGCTAATTAAGGTATATGCAAAAGGTGGCACTT	2100	
Qy	2101	AGGCCAATTTGCAAGTACAAAGATCAGCAAACTTGTAAATATCAGGAATTTGTTGCTACATT	2160	
Db	2101	AGGCCAATTTGCAAGTACAAAGATCAGCAAACTTGTAAATATCAGGAATTTGTTGCTACATT	2160	

QY 841 AATGGCCGCTGCTATCCTGAGACGCCCGGACATCACTGTGTCTAGAGAAATGCAATAGTAG 900
Db 1298 AATGGCCGCTGCTATCCTGAGACGCCCGGACATCACTGTGTCTAGAGAAATGCAATAGTAG 1357
QY 901 TACGGATAGCTGTAGCTCCGGTCCCTTCTAACAACCTCTGAGATACACCCGGTGTCTCC 960
Db 1358 TACGGATAGCTGTAGCTCCGGTCCCTTCTAACAACCTCTGAGATACACCCGGTGTCTCC 1417
QY 961 GCTGTGCCCATTAACCAAGTTGCCGTGAGAGTTGTGTGGCGCTGCCAGGCTGTGAAATG 1020
Db 1418 GCTGTGCCCATTAACCAAGTTGCCGTGAGAGTTGTGTGGCGCTGCCAGGCTGTGAAATG 1477
QY 1021 TATGAGGACTTGTCTTAACGAGCCCTGGCAACCTTTGGACTTTGAGCTGTAAACCCCCAG 1080
Db 1478 TATGAGGACTTGTCTTAACGAGCCCTGGCAACCTTTGGACTTTGAGCTGTAAACCCCCAG 1537
QY 1081 GCCATAAGTGTAAACCTGTATGCGTGTGTGTTAACGCCCTTGTGTTGCTGATGAGT 1140
Db 1538 GCCATAAGTGTAAACCTGTATGCGTGTGTGTTAACGCCCTTGTGTTGCTGATGAGT 1597
QY 1141 TGATGTAACTTTAATAAGGGTGAGATATGTTTACTTGCAATGCGCTGTAAATGGGGC 1200
Db 1598 TGATGTAACTTTAATAAGGGTGAGATATGTTTACTTGCAATGCGCTGTAAATGGGGC 1657
QY 1201 GGGGCTTAAAGGATATATATATGCGCGCGGTGCTAATCTGTGTTACATCTGACTGATGGA 1260
Db 1658 GGGGCTTAAAGGATATATATATGCGCGCGGTGCTAATCTGTGTTACATCTGACTGATGGA 1717
QY 1261 GGGTGGGAGTGTGTGGAAGATTTTCTGTGTGCTGATTAAGTTGCTGGAACAGAGCTCTAA 1320
Db 1718 GGGTGGGAGTGTGTGGAAGATTTTCTGTGTGCTGATTAAGTTGCTGGAACAGAGCTCTAA 1777
QY 1321 CAGTACTCTTGTGTTTGGAGGTTTCTGTGGGGCTCATCCAGGCAAAATTATGCTGAG 1380
Db 1778 CAGTACTCTTGTGTTTGGAGGTTTCTGTGGGGCTCATCCAGGCAAAATTATGCTGAG 1837
QY 1381 AATTAAGAGGATTAACAAGTGGGAATTTGAAGAGTTTGAATTCCTGTGTGAGCTGTT 1440
Db 1838 AATTAAGAGGATTAACAAGTGGGAATTTGAAGAGTTTGAATTCCTGTGTGAGCTGTT 1897
QY 1441 TGATCTTCTTGAATCTGGGTCAACAGCGCTTTTCCAGAGAAAGTTCATCAAGACTTTTGA 1500
Db 1898 TGATCTTCTTGAATCTGGGTCAACAGCGCTTTTCCAGAGAAAGTTCATCAAGACTTTTGA 1957
QY 1501 TTTTTCACACCGGGGGCGCGCTGCGGCTGTGCTTTTGTGAGTTTATAAAGATTA 1560
Db 1958 TTTTTCACACCGGGGGCGCGCTGCGGCTGTGCTTTTGTGAGTTTATAAAGATTA 2017
QY 1561 ATGAGCGAAGAAACCATCTGAGCGGGGGGTACCTGTGATTTTCTGGCCATGCACT 1620
Db 2018 ATGAGCGAAGAAACCATCTGAGCGGGGGGTACCTGTGATTTTCTGGCCATGCACT 2077
QY 1621 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGTACTGTGTCTTCCGTCCGCCCGGC 1680
Db 2078 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGTACTGTGTCTTCCGTCCGCCCGGC 2137
QY 1681 GATTAATCCGACGAGAGACAGACAGACAGAGAGAAACCCAGCGCGCGCGCAGGA 1740
Db 2138 GATTAATCCGACGAGAGACAGACAGACAGAGAGAAACCCAGCGCGCGCGCAGGA 2197
QY 1741 GCAGAGCCCATGTAACCGAGAGCGGCTGGAACCTTCCGGAATGAATGTTGTACAGTG 1800
Db 2198 GCAGAGCCCATGTAACCGAGAGCGGCTGGAACCTTCCGGAATGAATGTTGTACAGTG 2257
QY 1801 GCTGAACCTGTATCCAGAACTGAGACGATTTTGAACAATTACAGAGATGGCAGGGCTA 1860
Db 2258 GCTGAACCTGTATCCAGAACTGAGACGATTTTGAACAATTACAGAGATGGCAGGGCTA 2317
QY 1861 AAGGGGTTAAAGAGAGAGCGGGGGGCTTGTAGAGCTACAGAGAGGCTAAGAAATCTAGCT 1920
Db 2318 AAGGGGTTAAAGAGAGAGCGGGGGGCTTGTAGAGCTACAGAGAGGCTAAGAAATCTAGCT 2377

QY 1921 TTTAGCTTAATGACCAGACACCGGCTGAGTATTACTTTTCAACAGATCAAGATAT 1980
Db 2378 TTTAGCTTAATGACCAGACACCGGCTGAGTATTACTTTTCAACAGATCAAGATAT 2437
QY 1981 TGCGCTAATGAGCTTGATCTGTGGCGCAGAAAGATTCCATAGACAGCTGACCACTTAC 2040
Db 2438 TGCGCTAATGAGCTTGATCTGTGGCGCAGAAAGATTCCATAGACAGCTGACCACTTAC 2497
QY 2041 TGGCTGACGCCAGGGGATGATTTTGAAGAGCTATTTAGGGTATATGCAAAAGTGGCACTT 2100
Db 2498 TGGCTGACGCCAGGGGATGATTTTGAAGAGCTATTTAGGGTATATGCAAAAGTGGCACTT 2557
QY 2101 AGGCCAATTGCAAGTACCAATGATCAGCAACTTGTAAATATCAGAAATGTGTCTACATT 2160
Db 2558 AGGCCAATTGCAAGTACCAATGATCAGCAACTTGTAAATATCAGAAATGTGTCTACATT 2617
QY 2161 TCTGGGAACGGGGCGGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTAGATGTAGC 2220
Db 2618 TCTGGGAACGGGGCGGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTAGATGTAGC 2677
QY 2221 ATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAACGGGGTGGTATTTATGAAATGTAAAG 2280
Db 2678 ATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAACGGGGTGGTATTTATGAAATGTAAAG 2737
QY 2281 TTTTACGGCCCAATTTTACGGGTAGCGGTTTCCCTGGCCAATACCAACTTATCTACAC 2340
Db 2738 TTTTACGGCCCAATTTTACGGGTAGCGGTTTCCCTGGCCAATACCAACTTATCTACAC 2797
QY 2341 GGTGTAAAGCTTCTATGAGGTTTAAACAATACCTGTGTGGAAGCTTGGACGATGTAAAGGTT 2400
Db 2798 GGTGTAAAGCTTCTATGAGGTTTAAACAATACCTGTGTGGAAGCTTGGACGATGTAAAGGTT 2857
QY 2401 CGGGGCTGTGCTTTTACTGTCTGTGGAAGGGGTGTGTGTGCCCCCAAAAGCAGGCT 2460
Db 2858 CGGGGCTGTGCTTTTACTGTCTGTGGAAGGGGTGTGTGTGCCCCCAAAAGCAGGCT 2917
QY 2461 TCAATTAAGAAATGCGCTTTTGAAGAGGTATCCTTGGGTATCTGTCTGAGGTTAACTCC 2520
Db 2918 TCAATTAAGAAATGCGCTTTTGAAGAGGTATCCTTGGGTATCTGTCTGAGGTTAACTCC 2977
QY 2521 AGGGTGGCCACAATGTGGCTTCGACTGTGTGTTCTTCAATGTGAATGAAGCGTGGCT 2580
Db 2978 AGGGTGGCCACAATGTGGCTTCGACTGTGTGTTCTTCAATGTGAATGAAGCGTGGCT 3037
QY 2581 GTGATTAAGCATTAACATGTATGTGGCAACTGCGAGAGACAGGGCTCTCAGATGCTGACC 2640
Db 3038 GTGATTAAGCATTAACATGTATGTGGCAACTGCGAGAGACAGGGCTCTCAGATGCTGACC 3097
QY 2641 TGCTCGAACGGCAACTGTCACTGTGAGAACCAATTACAGTAGCGACCACTCTCGCAAG 2700
Db 3098 TGCTCGAACGGCAACTGTCACTGTGAGAACCAATTACAGTAGCGACCACTCTCGCAAG 3157
QY 2701 GCCTGGCAGTGTTTGAGCATTAATATCTGACCCGCTGTTCTTGAATTTGGGTAAACAG 2760
Db 3158 GCCTGGCAGTGTTTGAGCATTAATATCTGACCCGCTGTTCTTGAATTTGGGTAAACAG 3217
QY 2761 AGGGGGGTGTTCCTTCACTTACCTTACATGCAATTTGAGTACACTAAGATATGTGTAGCCC 2820
Db 3218 AGGGGGGTGTTCCTTCACTTACCTTACATGCAATTTGAGTACACTAAGATATGTGTAGCCC 3277
QY 2821 GAGAGCATGTCCAAAGGTGAACCTGMAAGGGGTGTTTGAACATGACATGAAGATCTGMAAG 2880
Db 3278 GAGAGCATGTCCAAAGGTGAACCTGMAAGGGGTGTTTGAACATGACATGAAGATCTGMAAG 3337
QY 2881 GTGCTAGGTATCGATGAGACCCGCAACAGGTGACACCTTGCAGGTGTGGGTAAACAT 2940
Db 3338 GTGCTAGGTATCGATGAGACCCGCAACAGGTGACACCTTGCAGGTGTGGGTAAACAT 3397
QY 2941 ATTAGGAACCAAGCTGTGATGTGAGATGTGACCGAGAGAGCTGAGCCCGATCACTTGGTG 3000
Db 3398 ATTAGGAACCAAGCTGTGATGTGAGATGTGACCGAGAGAGCTGAGCCCGATCACTTGGTG 3457
QY 3001 CTGGCTGACCCGCGCTGAGTTTGGCTTAGCGATGAATACAGATTGAG 3052

Db 3458 CTGGCCCTGACCCCGCGCTGAGTTGGCTCTAGCCAGTAAATACAGATTGAG 3509.

RESULT 3
US-10-766-307A-3
Sequence 3, Application US/10766307A
Publication No. US2004020263A1
GENERAL INFORMATION:
APPLICANT: Shanghai Sunway Biotech Co., LTD.
TITLE OF INVENTION: Treatment for Metastatic Cancer
FILE REFERENCE: 121300.00003
CURRENT APPLICATION NUMBER: US/10/766,307A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 32802
TYPE: DNA
ORGANISM: Adenovirus
US-10-766-307A-3

Query Match 100.0%; Score 3052; DB 21; Length 32802;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTGTAGTATTTATATACCCGGTGAATTCTCAAGAGCCACTCTTAGTCACGAGT 60
Db 459 CGTGTAGTATTTATATACCCGGTGAATTCTCAAGAGCCACTCTTAGTCACGAGT 518

Qy 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACTTATCTGCC 120
Db 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACTTATCTGCC 578

Qy 121 ACGAGGTGTTATTAACGGAAGAAATGGCGGCACTTTTGACACGCTGATCGAAGG 180
Db 579 ACGAGGTGTTATTAACGGAAGAAATGGCGGCACTTTTGACACGCTGATCGAAGG 638

Qy 181 TACGGCTGATTAATCTTCACCTCTAGCCATTTGAAACAACCTTACGAGACTGT 240
Db 639 TACGGCTGATTAATCTTCACCTCTAGCCATTTGAAACAACCTTACGAGACTGT 698

Qy 241 ATGATTTAGAGTACGCGCCCCCGAAGATCCCAACGAGAGCGGTTTCGAGATTTTC 300
Db 699 ATGATTTAGAGTACGCGCCCCCGAAGATCCCAACGAGAGCGGTTTCGAGATTTTC 758

Qy 301 CCGACTCTGTAATGTGGCGGTGACAGAAAGGATTGACTTCACTTTCCGCGGCGC 360
Db 759 CCGACTCTGTAATGTGGCGGTGACAGAAAGGATTGACTTCACTTTCCGCGGCGC 818

Qy 361 CCGGTTCTCCGAGACCGGCTCACTTTCGCGAGCCCGACAGCCGAGACGAGAGCCT 420
Db 819 CCGGTTCTCCGAGACCGGCTCACTTTCGCGAGCCCGACAGCCGAGAGAGCCT 878

Qy 421 TGGGTCCGGTTCTATGCGCAAACTTTGACGAGAGTATGATCTTACCTGCCAGAG 480
Db 879 TGGGTCCGGTTCTATGCGCAAACTTTGACGAGAGTATGATCTTACCTGCCAGAG 938

Qy 481 CTGCTTTCCACCGAGTACGAGAGATGAAAGAGGTGAGAGATTGTTAGATTATG 540
Db 939 CTGCTTTCCACCGAGTACGAGAGATGAAAGAGGTGAGAGATTGTTAGATTATG 998

Qy 541 TGGAGACCCCGGAGACGGTTGACAGTCTTGTCAATTACCCGAGGAATACGGGAGCC 600
Db 999 TGGAGACCCCGGAGACGGTTGACAGTCTTGTCAATTACCCGAGGAATACGGGAGCC 1058

Qy 601 CAGATATTAATGTGCTTGTGCTATATAGAGACCTGTGGCATGTTTGTCTACAGTAGT 660
Db 1059 CAGATATTAATGTGCTTGTGCTATATAGAGACCTGTGGCATGTTTGTCTACAGTAGT 1118

Qy 661 GAAATATTAAGGAGTGGGTGATAGAGTGTGGTTGGTGTGTAATTTTTTTTAT 720
Db 1119 GAAATATTAAGGAGTGGGTGATAGAGTGTGGTTGGTGTGTAATTTTTTTTAT 1178

Qy 721 TTTTACAGTTTGTGTTTAAAGATTTTGATTTGATTTTTTTTAAAGGCTCTGTGC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGATTTTGATTTGATTTTTTTTAAAGGCTCTGTGC 1238

Qy 781 TGAACCTGAGCCTGAGCCGAGCCAGAACCCGAGCCTGCAAGACTTCCGCGCTCA 840
Db 1239 TGAACCTGAGCCTGAGCCGAGCCAGAACCCGAGCCTGCAAGACTTCCGCGCTCA 1298

Qy 841 AATGCCCTGCTATCTGTGAGACGCCGAGACTCACTGTGCTAGAGATGCAATAGTAG 900
Db 1299 AATGCCCTGCTATCTGTGAGACGCCGAGACTCACTGTGCTAGAGATGCAATAGTAG 1358

Qy 901 TACGATAGCTGTGACTCCGCTCTTTTAAACACCTCTCTGAGATACAACCCGTGCTCC 960
Db 1359 TACGATAGCTGTGACTCCGCTCTTTTAAACACCTCTCTGAGATACAACCCGTGCTCC 1418

Qy 961 GCTGTGCCCATTAACCAAGTTCGAGAGATTGGTGGGCTGCGCAGGCTGGAATG 1020
Db 1419 GCTGTGCCCATTAACCAAGTTCGAGAGATTGGTGGGCTGCGCAGGCTGGAATG 1478

Qy 1021 TATCGAGACTTGTCTTAACGAGCCTGGGCAACTTTGACCTTGAGCTGTAAACGCCAG 1080
Db 1479 TATCGAGACTTGTCTTAACGAGCCTGGGCAACTTTGAGCTTGAGCTGTAAACGCCAG 1538

Qy 1081 GCCATTAAGTGTAAACCTGTGATTCGCTGTGCTTAAACGCTTTTGTCTGATGAGT 1140
Db 1539 GCCATTAAGTGTAAACCTGTGATTCGCTGTGCTTAAACGCTTTTGTCTGATGAGT 1598

Qy 1141 TGATGTAGTTTAAAGGTGATTAAGTTTAACTGTGATGCGCGTTAAATGGGCG 1200
Db 1599 TGATGTAGTTTAAAGGTGATTAAGTTTAACTGTGATGCGCGTTAAATGGGCG 1658

Qy 1201 GGGGCTTAAAGGTATTAATGCGCGGCTATATCTTGTGTTACATCTGACTATGGA 1260
Db 1659 GGGGCTTAAAGGTATTAATGCGCGGCTATATCTTGTGTTACATCTGACTATGGA 1718

Qy 1261 GGGTGGAGTGTGGAAGATTTTCTGCTGTGCTTAATCTGCTGGAACAGAGCTTAA 1320
Db 1719 GGGTGGAGTGTGGAAGATTTTCTGCTGTGCTTAATCTGCTGGAACAGAGCTTAA 1778

Qy 1321 CAGTACCTCTGTTTGGAGGTTCTGTGGGGCTCATCCAGGCAAGTAAAGTCTGAG 1380
Db 1779 CAGTACCTCTGTTTGGAGGTTCTGTGGGGCTCATCCAGGCAAGTAAAGTCTGAG 1838

Qy 1381 AATTAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1440
Db 1839 AATTAAGAGATTAACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1898

Qy 1441 TGATTTTGAATCTGGGTCAACGAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTGA 1500
Db 1899 TGATTTTGAATCTGGGTCAACGAGCGCTTTTCAAGAGAGGTCAATCAAGACTTTGA 1958

Qy 1501 TTTTTCACACCGGGGGCGCTGCGGCTGTGCTTTTGTAGTTTAAAGGATTA 1560
Db 1959 TTTTTCACACCGGGGGCGCTGCGGCTGTGCTTTTGTAGTTTAAAGGATTA 2018

Qy 1561 ATGAGAGGAAGAAACCATCTGAGCGGGGATACCTGTGATTTTCTGAGCATGACTCT 1620
Db 2019 ATGAGAGGAAGAAACCATCTGAGCGGGGATACCTGTGATTTTCTGAGCATGACTCT 2078

Qy 1621 GTGAGAGCGGTTGTGAGACAAAGAAATCGCTGTCTACTGTGTCTTCCGCGCGGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACAAAGAAATCGCTGTCTACTGTGTCTTCCGCGCGGC 2138

Qy 1681 GATTAATCCGACGAGAGAGACGAGACGAGAGAGGAGCCAGGCGCGGCGAGGA 1740
Db 2139 GATTAATCCGACGAGAGAGACGAGACGAGAGAGGAGCCAGGCGCGGCGAGGA 2198

Qy 1741 GCAGAGCCATGGAACCCGAGAGCGGCTGGAACCTCGGGAATGAATGTTTGAAGTGTG 1800
Db 2199 GCAGAGCCATGGAACCCGAGAGCGGCTGGAACCTCGGGAATGAATGTTTGAAGTGTG 2258

QY 1801 GCTGAACCTGATCCAGAACTGAGACGCAATTTGACAAATTAACAGAGATGGCGGGCTA 1860
|
|
|
Db 2259 GCTGAACCTGATCCAGAACTGAGACGCAATTTGACAAATTAACAGAGATGGCGGGCTA 2318
|
|
|
QY 1861 AAGGGGGTAAAGAGGAGCGGGGGGCTTTGTAGGCTACAGAGAGGCTTAGGAATCTAGCT 1920
|
|
|
Db 2319 AAGGGGGTAAAGAGGAGCGGGGGGCTTTGTAGGCTACAGAGAGGCTTAGGAATCTAGCT 2378
|
|
|
QY 1921 TTTAGCTTAATGACACAGACCGCTGAGGTATTTCTTTTCAACAGATCAAGATTAAT 1980
|
|
|
Db 2379 TTTAGCTTAATGACACAGACCGCTGAGGTATTTCTTTTCAACAGATCAAGATTAAT 2438
|
|
|
QY 1981 TGCCTAATGAGCTTGAATCTGCTGCGCAGAGATTTCCATAGAGACGCTGACCACTTAC 2040
|
|
|
Db 2439 TGCCTAATGAGCTTGAATCTGCTGCGCAGAGATTTCCATAGAGACGCTGACCACTTAC 2498
|
|
|
QY 2041 TGGCTGACACCGGGGATGATTTTGAAGAGGCTATTAAGGTATATGCAAGGTGGCACTT 2100
|
|
|
Db 2499 TGGCTGACACCGGGGATGATTTTGAAGAGGCTATTAAGGTATATGCAAGGTGGCACTT 2558
|
|
|
QY 2101 AGGCAGATTGCAAGTCAAGATCAGCAAACTTGTAATATACAGGAATTTGTTGCTACATT 2160
|
|
|
Db 2559 AGGCAGATTGCAAGTCAAGATCAGCAAACTTGTAATATACAGGAATTTGTTGCTACATT 2618
|
|
|
QY 2161 TCTGGAAACGGGGCCGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTAGATGTAGC 2220
|
|
|
Db 2619 TCTGGAAACGGGGCCGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTAGATGTAGC 2678
|
|
|
QY 2221 ATGATTAATATGTGGCCCGGGGGTCTTGCGATGGAACGGGGTGTATTATGATGTAAAG 2280
|
|
|
Db 2679 ATGATTAATATGTGGCCCGGGGGTCTTGCGATGGAACGGGGTGTATTATGATGTAAAG 2738
|
|
|
QY 2281 TTTACTGGCCCCCAATTTTAAAGGGTATCCGTGCGCAATACCAACTTAATCTTACAC 2340
|
|
|
Db 2739 TTTACTGGCCCCCAATTTTAAAGGGTATCCGTGCGCAATACCAACTTAATCTTACAC 2798
|
|
|
QY 2341 GGTGTAAAGCTTCTATGGGTTTAAACAATACCTGTGTGGAAGCCTGACGATGTAAAGGTT 2400
|
|
|
Db 2799 GGTGTAAAGCTTCTATGGGTTTAAACAATACCTGTGTGGAAGCCTGACGATGTAAAGGTT 2858
|
|
|
QY 2401 CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGTGTGTCCGCCCAAAAGCAAGGCT 2460
|
|
|
Db 2859 CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGTGTGTCCGCCCAAAAGCAAGGCT 2918
|
|
|
QY 2461 TCAATTAAGAAATGCTCTTTGAAAGGTATCCTTGGGTATCCTGTGAGGGGTAACTCC 2520
|
|
|
Db 2919 TCAATTAAGAAATGCTCTTTGAAAGGTATCCTTGGGTATCCTGTGAGGGGTAACTCC 2978
|
|
|
QY 2521 AGGGTGGCCCAATGTGGCTCCGACTGTGTGCTTCAATGCTAGTGAAGAAAGCGTGGCT 2580
|
|
|
Db 2979 AGGGTGGCCCAATGTGGCTCCGACTGTGTGCTTCAATGCTAGTGAAGAAAGCGTGGCT 3038
|
|
|
QY 2581 GTGATTAAGCAATTAATGTGTGTGGAACCTGCGAGAGCAGGGGCTCTCAGATGCTGAAC 2640
|
|
|
Db 3039 GTGATTAAGCAATTAATGTGTGTGGAACCTGCGAGAGCAGGGGCTCTCAGATGCTGAAC 3098
|
|
|
QY 2641 TGCCTGGACGGCAACTGCTGCTGTAAGACATTCACGTAAGCAGCACTCTCCGAAG 2700
|
|
|
Db 3099 TGCCTGGACGGCAACTGCTGCTGTAAGACATTCACGTAAGCAGCACTCTCCGAAG 3158
|
|
|
QY 2701 GCGCTGGCAAGTGTGAGCATTAATACTGACCGGCTGTTCTTGCAATTTGGGTAAAGG 2760
|
|
|
Db 3159 GCGCTGGCAAGTGTGAGCATTAATACTGACCGGCTGTTCTTGCAATTTGGGTAAAGG 3218
|
|
|
QY 2761 AGGGGGGGTGTCTTAACCTTAACCAATGCAATTTGAGTCACTTAAGATTTGCTTGAAGCC 2820
|
|
|
Db 3219 AGGGGGGGTGTCTTAACCTTAACCAATTTGAGTCACTTAAGATTTGCTTGAAGCC 3278
|
|
|
QY 2821 GAGAGCATGTCGAAGGTGAACCTGAACGGGGGTGTTTGAATGACATGAAGAATCTGGAAG 2880
|
|
|
Db 3279 GAGAGCATGTCGAAGGTGAACCTGAACGGGGGTGTTTGAATGACATGAAGAATCTGGAAG 3338
|
|
|
QY 2881 GTGCTGAGGTACGATGAGACCCGCAACGAGGTGAGAACCTTGCGAGTGTGGGTAAACAT 2940
|
|
|

Db 3339 GTGCTGAGTACGATGAGACCCGACAGGTGCAAGACCTTGCGAGTGTGGCGGTAAACAT 3398
|
|
|
QY 2941 ATTAGAACCAAGCTGTGATGCTGATGTGAACCGAGAGAGCTGAGCCCGATCACTTGCTG 3000
|
|
|
Db 3399 ATTAGAACCAAGCTGTGATGCTGATGTGAACCGAGAGAGCTGAGCCCGATCACTTGCTG 3458
|
|
|
QY 3001 CTGGCTGCAACCGCGCTGAGTGTGGCTTAGCGATGAAGTACAGATTGAG 3052
|
|
|
Db 3459 CTGGCTGCAACCGCGCTGAGTGTGGCTTAGCGATGAAGTACAGATTGAG 3510
|
|
|
RESULT 4
US-09-725-720-43
Sequence 43, Application US/09725720
Patent No. US20010049136A1
GENERAL INFORMATION:
APPLICANT: IMELER, Jean-Luc
APPLICANT: MEHTALI, Majid
APPLICANT: PAVIRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/725,720
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/379,452
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 029395-002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-725-720-43
Query Match 100.0%; Score 3052; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTGTAGTATTATTAACCGGGTGAAGTTCCTCAAGAGGCCACTTGAGTCCGAGAGT 60
|
|
|
Db 459 CGTGTAGTATTATTAACCGGGTGAAGTTCCTCAAGAGGCCACTTGAGTCCGAGAGT 518
|
|
|
QY 61 AGAGTTTCTCTCCGACCGCTCCGACACCGGGACTGAATAATGACATATTATCTGCC 120
|
|
|
Db 519 AGAGTTTCTCTCCGACCGCTCCGACACCGGGACTGAATAATGACATATTATCTGCC 578
|
|
|
QY 121 ACGAGAGTGTATTATTAACCGAAGAAATGGCGCCAGTCTTTTGGACACAGCTGATCGAAGG 180
|
|
|
Db 579 ACGAGAGTGTATTATTAACCGAAGAAATGGCGCCAGTCTTTTGGACACAGCTGATCGAAGG 638
|
|
|

QY 181 TACTGCTGATATCTTCCACTCTCTACCACTTTTGAACCACTACCTTCACGAACTGT 240
Db 639 TACTGCTGATATCTTCCACTCTCTACCACTTTTGAACCACTACCTTCACGAACTGT 698
QY 241 ATGATTTAGAGTGACGGGCCCCCGAAGATCCCAAGAGAGGGGTTTCGAGATTTTTC 300
Db 699 ATGATTTAGAGTGACGGGCCCCCGAAGATCCCAAGAGAGGGGTTTCGAGATTTTTC 758
QY 301 CCGACTCTGATATGTTGGCGGTGACGAGAGGATTTGACTCACTTTCCGCGCGGC 360
Db 759 CCGACTCTGATATGTTGGCGGTGACGAGAGGATTTGACTCACTTTCCGCGCGGC 818
QY 361 CCGGTTCTCCGAGCGGCTCACTTTCCGCGAGCCCGAGACGCGGACGAGAGCTT 420
Db 819 CCGGTTCTCCGAGCGGCTCACTTTCCGCGAGCCCGAGACGCGGAGAGAGCTT 878
QY 421 TGGGTCGGGTTTCTATGCAACCTTGTATCCGAGAGGTATGATCTTACCTGCGACGAGG 480
Db 879 TGGGTCGGGTTTCTATGCAACCTTGTATCCGAGAGGTATGATCTTACCTGCGACGAGG 938
QY 481 CTGGCTTTCCACCCAGTACGACGAGAGTGAAGAGGTGAGAGGTTGTGTAGATTATG 540
Db 939 CTGGCTTTCCACCCAGTACGACGAGAGTGAAGAGGTGAGAGGTTGTGTAGATTATG 998
QY 541 TGAAGACACCCCGGGGACGGTTGACAGGCTTGTCAATTATCACCGAGAGATACGGGGGACC 600
Db 999 TGAAGACACCCCGGGGACGGTTGACAGGCTTGTCAATTATCACCGAGAGATACGGGGGACC 1058
QY 601 CAGATATTATGTTGCTTGTCTATATGAGGACCTGTGAGCATGTTTCTACAGTAACT 660
Db 1059 CAGATATTATGTTGCTTGTCTATATGAGGACCTGTGAGCATGTTTCTACAGTAACT 1118
QY 661 GAAATTTATGAGGACGTGGGTGATAGAGTGTGGTTGGTGTGATTTTATTTTAT 720
Db 1119 GAAATTTATGAGGACGTGGGTGATAGAGTGTGGTTGGTGTGATTTTATTTTAT 1178
QY 721 TTTTACAGTTTGTGGTTTAAAGAAATTTTGTATGTGATTTTAAAGAGTCTGTGTC 780
Db 1179 TTTTACAGTTTGTGGTTTAAAGAAATTTTGTATGTGATTTTAAAGAGTCTGTGTC 1238
QY 781 TGAACCTGAGCTGAGCCGAGCCGAGAACCGGAGCTGCAAGACTTACCGCGGCTTAA 840
Db 1239 TGAACCTGAGCTGAGCCGAGCCGAGAACCGGAGCTGCAAGACTTACCGCGGCTTAA 1298
QY 841 AATGCGGCTGCTATCTGAGACGCGCCGACATCACTGTGTCTAGAGATGCAATAGTAG 900
Db 1299 AATGCGGCTGCTATCTGAGACGCGCCGACATCACTGTGTCTAGAGATGCAATAGTAG 1358
QY 901 TACGGATAGCTGTGACTCGGCTCTTCTTACACACCTTCTAGATACACCGGAGTCTCC 960
Db 1359 TACGGATAGCTGTGACTCGGCTCTTCTTACACACCTTCTAGATACACCGGAGTCTCC 1418
QY 961 GCTGCGCCCACTTAAACAGATTGCCGAGAGTGGTGGGGTGGCCAGGCTGGGAATG 1020
Db 1419 GCTGCGCCCACTTAAACAGATTGCCGAGAGTGGTGGGGTGGCCAGGCTGGGAATG 1478
QY 1021 TATCGAGAGCTTGTCTTAAAGAGCTTGGGCAACTTTGAGACTTGAAGCTTAAACGCCAG 1080
Db 1479 TATCGAGAGCTTGTCTTAAAGAGCTTGGGCAACTTTGAGACTTGAAGCTTAAACGCCAG 1538
QY 1081 GCCATAGGCTTAAACCTGTGATTGCGTGTGTGTAAAGCCTTTGTTGCTGAATGAGT 1140
Db 1539 GCCATAGGCTTAAACCTGTGATTGCGTGTGTGTAAAGCCTTTGTTGCTGAATGAGT 1598
QY 1141 TGATGTAGTTTAAAGAGGTGAGATATGTTTAACTTGACATGGCGGTAAATGGGGC 1200
Db 1599 TGATGTAGTTTAAAGAGGTGAGATATGTTTAACTTGACATGGCGGTAAATGGGGC 1658
QY 1201 GGGGCTTAAAGGATATATATGCGCGGTGGGCTAATCTTGTGTAATCTGACCTTATGGA 1260
Db 1659 GGGGCTTAAAGGATATATATGCGCGGTGGGCTAATCTTGTGTAATCTGACCTTATGGA 1718

QY 1261 GCGTTGGAGAGTGTGGAAGATTTTCTGTGTGCTTACTTGTCTGACACGAGCTTAA 1320
Db 1719 GCGTTGGAGAGTGTGGAAGATTTTCTGTGTGCTTACTTGTCTGACACGAGCTTAA 1778
QY 1321 CAGTACCTCTTGTTTGGAGGTTTCTGTGGGGCTCAATCCAGGCAAGTTAGTGTGAG 1380
Db 1779 CAGTACCTCTTGTTTGGAGGTTTCTGTGGGGCTCAATCCAGGCAAGTTAGTGTGAG 1838
QY 1381 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGCTTTGAAATCTGTGTGAGCTGTT 1440
Db 1839 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGCTTTGAAATCTGTGTGAGCTGTT 1898
QY 1441 TGATTTCTTGAATCTGGGTACACAGGCGCTTTTCCAGAGAAAGTCAACAAGCTTTGGA 1500
Db 1899 TGATTTCTTGAATCTGGGTACACAGGCGCTTTTCCAGAGAAAGTCAACAAGCTTTGGA 1958
QY 1501 TTTTTCACACCGGGGCGCGCTGGCGGCTGTTGCTTTTGAAGTTTATTAAGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGGCGGCTGTTGCTTTTGAAGTTTATTAAGATTA 2018
QY 1561 ATGAGCGAGAGAAACCATCTGAGCGGGGGTACCTGTGATTTTCTGGCATGATCT 1620
Db 2019 ATGAGCGAGAGAAACCATCTGAGCGGGGGTACCTGTGATTTTCTGGCATGATCT 2078
QY 1621 GTGAGAGCGGTTGTGAGACACAAGATGCGCTGTACTGTGTTCTTCCGTCGCGGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACACAAGATGCGCTGTACTGTGTTCTTCCGTCGCGGC 2138
QY 1681 GATATATCCGACGGGAGGACGACGACGACGAGAGAGACGAGCGGCGGCGAGGA 1740
Db 2139 GATATATCCGACGGGAGGACGACGACGACGAGAGAGAGACGAGCGGCGGCGAGGA 2198
QY 1741 GCAAGGCCATGGAACCCGAGAGCGGCTGTGAGCCTTGAGAAATGAATGTTTACAGGTG 1800
Db 2199 GCAAGGCCATGGAACCCGAGAGCGGCTGTGAGCCTTGAGAAATGAATGTTTACAGGTG 2258
QY 1801 GCTGAACGTATTCAGAACTGAGACGCAATTTTGAACAATTAACAGAGATGGGACGGGCTA 1860
Db 2259 GCTGAACGTATTCAGAACTGAGACGCAATTTTGAACAATTAACAGAGATGGGACGGGCTA 2318
QY 1861 AAGGGGTTAAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTAAGGAATTAAGT 1920
Db 2319 AAGGGGTTAAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGGCTAAGGAATTAAGT 2378
QY 1921 TTTAGCTTAATGACACAGACCGTCTGTAGTATTAATTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACACAGACCGTCTGTAGTATTAATTTTCAACAGATCAAGATTAAT 2438
QY 1981 TGGCTTAATGAGCTTGTCTGTGGCGGAGATTTTCAATAGACAGCTGACCACTTAC 2040
Db 2439 TGGCTTAATGAGCTTGTCTGTGGCGGAGATTTTCAATAGACAGCTGACCACTTAC 2498
QY 2041 TGGCTGACGACGAGGAGATTTTGAAGAGGCTTGAAGGTATATGCAAGGTGGCACTT 2100
Db 2499 TGGCTGACGACGAGGAGATTTTGAAGAGGCTTGAAGGTATATGCAAGGTGGCACTT 2558
QY 2101 AGGCGAATTTGCAAGTACAGATCAGCAACTTGAATATCAGGAATTTGTGTACTAT 2160
Db 2559 AGGCGAATTTGCAAGTACAGATCAGCAACTTGAATATCAGGAATTTGTGTACTAT 2618
QY 2161 TCTGGAGAACGGGGCGGAGGTGAGATATAGAGATAGAGGTGCTTTAGATGTAGC 2220
Db 2619 TCTGGAGAACGGGGCGGAGGTGAGATATAGAGATAGAGGTGCTTTAGATGTAGC 2678
QY 2221 ATGATTAATATGTAGGCGGGGCTTGTGACATGAGACGGGGTGTATATATGATAGTAAAG 2280
Db 2679 ATGATTAATATGTAGGCGGGGCTTGTGACATGAGACGGGGTGTATATATGATAGTAAAG 2738
QY 2281 TTATCTGGCCCAATTTTATGCGGTATCTGTGCAATACCACTTATCTTACAC 2340
Db 2739 TTATCTGGCCCAATTTTATGCGGTATCTGTGCAATACCACTTATCTTACAC 2798
QY 2341 GGTGTAAGCTTCTATGSGTTTAAACAATACCTGTGTGAAGCTGAGCCGATGTAAGGTT 2400

Db 2799 GGTGTAAGCTTCTATGGGTTTAACTATCTGTGTGAAAGCTGAGCCGATGTAAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTATCTGCTGTGAAAGGGGTGTGTGTCCGCCAAAAGAGAGGCT 2460
Db 2459 CGGGGCTGTGCTTTTATCTGCTGTGAAAGGGGTGTGTGTCCGCCAAAAGAGAGGCT 2918
Qy 2461 TCATTTAAGAAATGCTCTTTGAAAGGTATCCTTGGGTATCCTGTCTGAGGGTAACTCC 2520
Db 2919 TCAATTAAAGAAATGCTCTTTGAAAGGTATCCTTGGGTATCCTGTCTGAGGGTAACTCC 2978
Qy 2521 AGGGTGGCCCAATATGAGCTCCGACTGTGTGTTCTTCACTAGTGAAGAAAGGTGGCT 2580
Db 2979 AGGGTGGCCCAATATGAGCTCCGACTGTGTGTTCTTCACTAGTGAAGAAAGGTGGCT 3038
Qy 2581 GTGATTAAGCAATACTGTATGTGGCAATGCGAGACAGAGGCTCTCAGATCTGACC 2640
Db 3039 GTGATTAAGCAATACTGTATGTGGCAATGCGAGACAGAGGCTCTCAGATCTGACC 3098
Qy 2641 TGCTCGGACGGCAACTGTCACTGTGAAAGCAATTGACGAGCAAGCACTCTCGCAG 2700
Db 3099 TGCTCGGACGGCAACTGTCACTGTGAAAGCAATTGACGAGCAAGCACTCTCGCAG 3158
Qy 2701 GCTGCGCAAGTGTGTGACATTAAGTGAACCTGACCGCTGTCTTGCATTTGGGTAAACAG 2760
Db 3159 GCTGCGCAAGTGTGTGACATTAAGTGAACCTGACCGCTGTCTTGCATTTGGGTAAACAG 3218
Qy 2761 AGGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCACTAAGATTAATTCCTTGAGCCC 2820
Db 3219 AGGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCACTAAGATTAATTCCTTGAGCCC 3278
Qy 2821 GAGAGCATGTCCAGAGTGAACCTGAAAGGGGTGTGTCATGACCATGAAGATCTGAGAG 2880
Db 3279 GAGAGCATGTCCAGAGTGAACCTGAAAGGGGTGTGTCATGACCATGAAGATCTGAGAG 3338
Qy 2881 GTGCTGAGTACGATGAGACCCGACCAAGGTGACAGACCTGCGAGTGTGGCGTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGACCCGACCAAGGTGACAGACCTGCGAGTGTGGCGTAAACAT 3398
Qy 2941 ATTGGAACCAAGCTGTGATCTGTGATGTGACCGAGAGCTGAGAGCCCGATCACTTGGTG 3000
Db 3399 ATTGGAACCAAGCTGTGATCTGTGATGTGACCGAGAGCTGAGAGCCCGATCACTTGGTG 3458
Qy 3001 CTGGCTGACACCGCGGCTGATTTGGCTCTAGCGATGAAGATTAAGATTGAG 3052
Db 3459 CTGGCTGACACCGCGGCTGATTTGGCTCTAGCGATGAAGATTAAGATTGAG 3510

RESULT 5
US-09-782-378A-4
Sequence 4, Application US/09782378A
Patent No. US20020102731A1
GENERAL INFORMATION:
APPLICANT: Hearing, Patrick
APPLICANT: Bahou, Wadie
APPLICANT: Sandelon, Ziv
APPLICANT: Gnatenko, Dmitri
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONIB-04970
CURRENT APPLICATION NUMBER: US/09/782,378A
PRIOR FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/237,747
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 35935
TYPE: DNA
ORGANISM: Human adenovirus type 5
US-09-782-378A-4

Query Match 100.0%; Score 3052; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTGTATGTATTTATACCCGGTGAAGTTCTTCAAGAGGCCACTTTAGTGGCCAGCGAGT 60
Db 459 CGTGTATGTATTTATACCCGGTGAAGTTCTTCAAGAGGCCACTTTAGTGGCCAGCGAGT 518
Qy 61 AGAGTTTTCCTCCGAGCGCTCCGACACCGGGATCGAAATAGACATTTATCTGCC 120
Db 519 AGAGTTTTCCTCCGAGCGCTCCGACACCGGGATCGAAATAGACATTTATCTGCC 578
Qy 121 ACGGAGGTATTTATCCGAAGAAATGGCCGCACTTTTGGACACGCTGATCGAAGAG 180
Db 579 ACGGAGGTATTTATCCGAAGAAATGGCCGCACTTTTGGACACGCTGATCGAAGAG 638
Qy 181 TACTGGCTGATTAATCTTCCACTTCTAGCCATTTTGAACCACTTACCTTCAAGAACTGT 240
Db 639 TACTGGCTGATTAATCTTCCACTTCTAGCCATTTTGAACCACTTACCTTCAAGAACTGT 698
Qy 241 ATGATTTAGACGTGACGAGCCCGCAAGATCCCAACGAGAGGCGGTTTCGAGATTTTTC 300
Db 699 ATGATTTAGACGTGACGAGCCCGCAAGATCCCAACGAGAGGCGGTTTCGAGATTTTTC 758
Qy 301 CCGACTGTATATGTTGGCGGTGCAAGAGGATTTGACTTCACTTTTCGCGCGGC 360
Db 759 CCGACTGTATATGTTGGCGGTGCAAGAGGATTTGACTTCACTTTTCGCGCGGC 818
Qy 361 CCGGTTTCCGAGCGCGCTCACCTTCCCGGACCGCGAGCGCGAGCGAGAGGCT 420
Db 819 CCGGTTTCCGAGCGCGCTCACCTTCCCGGACCGCGAGCGCGAGCGAGAGGCT 878
Qy 421 TGGGTCCGTTTCTATGCAAACTTGTACCGGAGTGTATGATCTTACCTGCCACGAG 480
Db 879 TGGGTCCGTTTCTATGCAAACTTGTACCGGAGTGTATGATCTTACCTGCCACGAG 938
Qy 481 CTGGCTTTCACCCAGTGAAGAGATGAAGGTTGATGAGAGTTGTGTTAATTATG 540
Db 939 CTGGCTTTCACCCAGTGAAGAGATGAAGGTTGATGAGAGTTGTGTTAATTATG 998
Qy 541 TGAGGACCCCGGGCAAGTGTGAGGCTTGTCACTTACCCGAGGAATPACGGGGGACC 600
Db 999 TGAGGACCCCGGGCAAGTGTGAGGCTTGTCACTTACCCGAGGAATPACGGGGGACC 1058
Qy 601 CAGATATTATGTGTTCCCTTGTATATGAGACCTGTGCACTTGTCTACAGTAAGT 660
Db 1059 CAGATATTATGTGTTCCCTTGTATATGAGACCTGTGCACTTGTCTACAGTAAGT 1118
Qy 661 GAAATTTATGCGCAGTGGGTGATGAGTGGGTGGTGTGTGTTATTTTAT 720
Db 1119 GAAATTTATGCGCAGTGGGTGATGAGTGGGTGGTGTGTGTTATTTTAT 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGAAATTTGATTTTAAAGGTCCTGTC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGATTTTAAAGGTCCTGTC 1238
Qy 781 TGAACCTGAGCTGAGCCGACGAGCCGAGACCTTGCAGAACCTTACCCGCTCTTAA 840
Db 1239 TGAACCTGAGCTGAGCCGACGAGCCGAGACCTTGCAGAACCTTACCCGCTCTTAA 1298
Qy 841 AATGGCCCTGTCTATCTTGAAGCGCCGACATCACTGTGTCTTGAAGATTAAGTAG 900
Db 1299 AATGGCCCTGTCTATCTTGAAGCGCCGACATCACTGTGTCTTGAAGATTAAGTAG 1358
Qy 901 TAGGATAGCTGAGACCTCGGCTCTTAAACACCTCTGAGATTAACCCGGTGTGCC 960
Db 1359 TAGGATAGCTGAGACCTCGGCTCTTAAACACCTCTGAGATTAACCCGGTGTGCC 1418
Qy 961 GCTGTGCCCATTTAAACCAAGTTGCCGTGAGAGTTGTGGCGTCCGACAGGCTGTGAA 1020
Db 1419 GCTGTGCCCATTTAAACCAAGTTGCCGTGAGAGTTGTGGCGTCCGACAGGCTGTGAA 1478
Qy 1021 TATGAGAGCTTGCTTAAAGAGCTGGGCAACTTTTGAAGTTGAGCTGTAAAGCCCCAG 1080
Db 1479 TATGAGAGCTTGCTTAAAGAGCTGGGCAACTTTTGAAGTTGAGCTGTAAAGCCCCAG 1538

QY 1081 GCCATTAAGGTGTAACCTGTGATTGCGTGTGCTTAACGCCCTTGTGCTGAATGCT 1140
DB 1539 GCCATTAAGGTGTAACCTGTGATTGCGTGTGCTTAACGCCCTTGTGCTGAATGCT 1598
QY 1141 TGATGTAAGTTTAATTAAGGGTGAAGATTAATGTTTAACCTGATGGCGGTTAAATGGGGC 1200
DB 1599 TGATGTAAGTTTAATTAAGGGTGAAGATTAATGTTTAACCTGATGGCGGTTAAATGGGGC 1658
QY 1201 GGGGCTTAAGGTAATTAATGCGCGCGCTTAATCTTGTGTAACATCTGAACCTCATGGA 1260
DB 1659 GGGGCTTAAGGTAATTAATGCGCGCGCTTAATCTTGTGTAACATCTGAACCTCATGGA 1718
QY 1261 GGGCTTGGGAGCTTTGGAAGATTTTTCCTGCTGTGCTGAACCTTGTGTAACATCTGA 1320
DB 1719 GGGCTTGGGAGCTTTGGAAGATTTTTCCTGCTGTGCTGAACCTTGTGTAACATCTGA 1778
QY 1321 CAGTAACTCTGATTTTGGAGGTTTCTGTGGGGCTCATCCGAGGCAAGTTAGCTGAG 1380
DB 1779 CAGTAACTCTGATTTTGGAGGTTTCTGTGGGGCTCATCCGAGGCAAGTTAGCTGAG 1838
QY 1381 AATTAAAGGAGATTACAAGTGGGAATTTGAAGCTTTTGAATCTGTGGTGAAGCTTT 1440
DB 1839 AATTAAAGGAGATTACAAGTGGGAATTTGAAGCTTTTGAATCTGTGGTGAAGCTTT 1898
QY 1441 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAGGTCAACAAGCTTTGGA 1500
DB 1899 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAGGTCAACAAGCTTTGGA 1958
QY 1501 TTTTTCACACCGGGGGCGGCTGGGCTGCTGCTTTTGTGAGTTTAAAGGATTA 1560
DB 1959 TTTTTCACACCGGGGGCGGCTGGGCTGCTGCTTTTGTGAGTTTAAAGGATTA 2018
QY 1561 ATGAGAGGAAGAAAACCACTTGAAGCGGGGGTACCTGCTGATTTTTCGCCATGCACT 1620
DB 2019 ATGAGAGGAAGAAAACCACTTGAAGCGGGGGTACCTGCTGATTTTTCGCCATGCACT 2078
QY 1621 GTGAGAGCGGTTGTGAGACACAAGATCGCTGCTGATTTTTCGCCATGCACT 1680
DB 2079 GTGAGAGCGGTTGTGAGACACAAGATCGCTGCTGATTTTTCGCCATGCACT 2138
QY 1681 GATTAATCCGACCGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1740
DB 2139 GATTAATCCGACCGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2198
QY 1741 GCAGAGCCCATGGAACCCGAGAGCGGCTGGAACCTTGGGAAATGATTTGTCAGGTTG 1800
DB 2199 GCAGAGCCCATGGAACCCGAGAGCGGCTGGAACCTTGGGAAATGATTTGTCAGGTTG 2258
QY 1801 GCTGAACCTGATCCAGAACTGGAACGCAATTTTGAACAATTCAGAGATGGCAGGGCTA 1860
DB 2259 GCTGAACCTGATCCAGAACTGGAACGCAATTTTGAACAATTCAGAGATGGCAGGGCTA 2318
QY 1861 AAGGGGGTAAAGAGGAGCGGGGGCTTGTGAAGCTTACAGAGAGGCTTGAAGATCTTACT 1920
DB 2319 AAGGGGGTAAAGAGGAGCGGGGGCTTGTGAAGCTTACAGAGAGGCTTGAAGATCTTACT 2378
QY 1921 TTTAGCTTAATGACCAAGACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
DB 2379 TTTAGCTTAATGACCAAGACACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
QY 1981 TGCGCTAATGAGCTTGAATCTGCTGGCGCAAGATTAATTCATAGAGCAGCTGACCACTTAC 2040
DB 2439 TGCGCTAATGAGCTTGAATCTGCTGGCGCAAGATTAATTCATAGAGCAGCTGACCACTTAC 2498
QY 2041 TGCGCTGAGCCAGGGGAGTGAATTTTGAAGAGCTTATGAGGTAATTCGAAAAGTGGCCTT 2100
DB 2499 TGCGCTGAGCCAGGGGAGTGAATTTTGAAGAGCTTATGAGGTAATTCGAAAAGTGGCCTT 2558
QY 2101 AGGCGCAGATTGCAAGTACAGAGTACAGAACTTGTAAATATCAGGAATTTGTTGCTACATT 2160
DB 2559 AGGCGCAGATTGCAAGTACAGAGTACAGAACTTGTAAATATCAGGAATTTGTTGCTACATT 2618

QY 2161 TCTGGGAACGGGGCCGAGGTGAGATATGATTCGAGAGATAGGGTGGCTTTAGATGTAGC 2220
DB 2619 TCTGGGAACGGGGCCGAGGTGAGATATGATTCGAGAGATAGGGTGGCTTTAGATGTAGC 2678
QY 2221 ATGATTAATATATGTGCGGGGGGTGCTTGCAATGGAACGGGGGTGTTATTAATGAATGAAG 2280
DB 2679 ATGATTAATATATGTGCGGGGGGTGCTTGCAATGGAACGGGGGTGTTATTAATGAATGAAG 2738
QY 2281 TTTACTGGCCCCAATTTTAAAGGATGAGGTTTCTGTGGCAATTAACCAACTTATCTTACAC 2340
DB 2739 TTTACTGGCCCCAATTTTAAAGGATGAGGTTTCTGTGGCAATTAACCAACTTATCTTACAC 2798
QY 2341 GGTGTAAGCTTCTATGAGGTTTAAACATATCTGTGTGGAAGCTTGAACCGATGTAAAGGTT 2400
DB 2799 GGTGTAAGCTTCTATGAGGTTTAAACATATCTGTGTGGAAGCTTGAACCGATGTAAAGGTT 2858
QY 2401 CGGGGCTGTGCTTTTACTGCTGCGAAGGGGGGTGTTGTCGCCCCCAAAAGAGGGCT 2460
DB 2859 CGGGGCTGTGCTTTTACTGCTGCGAAGGGGGGTGTTGTCGCCCCCAAAAGAGGGCT 2918
QY 2461 TCAATTAAGAAATGCTCTTGTGAAGGTATCCTTGGGTATCTGTCTGAAGGTTAACTCC 2520
DB 2919 TCAATTAAGAAATGCTCTTGTGAAGGTATCCTTGGGTATCTGTCTGAAGGTTAACTCC 2978
QY 2521 AGGGTGGGCCCAATGTGCTCCGACTGTGTGCTTCAATGCTATGTAAGAAAGCTGGCT 2580
DB 2979 AGGGTGGGCCCAATGTGCTCCGACTGTGTGCTTCAATGCTATGTAAGAAAGCTGGCT 3038
QY 2581 GTGATTAAGCAATACATGTATGTGGAACCTGCGAGGACAGGGGCTCTCAATGCTGACC 2640
DB 3039 GTGATTAAGCAATACATGTATGTGGAACCTGCGAGGACAGGGGCTCTCAATGCTGACC 3098
QY 2641 TGCTCGAACCGCACTGTCACTGTGAGAACCAATTCAGTAGCAGCACTCTCGCAAG 2700
DB 3099 TGCTCGAACCGCACTGTCACTGTGAGAACCAATTCAGTAGCAGCACTCTCGCAAG 3158
QY 2701 GCTTGGCCAGTGTGTAAGCATATACATGACCCGCTGTTCTTGCATTTGGGTAAACAG 2760
DB 3159 GCTTGGCCAGTGTGTAAGCATATACATGACCCGCTGTTCTTGCATTTGGGTAAACAG 3218
QY 2761 AGGGGGGTGTTCCATACCTTACCAATGCAATTTGAGTCACTAAGATATGCTTGAAGCC 2820
DB 3219 AGGGGGGTGTTCCATACCTTACCAATGCAATTTGAGTCACTAAGATATGCTTGAAGCC 3278
QY 2821 GAGAGCATGTCAGAGGTGAACCTGAAACGGGTGTTTGAATGATGATGATGATGATGATG 2880
DB 3279 GAGAGCATGTCAGAGGTGAACCTGAAACGGGTGTTTGAATGATGATGATGATGATGATG 3338
QY 2881 GTGCTGAGTACGATGAGACCCGCAACAGGTGCAACCTTGGAGTGTGGCGTAAACAT 2940
DB 3339 GTGCTGAGTACGATGAGACCCGCAACAGGTGCAACCTTGGAGTGTGGCGTAAACAT 3398
QY 2941 ATTAGGAACCAAGCTGTGATGCTGATGATGACGAGAGAGCTGAAGGCCGATCACTGGTG 3000
DB 3399 ATTAGGAACCAAGCTGTGATGCTGATGATGACGAGAGAGCTGAAGGCCGATCACTGGTG 3458
QY 3001 CTGGCTGCAACCCGCGCTGAGTTTGGCTTGAACGATGAAGTAAAGATTGAG 3052
DB 3459 CTGGCTGCAACCCGCGCTGAGTTTGGCTTGAACGATGAAGTAAAGATTGAG 3510

RESULT 6
US-09-782-378A-5
; Sequence 5, Application US/09782378A
; Patent No. US20020102731A1
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandalon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: SNOYB-04970
; CURRENT APPLICATION NUMBER: US/09/782,378A

; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: Human adenovirus type 5
US-09-782-378A-5

Query Match 100.0%; Score 3052; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTGTAGTATTTTATACCCGGTGAATTCCTCAAGAGCCACTCTTAGTCCAGCCAGT 60
Db 459 CGTGTAGTATTTTATACCCGGTGAATTCCTCAAGAGCCACTCTTAGTCCAGCCAGT 518
QY 61 AGAGTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAATAATGACATTTATCTGCC 120
Db 519 AGAGTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAATAATGACATTTATCTGCC 578
QY 121 ACGGAGGTATTATACCGAAGAAATGCGCGCCAGTCTTTTGACCAAGCTGATCGAAGG 180
Db 579 ACGGAGGTATTATACCGAAGAAATGCGCGCAAGCTTTTGACAAGCTGATCGAAGG 638
QY 181 TACTGGCTGATTAATCTTCCACTCTCTAGCCATTTTGAAACCACTACCTTACGAACTGT 240
Db 639 TACTGGCTGATTAATCTTCCACTCTCTAGCCATTTTGAAACCACTACCTTACGAACTGT 698
QY 241 ATGATTTAGACGTAGCGGCCCCCGAAGATCCCAACGAGAGAGCGGTTTCGACAGATTTTTC 300
Db 699 ATGATTTAGACGTAGCGGCCCCCGAAGATCCCAACGAGAGAGCGGTTTCGACAGATTTTTC 758
QY 301 CCGACTCTGTAATGTTGGCGGTGACGAGAGGGAATTGACTTACTCACTTTTCGCGCGGCG 360
Db 759 CCGACTCTGTAATGTTGGCGGTGACGAGAGGGAATTGACTTACTCACTTTTCGCGCGGCG 818
QY 361 CCGGTTCTCCGAGACCGGCTCACTTTCCCGGACAGCCCGAGACGCCGAGACAGAGAGCT 420
Db 819 CCGGTTCTCCGAGACCGGCTCACTTTCCCGGACAGCCCGAGACGCCGAGAGAGAGCT 878
QY 421 TGGGTCGCGTTTCTATGSCAAACCTTGTACCGGAGGTGATGATCTTACCTGCCACGAG 480
Db 879 TGGGTCGCGTTTCTATGSCAAACCTTGTACCGGAGGTGATGATCTTACCTGCCACGAG 938
QY 481 CTGGCTTTCCACCGAGTACGACGAGATGAGAGGATGAGAGGTTTGTAGATTATG 540
Db 939 CTGGCTTTCCACCGAGTACGACGAGATGAGAGGATGAGAGGTTTGTAGATTATG 998
QY 541 TGGAGACACCCGGGGACGAGTTGACAGGTCTTGTCAATACCGAGAGAAATCGGGGAC 600
Db 999 TGGAGACACCCGGGGACGAGTTGACAGGTCTTGTCAATACCGAGAGAAATCGGGGAC 1058
QY 601 CAGATTAATATGTTGCTTGTGCTATATAGAGACCTGTGGCATGTTTGTCTACAGTAA 660
Db 1059 CAGATTAATATGTTGCTTGTGCTATATAGAGACCTGTGGCATGTTTGTCTACAGTAA 1118
QY 661 GAAATTAATGAGCAGTGGGTATAGAGTGTGGTTTGGTGTGTAATTTTTTTTAA 720
Db 1119 GAAATTAATGAGCAGTGGGTATAGAGTGTGGTTTGGTGTGTAATTTTTTTTAA 1178
QY 721 TTTTAAACAGTTTGTGTTTAAAGAAATTTTGTATTTGATTTTTTAAAGGTCTGTGTC 780
Db 1179 TTTTAAACAGTTTGTGTTTAAAGAAATTTTGTATTTGATTTTTTAAAGGTCTGTGTC 1238
QY 781 TGAACCTGAGCTGAGCCCGAGCCGAGAACCGGAGCTTCAAGACCTTACCCGCGCTTAA 840
Db 1239 TGAACCTGAGCTGAGCCCGAGCCGAGAACCGGAGCTTCAAGACCTTACCCGCGCTTAA 1298
QY 841 AATGGCGCTGCTATCTGAGACGCCCGACATCACTGTGTCTAGAGATCAATAGTAG 900
Db AATGGCGCTGCTATCTGAGACGCCCGACATCACTGTGTCTAGAGATCAATAGTAG 900

Db 1299 AATGGCGCTGCTATCTGAGACGCCCGACATCACTGTGTCTAGAGATCAATAGTAG 1358
QY 901 TACGGATAGCTGTGACTCGGCTCCTTACACACCTCTGAGTACACCGGAGTCCC 960
Db 1359 TACGGATAGCTGTGACTCGGCTCCTTACACACCTCTGAGTACACCGGAGTCCC 1418
QY 961 GCTGTGCCCATTAACCAAGTTGCCGTGAGAGTTGTGGCGCTGCGAGGCTGTGAATG 1020
Db 1419 GCTGTGCCCATTAACCAAGTTGCCGTGAGAGTTGTGGCGCTGCGAGGCTGTGAATG 1478
QY 1021 TATCGAGACTTGCTTTACAGAGCTGCGGCAACTTTTGGACTTGAAGCTGTAAAGCCCCAG 1080
Db 1479 TATCGAGACTTGCTTTACAGAGCTTGGGCAACTTTTGGACTTGAAGCTGTAAAGCCCCAG 1538
QY 1081 GCCATAGAGTGAACCTGTGATTTGCGTGTGGTTAAGCGCTTTGTTGCTGAATAGT 1140
Db 1539 GCCATAGAGTGAACCTGTGATTTGCGTGTGGTTAAGCGCTTTGTTGCTGAATAGT 1598
QY 1141 TGAATGATTTTAAATAAAGGTGAGATTAATGTTTAACTTGCAATGCGTGTAAATGGGGC 1200
Db 1599 TGAATGATTTTAAATAAAGGTGAGATTAATGTTTAACTTGCAATGCGTGTAAATGGGGC 1658
QY 1201 GGGGCTTAAAGGATATTAATGCGCGCTGAGCTAATCTTGTTACATCTGACTATGGA 1260
Db 1659 GGGGCTTAAAGGATATTAATGCGCGCTGAGCTAATCTTGTTACATCTGACTATGGA 1718
QY 1261 GGGCTTGGAGATTTTGGAGATTTTCTGCTGTGCTAATCTTGCTGGAACGAGCTCTAA 1320
Db 1719 GGGCTTGGAGATTTTGGAGATTTTCTGCTGTGCTAATCTTGCTGGAACGAGCTCTAA 1778
QY 1321 CAGTACCTCTTGTTTGAAGGTTTCTGTGGGGCTCATCCAGGCAAAATTAATGTCTGAG 1380
Db 1779 CAGTACCTCTTGTTTGAAGGTTTCTGTGGGGCTCATCCAGGCAAAATTAATGTCTGAG 1838
QY 1381 AATTAAGAGATTTACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGACTGTT 1440
Db 1839 AATTAAGAGATTTACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGACTGTT 1898
QY 1441 TGAATCTTTGAATCTGGGTACCGAGCGCTTTTCCAGAGAGGTCAATCAAGACTTTGGA 1500
Db 1899 TGAATCTTTGAATCTGGGTACCGAGCGCTTTTCCAGAGAGGTCAATCAAGACTTTGGA 1958
QY 1501 TTTTTCACACCGGGGCGCGCTGCGGCTGTGCTTTTGTAGTTTAAAGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGGCTGTGCTTTTGTAGTTTAAAGATTA 2018
QY 1561 ATGAGCGAAAGAAACCATCTGAGCGGGGGTACTCTGCTGATTTTCTGGCATGACT 1620
Db 2019 ATGAGCGAAAGAAACCATCTGAGCGGGGGTACTCTGCTGATTTTCTGGCATGACT 2078
QY 1621 GTGGAGAGCGGTTGTGAGACAAAGAAATGCGCTGTACTGTGTCTCCGTCGCGCCGGC 1680
Db 2079 GTGGAGAGCGGTTGTGAGACAAAGAAATGCGCTGTACTGTGTCTCCGTCGCGCCGGC 2138
QY 1681 GATTAATACGACCGAGAGAGCAGCAGCAGCAGAGAGAAACCGAGCGCGCGCGAGGA 1740
Db 2139 GATTAATACGACCGAGAGAGCAGCAGCAGCAGAGAGAAACCGAGCGCGCGCGAGGA 2198
QY 1741 GCAGAGCCCATGGAACCCGAGAGCCGCGCTGAGACCTTCGGGAATGAATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCCGCGCTGAGACCTTCGGGAATGAATGTTGTACAGGTG 2258
QY 1801 GCTGAACGTGATCCAGAACTGAGACGATTTTGAATTAACAGAGATGGGCAAGGGGCTA 1860
Db 2259 GCTGAACGTGATCCAGAACTGAGACGATTTTGAATTAACAGAGATGGGCAAGGGGCTA 2318
QY 1861 AAGGGGTTAAAGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTAGCT 1920
Db 2319 AAGGGGTTAAAGAGGAGCGGGGGCTTGTAGAGCTACAGAGAGGCTAGGAATCTAGCT 2378
QY 1921 TTTAGCTTAATGACACACCGTCTGAGGTATTAATTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACACACCGTCTGAGGTATTAATTTTCAACAGATCAAGATTAAT 2438

1981 TGGCTATATGACTTATGATCTGCGGAGAAATTTTCATAGAGACCTGACCTTAC 2040
2439 TGCCCTATATGACTTATGATCTGCGGAGAAATTTTCATAGAGACCTGACCTTAC 2498
2041 TGGCTGAGCGGAGGAGATTTTGAAGAGGCTATTAGGATATATGCAAGAGGACCTT 2100
2499 TGGCTGAGCGGAGGAGATTTTGAAGAGGCTATTAGGATATATGCAAGAGGACCTT 2558
2101 AGGCGAGATTGCAAGTACAGATCAGCAACTTTGAAATATCAGGAATTTGTTGCTAC 2160
2559 AGGCGAGATTGCAAGTACAGATCAGCAACTTTGAAATATCAGGAATTTGTTGCTAC 2618
2161 TCTGGGAAACGGGGCGGAGAGTGAATATGATACGAGATAGAGGCTTTTAAATGAT 2220
2619 TCTGGGAAACGGGGCGGAGAGTGAATATGATACGAGATAGAGGCTTTTAAATGAT 2678
2221 ATGATTAATATATGAGCGGAGGAGTGTGCAATGAGACGGGGTGTATTAATGATGTA 2280
2679 ATGATTAATATATGAGCGGAGGAGTGTGCAATGAGACGGGGTGTATTAATGATGTA 2738
2281 TTTTCTGGCCCCCAATTTTATAGCGGTATCTGCGCAATACCAACTTATCTTACAC 2340
2739 TTTTCTGGCCCCCAATTTTATAGCGGTATCTGCGCAATACCAACTTATCTTACAC 2798
2341 GGTGTAAGCTTCTATGAGGTTTAAACAATCCTGTGTGGAAGCCTGAGCCGATGTA 2400
2799 GGTGTAAGCTTCTATGAGGTTTAAACAATCCTGTGTGGAAGCCTGAGCCGATGTA 2858
2401 CGGGGCTGTGCTTTTATGCTGCTGGAAGGGGGTGTGTCCGCCCAAAAGAGGCT 2460
2859 CGGGGCTGTGCTTTTATGCTGCTGGAAGGGGGTGTGTCCGCCCAAAAGAGGCT 2918
2461 TCAATTAAGAAATGCTCTTTGAAAGGTATGATCTGTCTGAGGGTAACTCC 2520
2919 TCAATTAAGAAATGCTCTTTGAAAGGTATGATCTGTCTGAGGGTAACTCC 2978
2521 AGGGTGGCCCAATATGAGGCTCCGACTGTGAGTCTTCACTGATGTAAGAGGCT 2580
2979 AGGGTGGCCCAATATGAGGCTCCGACTGTGAGTCTTCACTGATGTAAGAGGCT 3038
2581 GTGATTAAGCAATATGAGTATGAGCAATGAGGAGCAAGGGCTCTCAATATGCTGAC 2640
3039 GTGATTAAGCAATATGAGTATGAGCAATGAGGAGCAAGGGCTCTCAATATGCTGAC 3098
2641 TGCTCGAGCGGCAATGCTGCTGAGAGCAATTCAGTAGCCAGCCTCTCGCAG 2700
3099 TGCTCGAGCGGCAATGCTGCTGAGAGCAATTCAGTAGCCAGCCTCTCGCAG 3158
2701 GCGTGGCCAGTGTGAGCAATTAATCACTGACCCGCTGTTCTTGCAATTTGGGTAAC 2760
3159 GCGTGGCCAGTGTGAGCAATTAATCACTGACCCGCTGTTCTTGCAATTTGGGTAAC 3218
2761 AGGGGGGTGTTCTTACCTTAACCAATGCAATTTGATCACTTAAGATTTTCTTGAAGCC 2820
3219 AGGGGGGTGTTCTTACCTTAACCAATGCAATTTGATCACTTAAGATTTTCTTGAAGCC 3278
2821 GAGAGCATGCTCAAGAGTGAACCTGAAACGGGGTGTGTCATGACCAATGAAGCTGAA 2880
3279 GAGAGCATGCTCAAGAGTGAACCTGAAACGGGGTGTGTCATGACCAATGAAGCTGAA 3338
2881 GTGCTGAGTACGATGAGACCCGCAACAGGTGAGACCCCTGAGAGTGTGGCGTAACAT 2940
3339 GTGCTGAGTACGATGAGACCCGCAACAGGTGAGACCCCTGAGAGTGTGGCGTAACAT 3398
2941 ATTAGGAACCAAGCTGTGATGCTGATGTAATGACCAAGAGCTGAGGCCGATCACTT 3000
3399 ATTAGGAACCAAGCTGTGATGCTGATGTAATGACCAAGAGCTGAGGCCGATCACTT 3458
3001 CTGAGCTGACACCCGCGCTGAGTTGGCTCTAGCGATGAAATACAGATTGAG 3052
3459 CTGAGCTGACACCCGCGCTGAGTTGGCTCTAGCGATGAAATACAGATTGAG 3510

RESULT 7
US-09-739-007-43
; Sequence 43, Application US/09739007
; Publication No. US20030170885A1
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; MEHTALI, Majid
; PAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; COMPLEMENTATION LINES
; NUMBER OF SEQUENCE: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,007
; FILING DATE: 19-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/379,452
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35935 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-739-007-43
Query Match 100.0%; Score 3052; DB 10; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTGTAGTATTAATACCCGAGTTCCTCAAGAGGCACTCTTGAAGTCCAGCGAGT 60
DB 459 CGTGTAGTATTAATACCCGAGTTCCTCAAGAGGCACTCTTGAAGTCCAGCGAGT 518
QY 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAATGAGACATATATCTGCC 120
DB 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAATGAGACATATATCTGCC 578
QY 121 ACGGAGGTATTAACGGAATAATGCGCGCAGTCTTTTGAACAGAGTGAATCGAAGAG 180
DB 579 ACGGAGGTATTAACGGAATAATGCGCGCAGTCTTTTGAACAGAGTGAATCGAAGAG 638
QY 181 TACTGCTGATATCTTCACTCTAGCCATTTTGAACCACTTACCTTACGAACTGT 240
DB 639 TACTGCTGATATCTTCACTCTAGCCATTTTGAACCACTTACCTTACGAACTGT 698
QY 241 ATGATTTAGAGTACGCGCCCGGAGATCCCAAGAGAGCGGTTTCCGAGATTTTTC 300
DB 699 ATGATTTAGAGTACGCGCCCGGAGATCCCAAGAGAGCGGTTTCCGAGATTTTTC 758
QY 301 CCGACTGTATATGTGGCGGTGAGGAAGGATTACTCACTTTCCGCGCGGCGC 360

Db 759 CCGACTGTATGTTGGCGGTGACAGAAAGGATTGACTTACCTTTTCCGCGGCGC 818
Qy 361 CCGGTTCTCCGGAGCCGCTCACTTTTCCGGCAGCCCGAGACGCCGAGCAGAGAGCTT 420
Db 819 CCGGTTCTCCGGAGCCGCTCACTTTTCCGGCAGCCCGAGACGCCGAGCAGAGAGCTT 878
Qy 421 TGGTCCGGTTTCTATGCGCAAACTTTGTAACCGAGAGTGAATGATCTTTCCTGCCACGAG 480
Db 879 TGGGTTCCGGTTTCTATGCGCAAACTTTGTAACCGAGAGTGAATGATCTTTCCTGCCACGAG 938
Qy 481 CTGGCTTTCCACCCGAGCAGCAGAGATGAAGAAGGTGAGAGTTGTGTAGATTATG 540
Db 939 CTGGCTTTCCACCCGAGCAGCAGAGATGAAGAAGGTGAGAGTTGTGTAGATTATG 998
Qy 541 TGGAGCAACCCCGGACAGGTTGCAAGTCTTGTCAATATCACCGAGAGAAATCGGGGAC 600
Db 999 TGGAGCAACCCCGGACAGGTTGCAAGTCTTGTCAATATCACCGAGAGAAATCGGGGAC 1058
Qy 601 CAGATATATATGTTGCTTGTCTATATAGAGACCTGTGGCATGTTGTCTACAGTAA 660
Db 1059 CAGATATATATGTTGCTTGTCTATATAGAGACCTGTGGCATGTTGTCTACAGTAA 1118
Qy 661 GAAATATATGAGGCAAGTGTGATAGAGTGTGGTTGTGTGATATTTTTTTTAA 720
Db 1119 GAAATATATGAGGCAAGTGTGATAGAGTGTGGTTGTGTGATATTTTTTTTAA 1178
Qy 721 TTTTACGTTTTGTGCTTAAAGAAATTTGTATGTGATTTTTTTTAAAGTCTGTGTC 780
Db 1179 TTTTACGTTTTGTGCTTAAAGAAATTTGTATGTGATTTTTTTTAAAGTCTGTGTC 1238
Qy 781 TGAACCTGAGCCTGAGCCGAGCCAGAACCCGAGCCTGCAAGACTACCCGCGCTCTAA 840
Db 1239 TGAACCTGAGCCTGAGCCGAGCCAGAACCCGAGCCTGCAAGACTACCCGCGCTCTAA 1298
Qy 841 AATGGCGCTGCTATCTGAGACGCGCAGCATCACTGTGTCTAGAGATCAATAGTAG 900
Db 1299 AATGGCGCTGCTATCTGAGACGCGCAGCATCACTGTGTCTAGAGATCAATAGTAG 1358
Qy 901 TAGGATAGCTGTGACTCCGCTCTTCTAACACACTCCTGAGATACACCCGCGGTGCC 960
Db 1359 TAGGATAGCTGTGACTCCGCTCTTCTAACACACTCCTGAGATACACCCGCGGTGCC 1418
Qy 961 GCTGTGCCCCATTAAACAGTTGCGTGAAGATTGTGAGCGTGCAGCGCTGGAATG 1020
Db 1419 GCTGTGCCCCATTAAACAGTTGCGTGAAGATTGTGAGCGTGCAGCGCTGGAATG 1478
Qy 1021 TATGAGAGACTTGCTTAAACGAGCCTGAGCAACTTTGAGCTTGAAGCTGTAAACGCC 1080
Db 1479 TATGAGAGACTTGCTTAAACGAGCCTGAGCAACTTTGAGCTTGAAGCTGTAAACGCC 1538
Qy 1081 GCCATTAAGTGTAAACCTGTGATTGCGTGTGTTAACGCTTGTGTGTAATGAT 1140
Db 1539 GCCATTAAGTGTAAACCTGTGATTGCGTGTGTTAACGCTTGTGTGTAATGAT 1598
Qy 1141 TGAATGAATTAATAAGGTGAGATATGTTTAACTTGCATGGCGTGTAAATGAGG 1200
Db 1599 TGAATGAATTAATAAGGTGAGATATGTTTAACTTGCATGGCGTGTAAATGAGG 1658
Qy 1201 GGGGCTTAAAGGATATATATGCGCGCTGAGCTTATCTTGTTACATCTGACCTCAT 1260
Db 1659 GGGGCTTAAAGGATATATATATGCGCGCTGAGCTTATCTTGTTACATCTGACCTCAT 1718
Qy 1261 GGGCTTGGAGATGTTTGAAGATTTTCTGCTGTGCTTAACTTGTGGAACGAGCTCT 1320
Db 1719 GGGCTTGGAGATGTTTGAAGATTTTCTGCTGTGCTTAACTTGTGGAACGAGCTCT 1778
Qy 1321 CAGTACTCTTGTGTTTGAAGTCTGTGAGGCTCAATCCAGGCAAAATTAATGCTGAG 1380
Db 1779 CAGTACTCTTGTGTTTGAAGTCTGTGAGGCTCAATCCAGGCAAAATTAATGCTGAG 1838
Qy 1381 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGACTTTTGAATCTGTGTGAGCTG 1440
Db 1839 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGACTTTTGAATCTGTGTGAGCTG 1898

Qy 1441 TGATTTCTTGAATCTGGGTCAACGAGCGCTTTTCCAGAGAAAGTCATCAAGACTTTGGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACGAGCGCTTTTCCAGAGAAAGTCATCAAGACTTTGGA 1958
Qy 1501 TTTTTCACACCGGGGGCGCTGCGGCTGTGCTTTTGTGAGTTTATTAAGATTA 1560
Db 1959 TTTTTCACACCGGGGGCGCTGCGGCTGTGCTTTTGTGAGTTTATTAAGATTA 2018
Qy 1561 ATGAGCGAAAGAAACCATCTGAGCGGGGGTACCTGCTGATTTTCTGCGCATGCACT 1620
Db 2019 ATGAGCGAAAGAAACCATCTGAGCGGGGGTACCTGCTGATTTTCTGCGCATGCACT 2078
Qy 1621 GTGAGAGCGGTTGTGACACAAAGATTCGCTGTCTGTGTCTTCCGCGCGCGC 1680
Db 2079 GTGAGAGCGGTTGTGACACAAAGATTCGCTGTCTGTGTCTTCCGCGCGCGC 2138
Qy 1681 GATTAATACGACCGAGAGAGCAGCAGCAGCAGAGAGAAAGCCAGCGCGCGCAGGA 1740
Db 2139 GATTAATACGACCGAGAGAGCAGCAGCAGCAGAGAGAAAGCCAGCGCGCGCAGGA 2198
Qy 1741 GCAGAGCCATGGAACCCGAGAGCCGCGCTGAGCCTTGGGAATGAATGTTGTAACAG 1800
Db 2199 GCAGAGCCATGGAACCCGAGAGCCGCGCTGAGCCTTGGGAATGAATGTTGTAACAG 2258
Qy 1801 GCTGAAGTATCCAGAACTGAGACGCAATTTGACATTAACAGAGATGGGCAAGGCTA 1860
Db 2259 GCTGAAGTATCCAGAACTGAGACGCAATTTGACATTAACAGAGATGGGCAAGGCTA 2318
Qy 1861 AAGGGGTTAAAGAGGAGCGGGGGCTTGTAGAGCTTACAGAGAGGCTAGGAATCTAG 1920
Db 2319 AAGGGGTTAAAGAGGAGCGGGGGCTTGTAGAGCTTACAGAGAGGCTAGGAATCTAG 2378
Qy 1921 TTTTACCTTAATGACACAGACACCGTCTGATGTTTACTTTTCAACGATCAAGATTA 1980
Db 2379 TTTTACCTTAATGACACAGACACCGTCTGATGTTTACTTTTCAACGATCAAGATTA 2438
Qy 1981 TGGGCTTAATGAGCTGATCTGCTGGGAGAAATTCATPAGAGAGCTGACACACTTAC 2040
Db 2439 TGGGCTTAATGAGCTGATCTGCTGGGAGAAATTCATPAGAGAGCTGACACACTTAC 2498
Qy 2041 TGGCTGAGCAGGGGATGATTTTGAAGAGCTATTAGGATATGCAAGGTGGCACTT 2100
Db 2499 TGGCTGAGCAGGGGATGATTTTGAAGAGCTATTAGGATATGCAAGGTGGCACTT 2558
Qy 2101 AGGCGAGATTGCAATTAACAAGTACGAAACTTGTAAATATCAGGAATTTGTTGCTAC 2160
Db 2559 AGGCGAGATTGCAATTAACAAGTACGAAACTTGTAAATATCAGGAATTTGTTGCTAC 2618
Qy 2161 TCTGGGAAAGGGGGCGAGGTGAGATGATACGAGAGATGGGGTGGCTTTAGATGTA 2220
Db 2619 TCTGGGAAAGGGGGCGAGGTGAGATGATACGAGAGATGGGGTGGCTTTAGATGTA 2678
Qy 2221 ATGATTAATATGTGCGCGGGGTGCTTGGCATGAGCGGGGTGTTATTATGATGTA 2280
Db 2679 ATGATTAATATGTGCGCGGGGTGCTTGGCATGAGCGGGGTGTTATTATGATGTA 2738
Qy 2281 TTTTACTGGCCCCAATTTTACCGGTGCGTTTTCTGTGCAATACCACTTATCTTACAC 2340
Db 2739 TTTTACTGGCCCCAATTTTACCGGTGCGTTTTCTGTGCAATACCACTTATCTTACAC 2798
Qy 2341 GGTGTAGCTTCTATGAGGTTTAAACAATACCTGTGTGGAACCTGGAACGATGAAG 2400
Db 2799 GGTGTAGCTTCTATGAGGTTTAAACAATACCTGTGTGGAACCTGGAACGATGAAG 2858
Qy 2401 CCGGGCTGTGCTTTTACTGCTGTGAAGCGGGGTGTGTGTGCGCCCAAAAGCAGG 2460
Db 2859 CCGGGCTGTGCTTTTACTGCTGTGAAGCGGGGTGTGTGTGCGCCCAAAAGCAGG 2918
Qy 2461 TCAATTAAGAAATGCTCTTTTGAAGGTGTAACCTTGGGTATCTGTGTGAGGTTA 2520
Db 2919 TCAATTAAGAAATGCTCTTTTGAAGGTGTAACCTTGGGTATCTGTGTGAGGTTA 2978

Qy 2521 AGGGTGGCCCAATGTTGGCTCCGACGTGGTTGCTTCAATGTAAGTAAAGGCTGCT 2580
Db 2579 AGGGTGGCCCAATGTTGGCTCCGACGTGGTTGCTTCAATGTAAGTAAAGGCTGCT 3038
Qy 2581 GTGATTAAGCATACATGTAATGTGGCACTGCGAGGACAGGGCTCTCAGATCTGACC 2640
Db 3039 GTGATTAAGCATACATGTAATGTGGCACTGCGAGGACAGGGCTCTCAGATCTGACC 3098
Qy 2641 TGCTCGAGCGCAACTGTCACTGCTGTGAAGACATTTCAGTACGACCACTCTCGCAG 2700
Db 3099 TGCTCGAGCGCAACTGTCACTGCTGTGAAGACATTTCAGTACGACCACTCTCGCAG 3158
Qy 2701 GCGTGGCAGTGTGAGCATACATGACCGGCTGCTTGCATTTGGGTAAGAG 2760
Db 3159 GCGTGGCAGTGTGAGCATACATGACCGGCTGCTTGCATTTGGGTAAGAG 3218
Qy 2761 AGGGGGGTGTTCTTACCTTACCAATGCAATTGAGTCACTAAGATTTGCTTGAGCCC 2820
Db 3219 AGGGGGGTGTTCTTACCTTACCAATGCAATTGAGTCACTAAGATTTGCTTGAGCCC 3278
Qy 2821 GAGAGCATGTCGAAGTGGAACCTGGAACGGGGTGTGACATGACCATGAAGATCTGAG 2880
Db 3279 GAGAGCATGTCGAAGTGGAACCTGGAACGGGGTGTGACATGACCATGAAGATCTGAG 3338
Qy 2881 GTGCTGAGTACATGAGACCCGACAGGTGAGACCTGCGAGTGTGGCGTAACAT 2940
Db 3339 GTGCTGAGTACATGAGACCCGACAGGTGAGACCTGCGAGTGTGGCGTAACAT 3398
Qy 2941 ATTAGAACAAGCTGTGATGCTGATGTGACCGAGAGCTGAGGCGCATCTTGAGTG 3000
Db 3399 ATTAGAACAAGCTGTGATGCTGATGTGACCGAGAGCTGAGGCGCATCTTGAGTG 3458
Qy 3001 CTGGCTCTGACCCGCGCTGAGTTGGCTCTAGCGATGAAGTACAGATTGAG 3052
Db 3459 CTGGCTCTGACCCGCGCTGAGTTGGCTCTAGCGATGAAGTACAGATTGAG 3510

RESULT 8
US-10-264-839-12
/ Sequence 12, Application US/10264839
/ Publication No. US20040086485A1
/ GENERAL INFORMATION:
/ APPLICANT: AGUILAR-CORDOVA, CARLOS ESTUARDO
/ TITLE OF INVENTION: CHIMERIC VIRAL VECTORS FOR GENE THERAPY
/ FILE REFERENCE: 13087-105 US
/ CURRENT APPLICATION NUMBER: US/10/264,839
/ PRIOR FILING DATE: 2002-10-04
/ PRIOR APPLICATION NUMBER: 60/327,179
/ PRIOR FILING DATE: 2001-10-04
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 35935
/ TYPE: DNA
/ ORGANISM: Adenovirus
/ FEATURE:
/ OTHER INFORMATION: Adenovirus serotype 5
US-10-264-839-12

Query Match 100.0%; Score 3052; DB 19; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGTAGTGTATTATACCGGGTGAAGTTCCTCAAGAGGCCACTTGTAGTCCAGCGAGT 60
Db 459 CGGTAGTGTATTATACCGGGTGAAGTTCCTCAAGAGGCCACTTGTAGTCCAGCGAGT 518
Qy 61 AGAGTTTTCCTCCGAGCGGCTCCGACACCGGAGCTGAAATGACATATTATCTGCC 120
Db 519 AGAGTTTTCCTCCGAGCGGCTCCGACACCGGAGCTGAAATGACATATTATCTGCC 578
Qy 121 ACGAGGTGTTATTATACGAAGAAATGCGCGCACTCTTTGGACACAGCTGATCGAAGG 180

Db 579 ACGAGGTGTTATTATACGAAGAAATGCGCGCACTCTTTGGACACAGCTGATCGAAGG 638
Qy 181 TACTGCTGTATATCTTCCACCTCTACCAATTTGAAACCACTTACCTTACGAAGCTGT 240
Db 639 TACTGCTGTATATCTTCCACCTCTACCAATTTGAAACCACTTACCTTACGAAGCTGT 698
Qy 241 ATGATTTAGACGTGACGGCCCCGGAAGATCCCAACGAGAGGCGGTTTCGAGATTTTTC 300
Db 699 ATGATTTAGACGTGACGGCCCCGGAAGATCCCAACGAGAGGCGGTTTCGAGATTTTTC 758
Qy 301 CCGACTCTGTAATGTTGGCGGTGAGAGGATTTGACTTACTCACTTTTCCGCGCGC 360
Db 759 CCGACTCTGTAATGTTGGCGGTGAGAGGATTTGACTTACTCACTTTTCCGCGCGC 818
Qy 361 CCGGTTCTCGGAGCGGCTTACCTTTCCCGGAGCCCGAGACCGGAGCAGAGAGCTT 420
Db 819 CCGGTTCTCGGAGCGGCTTACCTTTCCCGGAGCCCGAGACCGGAGCAGAGAGCTT 878
Qy 421 TGGGTCCGGTTTCTATGCAAACTTGTACCGAGGTGATCGATCTTACCTGCAAGG 938
Db 879 TGGGTCCGGTTTCTATGCAAACTTGTACCGAGGTGATCGATCTTACCTGCAAGG 938
Qy 481 CTGGCTTTCACCAAGAGAGAGAGATGAAGAGGTGAGAGTTGTGTTAGATTATG 540
Db 939 CTGGCTTTCACCAAGAGAGAGATGAAGAGGTGAGAGTTGTGTTAGATTATG 998
Qy 541 TGAAGACCCCGGACGAGTTGCAAGTCTTGTCAATTATCAACCGAGGAATACGGGAGAC 600
Db 999 TGAAGACCCCGGACGAGTTGCAAGTCTTGTCAATTATCAACCGAGGAATACGGGAGAC 1058
Qy 601 CAGATATTATGTTGCTGCTTGTATATGAGACCTGTGCATGTTGTCTACAGTAAGT 660
Db 1059 CAGATATTATGTTGCTGCTTGTATATGAGACCTGTGCATGTTGTCTACAGTAAGT 1118
Qy 661 GAAATATTAGGAGAGTGGATGATGAGTGGGTTGGTGGTAATTTTTTTTAAAT 720
Db 1119 GAAATATTATGAGAGTGGATGATGAGTGGGTTGGTGGTAATTTTTTTTAAAT 1178
Qy 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGATTTTAAAGTCTGTGTC 780
Db 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGATTTTAAAGTCTGTGTC 1238
Qy 781 TGAACCTGAGACCGGCGGACGAGAACCGGAGCTGCAAGACTTACCGGCGTCTTAA 840
Db 1239 TGAACCTGAGACCGGCGGACGAGAACCGGAGCTGCAAGACTTACCGGCGTCTTAA 1298
Qy 841 AATGGCGCTGTATCTGTAGACGCGCGACATCACTGTGCTAGAGATGCAATAGTAG 900
Db 1299 AATGGCGCTGTATCTGTAGACGCGCGACATCACTGTGCTAGAGATGCAATAGTAG 1358
Qy 901 TACGATAGCTGTGACTCCGGTCTTTTAAACAACCTCTGAGATACACCGGAGTCC 960
Db 1359 TACGATAGCTGTGACTCCGGTCTTTTAAACAACCTCTGAGATACACCGGAGTCC 1418
Qy 961 GCTGTGCCCCATTAAACCAAGTTGCGGTAGAGTTGTGGGCGTCCAGAGCTGTGAATG 1020
Db 1419 GCTGTGCCCCATTAAACCAAGTTGCGGTAGAGTTGTGGGCGTCCAGAGCTGTGAATG 1478
Qy 1021 TATCGAGGACTGTGATACGAGCTGGGCAACCTTGGACTTGAAGCTGTAAACGCCCCAG 1080
Db 1479 TATCGAGGACTGTGATACGAGCTGGGCAACCTTGGACTTGAAGCTGTAAACGCCCCAG 1538
Qy 1081 GCCATAAGGTGTAACCTGTGATTCGTGTGTGTTAAAGCCTTTGTGTGTAATAGT 1140
Db 1539 GCCATAAGGTGTAACCTGTGATTCGTGTGTGTTAAAGCCTTTGTGTGTAATAGT 1598
Qy 1141 TGAATGTAAGTTTAAATGAAGGTGAGATTAATGTTTAACTGATGCGCTTAAATGGGCG 1200
Db 1599 TGAATGTAAGTTTAAATGAAGGTGAGATTAATGTTTAACTGATGCGCTTAAATGGGCG 1658
Qy 1201 GGGGCTTAAAGGATATATATGCGCGTGGGCTAATCTTGGTTACATCTGACCTCATGA 1260
Db 1659 GGGGCTTAAAGGATATATATGCGCGTGGGCTAATCTTGGTTACATCTGACCTCATGA 1718

1261 GCGTGGAGAGTGTGGAGATTTTCTGCTGCGTAATCTGCTGAAAGAGCTCTAA 1320
1719 GCGTTGGAGAGTGTGGAGATTTTCTGCTGCGTAATCTGCTGAAAGAGCTCTAA 1778
1321 CAGTACCTCTTGTTTGGAGAGTGTGCGGCTCATCCAGGCAAGTTAGTCTGAG 1380
1779 CAGTACCTCTTGTTTGGAGAGTGTGCGGCTCATCCAGGCAAGTTAGTCTGAG 1838
1381 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGCTTTTGAATTCCTGTGTAGCTGT 1440
1839 AATTAAGAGAGATTAACAAGTGGAAATTTGAAGCTTTTGAATTCCTGTGTAGCTGT 1898
1441 TGATTTCTTGAATCTGCGTCAACAGAGCTTTTCCAGAGAAAGCTCATCAAGCTTTGGA 1500
1899 TGATTTCTTGAATCTGCGTCAACAGAGCTTTTCCAGAGAAAGCTCATCAAGCTTTGGA 1958
1501 TTTTTCACACCGGGGCGCGCTGCGGCTGCTGTGCTTTTGAAGTTTATTAAGATTA 1560
1959 TTTTTCACACCGGGGCGCGCTGCGGCTGCTGTGCTTTTGAAGTTTATTAAGATTA 2018
1561 ATGAGAGGAGAAACCCATCTGAGAGCGGGGGGTACTGCTGATTTTCTGCGCATGCTCT 1620
2019 ATGAGAGGAGAAACCCATCTGAGAGCGGGGGGTACTGCTGATTTTCTGCGCATGCTCT 2078
1621 GTGAGAGAGCGGTTGTGAGACACAAGAAATCGCTGCTACTGTTGCTTCCGTCGCGCGG 1680
2079 GTGAGAGAGCGGTTGTGAGACACAAGAAATCGCTGCTACTGTTGCTTCCGTCGCGCGG 2138
1681 GATTAATCCGACGAGAGAGCAGCAGCAGCAGCAGAGAGAGCCAGCGCGCGCAGGA 1740
2139 GATTAATCCGACGAGAGAGCAGCAGCAGCAGCAGAGAGAGCCAGCGCGCGCAGGA 2198
1741 GCAGAGCCCATGGAACCCGAGAGCGGCTGGAACCTTGGGAAATGAATGTTGTACAGGTG 1800
2199 GCAGAGCCCATGGAACCCGAGAGCGGCTGGAACCTTGGGAAATGAATGTTGTACAGGTG 2258
1801 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGATGGGCGAGGCTA 1860
2259 GCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGATGGGCGAGGCTA 2318
1861 AAGGGGGTAAAGAGAGAGCGGGGGGCTTTGTAGGCTTACAGAGAGGCTTAGAATCTA 1920
2319 AAGGGGGTAAAGAGAGAGCGGGGGGCTTTGTAGGCTTACAGAGAGGCTTAGAATCTA 2378
1921 TTTAGCTTAAAGACCAAGCACCGGCTCTGAGGTATTAATTTTCAACAGATCAAGATTA 1980
2379 TTTAGCTTAAAGACCAAGCACCGGCTCTGAGGTATTAATTTTCAACAGATCAAGATTA 2438
1981 TGCGCTAATGAGCTTGAATCTGCTGGCGAGAAAGTATTCATAGAGCAGCTGACCTTAC 2040
2439 TGCGCTAATGAGCTTGAATCTGCTGGCGAGAAAGTATTCATAGAGCAGCTGACCTTAC 2498
2041 TGCGTGCAGCCAGGGGATGATTTTGAAGAGGCTTATTAAGGATTAATGCAAGGTGCACTT 2100
2499 TGCGTGCAGCCAGGGGATGATTTTGAAGAGGCTTATTAAGGATTAATGCAAGGTGCACTT 2558
2101 AGGCGCAATTCGAAAGTACAAAGTACAGCAACTTGTAAATATCAGAGATTTGTTGCTACCTT 2160
2559 AGGCGCAATTCGAAAGTACAAAGTACAGCAACTTGTAAATATCAGAGATTTGTTGCTACCTT 2618
2161 TCTGGGAAACGGGGCGAGAGTGAATGATACGAGAGGTTAGGGTGGCTTTAGATGATGAC 2220
2619 TCTGGGAAACGGGGCGAGAGTGAATGATACGAGAGGTTAGGGTGGCTTTAGATGATGAC 2678
2221 ATGATTAATATGTGGCGCGGGGTGCTTGGCATGAGCGGGGTGTTATTAATGATGATGAG 2280
2679 ATGATTAATATGTGGCGCGGGGTGCTTGGCATGAGCGGGGTGTTATTAATGATGATGAG 2738
2281 TTTTACTGGCCCCAATTTTAAAGGATACGTTTCTGCGCAATACCAACCTTATCTTACAC 2340
2739 TTTTACTGGCCCCAATTTTAAAGGATACGTTTCTGCGCAATACCAACCTTATCTTACAC 2798

2341 GGTGTAAGCTTTCTATGGGTTTAAACAATACCTGTGTGGAAGCGTGGACGATGAAGGTT 2400
2799 GGTGTAAGCTTTCTATGGGTTTAAACAATACCTGTGTGTGGAAGCGTGGACGATGAAGGTT 2858
2401 CGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGTGTGTGCGCCCCAAAAGCAGGCT 2460
2859 CGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGTGTGTGCGCCCCAAAAGCAGGCT 2918
2461 TCAATTAAGAAATGCTTTTGAAGAGGTGATCCTTGGGATTCCTGTGAGAGGTTAACTCC 2520
2919 TCAATTAAGAAATGCTTTTGAAGAGGTGATCCTTGGGATTCCTGTGAGAGGTTAACTCC 2978
2521 AGGCTGGCCCAATGTGAGCTCCGACTGTGTGCTTCAATGTAGTGAAGAAAGCGTGGCT 2580
2979 AGGCTGGCCCAATGTGAGCTCCGACTGTGTGCTTCAATGTAGTGAAGAAAGCGTGGCT 3038
2581 GTGATTAAGCAATTAATGTATGTGCAACTGCGAGAGCAGAGGCGCTCTCAGATCTGACC 2640
3039 GTGATTAAGCAATTAATGTATGTGCAACTGCGAGAGCAGAGGCGCTCTCAGATCTGACC 3098
2641 TGCTGGAGCGGCAATGTATGTGCAACTGCGAGAGCAGATTCAGTACGACCACTCTCGCAG 2700
3099 TGCTGGAGCGGCAATGTATGTGCAACTGCGAGAGCAGATTCAGTACGACCACTCTCGCAG 3158
2701 GCCTGGCAGAGTGTGAGCAATTAATCATACTGACCCGCTGTCTTCAATTTGGGTTAACAG 2760
3159 GCCTGGCAGAGTGTGAGCAATTAATCATACTGACCCGCTGTCTTCAATTTGGGTTAACAG 3218
2761 AGGGGGGTGTCTTCACTTAACTCAATGCAATTTAGTCACTAATAGATTTGCTTGAAGCC 2820
3219 AGGGGGGTGTCTTCACTTAACTCAATGCAATTTAGTCACTAATAGATTTGCTTGAAGCC 3278
2821 GAGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTGAACATGACATGAAGATGATCGAG 2880
3279 GAGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTGAACATGACATGAAGATGATCGAG 3338
2881 GTGCTGAGTACATGATGAGACCCGACAGGAGTGCAGACCTGCGAGTGTGGCGTTAAACAT 2940
3339 GTGCTGAGTACATGATGAGACCCGACAGGAGTGCAGACCTGCGAGTGTGGCGTTAAACAT 3398
2941 ATTGGAACCAAGCTGTGATGTCTGATGTGACCGAGAGCTGAGAGCCCGATCACTTGGTG 3000
3399 ATTGGAACCAAGCTGTGATGTCTGATGTGACCGAGAGCTGAGAGCCCGATCACTTGGTG 3458
3001 CTGGCCCTGACCCGCGCTGAGTGTGGCTTACGAGTGAAGTAAAGATTGAG 3052
3459 CTGGCCCTGACCCGCGCTGAGTGTGGCTTACGAGTGAAGTAAAGATTGAG 3510

RESULT 9
US-10-432-989-1
Sequence 1, Application US/10432989
Publication No. US20040097455A1
GENERAL INFORMATION:
APPLICANT: Armendariz Borunda, Juan
APPLICANT: Aquilar Cordova, Saturno
TITLE OR INVENTION: Recombinant viral and non-viral vectors
TITLE OR INVENTION: containing the human gene of the urokinase plasminogen
TITLE OF INVENTION: activator and their utility in the treatment of various
TITLE OF INVENTION: types of fibrosis such as hepatic, renal, pulmonary,
TITLE OF INVENTION: pancreatic, heart fibrosis as well as hypertrophic scars
FILE REFERENCE: 5585-035-999(205/19071)
CURRENT APPLICATION NUMBER: US/10/432,989
CURRENT FILING DATE: 2003-10-24
PRIOR APPLICATION NUMBER: PCT/MX00/00050
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: MX011713
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 35935
TYPE: DNA

/ ORGANISM: Human adenovirus type 5
US-10-432-989-1

Query Match 100.0%; Score 3052; DB 19; Length 35935;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTGATGCTATTTATACCCGGTGAATTCCTCAAGAGCCACTCTTGAGTGCACGAGT 60
DB CGTGATGCTATTTATACCCGGTGAATTCCTCAAGAGCCACTCTTGAGTGCACGAGT 518
QY 459 CGTGATGCTATTTATACCCGGTGAATTCCTCAAGAGCCACTCTTGAGTGCACGAGT 518
DB AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAAATGAGCATTTATCTGCC 120
QY 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAAATGAGCATTTATCTGCC 578
DB AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAAATGAGCATTTATCTGCC 578
QY 121 ACGGAGGTGTTATTAACGAGAAATGGCCGCGCATTTTGGACCAAGCTGATCGAAGAG 180
DB ACGGAGGTGTTATTAACGAGAAATGGCCGCGCATTTTGGACCAAGCTGATCGAAGAG 638
QY 181 TACGTGCTGATTAATCTTCACTCTAGCCATTTTGAACCACTACCTTCAAGAACTGT 240
DB TACGTGCTGATTAATCTTCACTCTAGCCATTTTGAACCACTACCTTCAAGAACTGT 698
QY 639 TACGTGCTGATTAATCTTCACTCTAGCCATTTTGAACCACTACCTTCAAGAACTGT 698
DB 241 ATGATTTAGACGTGACGCGCCCGGAAAGATCCCAAGAGAGCGGTTTCCGAGATTTTTC 300
QY 699 ATGATTTAGACGTGACGCGCCCGGAAAGATCCCAAGAGAGCGGTTTCCGAGATTTTTC 758
DB 301 CCGACTCTGTAATGTTGGCGGTGACGAAAGGATTTGACTTCACTTTTCCGCGCGGC 360
QY 759 CCGACTCTGTAATGTTGGCGGTGACGAAAGGATTTGACTTCACTTTTCCGCGCGGC 818
DB 361 CCGGTTCTCCGAGCGCGCTCACTTTTCCGCGAGCCCGAGAGCGCGGAGAGAGCTT 420
QY 819 CCGGTTCTCCGAGCGCGCTCACTTTTCCGCGAGCCCGAGAGCGCGGAGAGAGCTT 878
DB 421 TGGGTCCGGTTTCTATGCAAACTTGTACGAGAGGTGATGATCTTTCCTGCCAGAG 480
QY 879 TGGGTCCGGTTTCTATGCAAACTTGTACGAGAGGTGATGATCTTTCCTGCCAGAG 938
DB 481 CTGGCTTTCCACCCAGTGAACGAGATGAAAGAGGTGAGAGGTTTGTGTAATATG 540
QY 939 CTGGCTTTCCACCCAGTGAACGAGATGAAAGAGGTGAGAGGTTTGTGTAATATG 998
DB 541 TGGAGCAACCCCGGAGCGGTGCAAGTCTTGTCAATTAACCGAGAAATCGGGGAGCC 600
QY 999 TGGAGCAACCCCGGAGCGGTGCAAGTCTTGTCAATTAACCGAGAAATCGGGGAGCC 1058
DB 601 CAGATATTAATGTTGCTTGTATATAGAGACCTGAGGATGTTTGTCTACAGTAAGT 660
QY 1059 CAGATATTAATGTTGCTTGTATATAGAGACCTGAGGATGTTTGTCTACAGTAAGT 1118
DB 661 GAAATTAATGAGGAGTGGGTGATAGAGTGTGAGTGTGTAATTTTTTTTTTAAAT 720
QY 1119 GAAATTAATGAGGAGTGGGTGATAGAGTGTGAGTGTGTAATTTTTTTTTTAAAT 1178
DB 721 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTAATTTTTTAAAGGTCTGTGTC 780
QY 1179 TTTTACAGTTTGTGTTTAAAGAAATTTGTATGTAATTTTTTAAAGGTCTGTGTC 1238
DB 781 TGAACCTGAGCCTGAGCCGAGCCGAGAACCGGAGCTGCAAGACCTTACCGCGCTCAA 840
QY 1239 TGAACCTGAGCCTGAGCCGAGCCGAGAACCGGAGCTGCAAGACCTTACCGCGCTCAA 1298
DB 841 AATGAGCGCTGCTATCTGAGACGCGCGACATCACTGTGTCTAGAGAAATCAATAGTAG 900
QY 1299 AATGAGCGCTGCTATCTGAGACGCGCGACATCACTGTGTCTAGAGAAATCAATAGTAG 1358
DB 901 TACGGAATAGCTGTGACTCCGCTCTTCAACACACTCTGAGATCAACCGGAGGTCCC 960
QY 1359 TACGGAATAGCTGTGACTCCGCTCTTCAACACACTCTGAGATCAACCGGAGGTCCC 1418
DB 961 GCTGTGCCCCATTAACCAAGTTGCGGTGAGAGTGTGAGGCGTCCCAAGGCTGGAATG 1020
QY GCTGTGCCCCATTAACCAAGTTGCGGTGAGAGTGTGAGGCGTCCCAAGGCTGGAATG 1020
DB GCTGTGCCCCATTAACCAAGTTGCGGTGAGAGTGTGAGGCGTCCCAAGGCTGGAATG 1020

DB 1419 GCTGTGCCCCATTAACCAAGTTGCGGTGAGAGTGTGAGGCGTCCCAAGGCTGGAATG 1478
QY 1021 TATGAGGACTTGTCTTAACGAGCCTGGCAACCTTTGACTGAGCTGTAAACGCCCCAG 1080
DB 1479 TATGAGGACTTGTCTTAACGAGCCTGGCAACCTTTGACTGAGCTGTAAACGCCCCAG 1538
QY 1081 GCCATAGGTGTAACCTGTGATTTGCGTGTGTTAAACGCTTTGTTGCTGAATGAT 1140
DB 1539 GCCATAGGTGTAACCTGTGATTTGCGTGTGTTAAACGCTTTGTTGCTGAATGAT 1598
QY 1141 TGAATGATTTTAAAGGAGTGAATAGTTTAACTGATGAGCGGTTAAATGGGGC 1200
DB 1599 TGAATGATTTTAAAGGAGTGAATAGTTTAACTGATGAGCGGTTAAATGGGGC 1658
QY 1201 GGGGCTTAAAGGATATATATGCGCGGTGCTAATCTTGTGTAACATCTGACCTCATGA 1260
DB 1659 GGGGCTTAAAGGATATATATGCGCGGTGCTAATCTTGTGTAACATCTGACCTCATGA 1718
QY 1261 GCGTTGGAGGTGTTGGAAGATTTTCTGTGTGCTGATTAACCTTGTGTAACAGCTCTTA 1320
DB 1719 GCGTTGGAGGTGTTGGAAGATTTTCTGTGTGCTGATTAACCTTGTGTAACAGCTCTTA 1778
QY 1321 CAGTACCTCTTGTGTAAGTCTGTGGGCTCATCCGAGCAAGTTAGTGTGAG 1380
DB 1779 CAGTACCTCTTGTGTAAGTCTGTGGGCTCATCCGAGCAAGTTAGTGTGAG 1838
QY 1381 AATTAAAGAGATTAACAAGTGGAAATTTGAAGAGCTTTGAAATCTGTGTGAGCTGTT 1440
DB 1839 AATTAAAGAGATTAACAAGTGGAAATTTGAAGAGCTTTGAAATCTGTGTGAGCTGTT 1898
QY 1441 TGATTTCTTGAATCTGGGTCAACAGCGCTTTTCCAGAGAAAGTCAATCAAGCTTGTGA 1500
DB 1899 TGATTTCTTGAATCTGGGTCAACAGCGCTTTTCCAGAGAAAGTCAATCAAGCTTGTGA 1958
QY 1501 TTTTTCACACCGGGGCGCGCTGCGGCTGTGCTTTTGAATTTAAAGGATTA 1560
DB 1959 TTTTTCACACCGGGGCGCGCTGCGGCTGTGCTTTTGAATTTAAAGGATTA 2018
QY 1561 ATGAGCGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTTCGACATGATCT 1620
DB 2019 ATGAGCGAAGAAACCATCTGAGCGGGGGTACCTGTGATTTTTCGACATGATCT 2078
QY 1621 GTGAGAGCGGTGTGAGACCAAGAAATCGCTCTACTTGTGCTTCCGTCGCCCGCC 1680
DB 2079 GTGAGAGCGGTGTGAGACCAAGAAATCGCTCTACTTGTGCTTCCGTCGCCCGCC 2138
QY 1681 GATAATCCGACGAGAGGAGGACGACGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
DB 2139 GATAATCCGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2198
QY 1741 GCAGAGCCCATGGAACCCGAGAGCGCGCTGGAACCTTCGGAATGAAATGTTGTACAGGTG 1800
DB 2199 GCAGAGCCCATGGAACCCGAGAGCGCGCTGGAACCTTCGGAATGAAATGTTGTACAGGTG 2258
QY 1801 GCTGAATCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGATGGGAGGCTTA 1860
DB 2259 GCTGAATCTGTATCCAGAACTGAGACGCAATTTTGAACAATTAAGAGATGGGAGGCTTA 2318
QY 1861 AAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGGAGGCTAGGAATCTAGCT 1920
DB 2319 AAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTACAGAGAGGAGGCTAGGAATCTAGCT 2378
QY 1921 TTTAGCTTAATGACACAGACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 1980
DB 2379 TTTAGCTTAATGACACAGACCGTCTGAGTGTATTAATTTTCAACAGATCAAGATTAAT 2438
QY 1981 TGGCTTAATGAGCTGTATCTGTGCGGAGCAAGATTTCCATATAGAGCTGACCACTTAC 2040
DB 2439 TGGCTTAATGAGCTGTATCTGTGCGGAGCAAGATTTCCATATAGAGCTGACCACTTAC 2498
QY 2041 TGGCTGAGCCAGGGAGATGATTTTGAAGAGCTTTAGGGATATGCAAAAGGTGGCACTT 2100
DB 2499 TGGCTGAGCCAGGGAGATGATTTTGAAGAGCTTTAGGGATATGCAAAAGGTGGCACTT 2558

QY 2101 AGGCCAATTGCAGTACAGATCAGCAAACTTGTAAATATACAGAAATGTTGCTACATT 2160
DB 2559 AGGCCAATTGCAGTACAGATCAGCAAACTTGTAAATATACAGAAATGTTGCTACATT 2618
QY 2161 TCTGGGAACGGGGCCGAGGTGAGATAGATACGAGAGTAAAGGTGAGCTTTAGATGAGC 2220
DB 2619 TCTGGGAACGGGGCCGAGGTGAGATAGATACGAGAGTAAAGGTGAGCTTTAGATGAGC 2678
QY 2221 ATGATTAATATGTGGCCGGGGGTGCTTGGCATGACGAGGGTGTATTATGATGATGAGG 2280
DB 2679 ATGATTAATATGTGGCCGGGGGTGCTTGGCATGACGAGGGTGTATTATGATGATGAGG 2738
QY 2281 TTTTCTGGCCCCCAATTTTAAAGGTGATACGGTTTCCGCGCAATACCAACCTTATCCTACAC 2340
DB 2739 TTTTCTGGCCCCCAATTTTAAAGGTGATACGGTTTCCGCGCAATACCAACCTTATCCTACAC 2798
QY 2341 GGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGTGAGAGCCTGGAACCGATGTAAGGTT 2400
DB 2799 GGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGTGAGAGCCTGGAACCGATGTAAGGTT 2858
QY 2401 CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGTGTGTGCTGCCCAAAAGCAGGCT 2460
DB 2859 CGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGTGTGTGCTGCCCAAAAGCAGGCT 2918
QY 2461 TCAATTAAGAAATGCTCTTTGAAAGGTGATCCTTGGGTATCCTGTGAGAGGTGATCCTC 2520
DB 2919 TCAATTAAGAAATGCTCTTTGAAAGGTGATCCTTGGGTATCCTGTGAGAGGTGATCCTC 2978
QY 2521 AGGGTGGCCCAAAATGTGGCTCCGACTGTGTGCTTCAATGATGTAAGAAAGGTGCT 2580
DB 2979 AGGGTGGCCCAAAATGTGGCTCCGACTGTGTGCTTCAATGATGTAAGAAAGGTGCT 3038
QY 2581 GTGATTAAGCAATTAATGTGTATGTGGCACTGCGAGACAGAGGCTCTCAGATGCTGACC 2640
DB 3039 GTGATTAAGCAATTAATGTGTATGTGGCACTGCGAGACAGAGGCTCTCAGATGCTGACC 3098
QY 2641 TGTCTGGAGCGGCACTGTCACTGTGGAAGACATTCGATGACAGCACTCTCGCAG 2700
DB 3099 TGTCTGGAGCGGCACTGTCACTGTGGAAGACATTCGATGACAGCACTCTCGCAG 3158
QY 2701 GCTGTGGCAAGTGTGTGAGCATTAATACATACTGACCGGCTGTCTTGTGATGGGTAAACAG 2760
DB 3159 GCTGTGGCAAGTGTGTGAGCATTAATACATACTGACCGGCTGTCTTGTGATGGGTAAACAG 3218
QY 2761 AGGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCACTAAGATATTGCTTGAAGCCC 2820
DB 3219 AGGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCACTAAGATATTGCTTGAAGCCC 3278
QY 2821 GAGAGCAATGTCCAAGGTGAACCTGAAACGGGGTGTGTGATGATGACATCAATGAAGATCTGAGAG 2880
DB 3279 GAGAGCAATGTCCAAGGTGAACCTGAAACGGGGTGTGTGATGATGACATCAATGAAGATCTGAGAG 3338
QY 2881 GTGTGAGTACGATGAGAACCCGACCAAGGTGACAGACCTGCGAGTGTGGCGGTAAACAT 2940
DB 3339 GTGTGAGTACGATGAGAACCCGACCAAGGTGACAGACCTGCGAGTGTGGCGGTAAACAT 3398
QY 2941 ATTAGGAACCAAGCTGTGTATGCTGATGTGACCCGAGAGCTGAGAGCCCGATCATTGTGTG 3000
DB 3399 ATTAGGAACCAAGCTGTGTATGCTGATGTGACCCGAGAGCTGAGAGCCCGATCATTGTGTG 3458
QY 3001 CTGGGCTGACCCGCGCTGAGTTTGGCTCTGAGCATGAATACAGATTGAG 3052
DB 3459 CTGGGCTGACCCGCGCTGAGTTTGGCTCTGAGCATGAATACAGATTGAG 3510

RESULT 10

US-10-766-307A-4
; Sequence 4, Application US/10766307A
; Publication No. US20040202663A1
; GENERAL INFORMATION:
; APPLICANT: Shanghai Sunway Biotech Co., LTD.
; TITLE OF INVENTION: Treatment for Metastatic Cancer

FILE REFERENCE: 121300.00003
; CURRENT APPLICATION NUMBER: US/10/766,307A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: adenovirus
US-10-766-307A-4

Query Match 100.0%; Score 3052; DB 21; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTGTAGTATTAATATATCCCGGTGAGTTCTCTCAAGAGCCACTTTAGTCCAGCGAGT 60
DB 459 CGTGTAGTATTAATATATCCCGGTGAGTTCTCTCAAGAGCCACTTTAGTCCAGCGAGT 518
QY 61 AGAGTTTCTCTCCGAGCGCTCCGACACCGGAGCTGAATAATGACATTAATCTGCC 120
DB 519 AGAGTTTCTCTCTCCGAGCGCTCCGACACCGGAGCTGAATAATGACATTAATCTGCC 578
QY 121 ACGAGGTGTTATTAACGAAATATGACCGCACTCTTTGACACAGCTGATCGAAGAG 180
DB 579 ACGAGGTGTTATTAACGAAATATGACCGCACTCTTTGACACAGCTGATCGAAGAG 638
QY 181 TACTGGCTGATTAATCTTCCACTCTCTAGCCATTTTGAACCACTTCCCTTACAGAACTGT 240
DB 639 TACTGGCTGATTAATCTTCCACTCTCTAGCCATTTTGAACCACTTCCCTTACAGAACTGT 698
QY 241 ATGATTTAGAAGTGAAGGCCCCGGAAGATCCAAAGAGAGAGCGGTTTCCGAGATTTTTC 300
DB 699 ATGATTTAGAAGTGAAGGCCCCGGAAGATCCAAAGAGAGAGCGGTTTCCGAGATTTTTC 758
QY 301 CCGACTGTATATGTTGCGGTGAGAGAGGATGATTAATCACTTCTTCCGCGGCGC 360
DB 759 CCGACTGTATATGTTGCGGTGAGAGAGGATGATTAATCACTTCTTCCGCGGCGC 818
QY 361 CCGGTTCTCCGAGCGGCTTCACTTCTCCGAGCGCCGAGAGCCGAGAGAGAGCT 420
DB 819 CCGGTTCTCCGAGCGGCTTCACTTCTCCGAGCGCCGAGAGCCGAGAGAGAGCT 878
QY 421 TGGGTCCGGTTTCTATATCCAAACCTTGTACCGAGGTGATGATCTTAACCTGACAGAG 480
DB 879 TGGGTCCGGTTTCTATATCCAAACCTTGTACCGAGGTGATGATCTTAACCTGACAGAG 938
QY 481 CTGGCTTTCAACCCAGTACGACGAGGATGAAGAGGTGAGAGTTTGTGTAGATTATG 540
DB 939 CTGGCTTTCAACCCAGTACGACGAGGATGAAGAGGTGAGAGTTTGTGTAGATTATG 998
QY 541 TGGAGCACCCCGGCAAGGTGTGAGGCTTGTCAATTATCAACCGAGAGAAATACGGGGAGC 600
DB 999 TGGAGCACCCCGGCAAGGTGTGAGGCTTGTCAATTATCAACCGAGAGAAATACGGGGAGC 1058
QY 601 CAGATTAATATGTGTCTTGTGCTATATGAGACCTGTGCATGTTGTCTACAGTAAGT 660
DB 1059 CAGATTAATATGTGTCTTGTGCTATATGAGACCTGTGCATGTTGTCTACAGTAAGT 1118
QY 661 GAAATTAATGAGGAGTGTGATAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
DB 1119 GAAATTAATGAGGAGTGTGATAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1178
QY 721 TTTTACAGTTTGT 780
DB 1179 TTTTACAGTTTGT 1238
QY 781 TGAACCTGAGCTGAGCCGAGCCAGAACCGAGCTGCAAGACCTACCCGCTCTCTAA 840
DB 1239 TGAACCTGAGCTGAGCCGAGCCAGAACCGAGCTGCAAGACCTACCCGCTCTCTAA 1298
QY 841 AATGGCCCTGTATCTGTGAGCGCCGAGATCACTGTGTCTTGAAGATGCAATAGTAG 900

Db 1299 AATGGCGCTGCTATCCTGAGAACCGCCGACATCACCTGTCTAGAGATGCAATAGTAG 1358
Qy 901 TACGGATAGCTGTGACTCCGGTCTTCTTAACACACCTCTGAGATACACCCGGTGTCC 960
Db 1359 TACGGATAGCTGTGACTCCGGTCTTCTTAACACACCTCTGAGATACACCCGGTGTCC 1418
Qy 961 GCTGCGCCCATTAACAGATGGCCGTGAGATGGTGGGGGTGCGGAGGCTGTGGAAATG 1020
Db 1419 GCTGCGCCCATTAACAGATGGCCGTGAGATGGTGGGGGTGCGGAGGCTGTGGAAATG 1478
Qy 1021 TATGAGAGACTTGTCTTAACGAGCCTGGCAACCTTTGACTTGAAGCTTAACGCCGAG 1080
Db 1479 TATGAGAGACTTGTCTTAACGAGCCTGGCAACCTTTGACTTGAAGCTTAACGCCGAG 1538
Qy 1081 GCCATTAAGGTGTAACCTGTGATTCGCTGTGTGTTAACGCTTTGTTTGTCTGAATGAT 1140
Db 1539 GCCATTAAGGTGTAACCTGTGATTCGCTGTGTGTTAACGCTTTGTTTGTCTGAATGAT 1598
Qy 1141 TGATGTAACTTAAATTAAGGGTGAAGATTAATGTTTAACTTGAATGGCGTTAAATGGGGC 1200
Db 1599 TGATGTAACTTAAATTAAGGGTGAAGATTAATGTTTAACTTGAATGGCGTTAAATGGGGC 1658
Qy 1201 GGGGCTTAAAGGGTATATATATGCGCCGTGGCTAATCTTGGTTACATCTGACTGATGGA 1260
Db 1659 GGGGCTTAAAGGGTATATATATGCGCCGTGGCTAATCTTGGTTACATCTGACTGATGGA 1718
Qy 1261 GGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCTAATCTTGTGAAACAGAGCTTAA 1320
Db 1719 GGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCTAATCTTGTGAAACAGAGCTTAA 1778
Qy 1321 CAGTAACCTCTGTTTGGAGAGTTTCTGTGGGGCTCAATCCGAGCAAGTTAGTCTGAG 1380
Db 1779 CAGTAACCTCTGTTTGGAGAGTTTCTGTGGGGCTCAATCCGAGCAAGTTAGTCTGAG 1838
Qy 1381 AATTAAGAGAGATTACAAGTGGAAATTTGAAGACTTTTGAATCTGTGGTGAAGCTTT 1440
Db 1839 AATTAAGAGAGATTACAAGTGGAAATTTGAAGACTTTTGAATCTGTGGTGAAGCTTT 1898
Qy 1441 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCATCAAGACTTTGGA 1500
Db 1899 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAAAGTCATCAAGACTTTGGA 1958
Qy 1501 TTTTTCACACCGGGGCGCGCTGCGGCTGTGCTTTTGAAGTTTAAAGAGATAA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGGCTGTGCTTTTGAAGTTTAAAGAGATAA 2018
Qy 1561 ATGAGCGAAGAAACCATCTGAGCGGGGGGTACTCTGTGATTTTGTGGCATGCACT 1620
Db 2019 ATGAGCGAAGAAACCATCTGAGCGGGGGGTACTCTGTGATTTTGTGGCATGCACT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACACAGAAATCGCTGTGTAATGTTTCTTCCGTCCGCCGCC 1680
Db 2079 GTGAGAGCGGTTGTGAGACACAGAAATCGCTGTGTAATGTTTCTTCCGTCCGCCGCC 2138
Qy 1681 GATTAATCCGACGAGAGACAGACAGACAGAGAGAAAGCCAGCGCGCGCGCAGAGA 1740
Db 2139 GATTAATCCGACGAGAGACAGACAGACAGAGAGAAAGCCAGCGCGCGCGCAGAGA 2198
Qy 1741 GCAAGAGCCATGGAACCGAGAGCGGCTGGAACCTCTGGGAATGAATGTTGTAAGGTG 1800
Db 2199 GCAAGAGCCATGGAACCGAGAGCGGCTGGAACCTCTGGGAATGAATGTTGTAAGGTG 2258
Qy 1801 GCTAACTGTATCCAGAACTGAGACGCAATTTTGAACATTAAGAGAGATGGCAGGGGCTA 1860
Db 2259 GCTAACTGTATCCAGAACTGAGACGCAATTTTGAACATTAAGAGAGATGGCAGGGGCTA 2318
Qy 1861 AAGGGGGTAAAGAGAGAGAGCGGGGGCTTGTAGGTAAAGAGAGAGCTTAAGAACTTACT 1920
Db 2319 AAGGGGGTAAAGAGAGAGAGCGGGGGCTTGTAGGTAAAGAGAGCTTAAGAACTTACT 2378
Qy 1921 TTTAGCTTAATGACAGACACCGTCTGTAGTGTATTAATCTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACAGACACCGTCTGTAGTGTATTAATCTTTCAACAGATCAAGATTAAT 2438

Qy 1981 TGGCTTAATGACTTGAATCTGCTGCCAGAAATTAATTCATAGAGCAGCTGACCACTTAC 2040
Db 2439 TGGCTTAATGACTTGAATCTGCTGCCAGAAATTAATTCATAGAGCAGCTGACCACTTAC 2498
Qy 2041 TGGCTGAGCCAGGGGAGATTTTGAAGAGGCTATTGAGGATATGCAAGAGTGGCACTT 2100
Db 2499 TGGCTGAGCCAGGGGAGATTTTGAAGAGGCTATTGAGGATATGCAAGAGTGGCACTT 2558
Qy 2101 AGGCAAGTTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGAAATTTGTGTACATT 2160
Db 2559 AGGCAAGTTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGAAATTTGTGTACATT 2618
Qy 2161 TCTGGAAACGGGGCCGAGAGTGAAGATAGATACGAGAGATAGGGTCCCTTAATGATGAGC 2220
Db 2619 TCTGGAAACGGGGCCGAGAGTGAAGATAGATACGAGAGATAGGGTCCCTTAATGATGAGC 2678
Qy 2221 ATGATTAATATATGAGCCGGGGGTGCTTGGCAATGGAACGGGGGTGTTATTAAGATGAAG 2280
Db 2679 ATGATTAATATATGAGCCGGGGGTGCTTGGCAATGGAACGGGGGTGTTATTAAGATGAAG 2738
Qy 2281 TTTACTGGCCCAATTTTAAAGCGTACAGTATTTCTTGGCCAAATACCAACTTATCTTACAC 2340
Db 2739 TTTACTGGCCCAATTTTAAAGCGTACAGTATTTCTTGGCCAAATACCAACTTATCTTACAC 2798
Qy 2341 GGTGTAAAGCTTCTATGAGGTTTAAACAATACCTGTGTGAGAGCTGGAACGATGAAGGTT 2400
Db 2799 GGTGTAAAGCTTCTATGAGGTTTAAACAATACCTGTGTGAGAGCTGGAACGATGAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTAACTGTGCTGGAAGGGGGGTGTGTGCCCCCAAAAGAGGGCT 2460
Db 2859 CGGGGCTGTGCTTTTAACTGTGCTGGAAGGGGGGTGTGTGCCCCCAAAAGAGGGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTGTGAAGAGTGTACTTGTGGTATCTGTCTGAGGGTAACTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTGTGAAGAGTGTACTTGTGGTATCTGTCTGAGGGTAACTCC 2978
Qy 2521 AGGGTGCCCAACAATGTGGCTCCGACTGTGTGTTCTTATGCTAGTGAAGAGTGGCT 2580
Db 2979 AGGGTGCCCAACAATGTGGCTCCGACTGTGTGTTCTTATGCTAGTGAAGAGTGGCT 3038
Qy 2581 GTGATTAAGCAATAATGATATGAGCAATGAGGAGACAGGGGCTCTCAGATGCTGACC 2640
Db 3039 GTGATTAAGCAATAATGATATGAGCAATGAGGAGACAGGGGCTCTCAGATGCTGACC 3098
Qy 2641 TGCTGGACGGCAACTGTCACTTGTGAAGACCAATTCAGTACGATGACAGCACTCTGCAAG 2700
Db 3099 TGCTGGACGGCAACTGTCACTTGTGAAGACCAATTCAGTACGATGACAGCACTCTGCAAG 3158
Qy 2701 GCTGGCCAGTGTGTAAGCATATGACCCGCTGTCTTGTGCAATTTGGGTAAACAGG 2760
Db 3159 GCTGGCCAGTGTGTAAGCATATGACCCGCTGTCTTGTGCAATTTGGGTAAACAGG 3218
Qy 2761 AGGGGGGTGTTCCACTTACCAATGCAATTTGAGTGAACCTAAGATATGCTTGAAGGCC 2820
Db 3219 AGGGGGGTGTTCCACTTACCAATGCAATTTGAGTGAACCTAAGATATGCTTGAAGGCC 3278
Qy 2821 GAGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTGTAACAATGACATGAAGATCTGGAAG 2880
Db 3279 GAGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTGTAACAATGACATGAAGATCTGGAAG 3338
Qy 2881 GTGCTGAGTACGATGAGACCCGCAACAGGTGACAGCCCTGCGAGTGTGGCGGTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGACCCGCAACAGGTGACAGCCCTGCGAGTGTGGCGGTAAACAT 3398
Qy 2941 ATTAGGAACAGAGCTGTGATGTGATGTGACCGAGGAGCTGAGGGCCGATCACTTGGTG 3000
Db 3399 ATTAGGAACAGAGCTGTGATGTGATGTGACCGAGGAGCTGAGGGCCGATCACTTGGTG 3458
Qy 3001 CTGGCTTGACCCGCGCTGAGTGTGGCTTACGATGAAGATACAGATTGAG 3052
Db 3459 CTGGCTTGACCCGCGCTGAGTGTGGCTTACGATGAAGATACAGATTGAG 3510

```
RESULT 11
US-10-492-178-8
Sequence 8, Application US/10492178
Publication No. US20040247615A1
GENERAL INFORMATION:
APPLICANT: Emimi, Emilio A.
APPLICANT: Kaskow, David C.
APPLICANT: Bett, Andrew J.
APPLICANT: Shiver, John W.
APPLICANT: Nicolsia, Alfredo
APPLICANT: Lahm, Armin
APPLICANT: Luzago, Alessandra
APPLICANT: Corlese, Riccardo
APPLICANT: Colloca, Stefano
TITLE OF INVENTION: HEPATITIS C VIRUS VACCINE
FILE REFERENCE: ITR0015TP
CURRENT APPLICATION NUMBER: US/10/492,178
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: PCT/US02/32512
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/363,774
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/328,655
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 35935
TYPE: DNA
ORGANISM: Adenovirus serotype 6
US-10-492-178-8

Query Match      100.0%; Score 3052; DB 21; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTGTAGTATTTATATCCCGGTGAGTTCTCAAGAGCCACTCTTGAGTCCAGCAGT 60
DB      459 CGTGTAGTATTTATATCCCGGTGAGTTCTCAAGAGCCACTCTTGAGTCCAGCAGT 518
QY      61 AGAGTTTCTCTCCGAGCGGCTCCGACACCGGGACTGAAATGACATATATCTGCC 120
DB      519 AGAGTTTCTCTCCGAGCGGCTCCGACACCGGGACTGAAATGACATATATCTGCC 578
QY      121 ACGGAGGTATATACGGAAGAAATGCGCGCAGCTTTTGACACAGTGTGAAAGG 180
DB      579 ACGGAGGTATATACGGAAGAAATGCGCGCAGCTTTTGACACAGTGTGAAAGG 638
QY      181 TACTGCTGATATCTTCACTCTAGCCATTTTGAACACACTTACCTTACGACAGT 240
DB      639 TACTGCTGATATCTTCACTCTAGCCATTTTGAACACACTTACCTTACGACAGT 698
QY      241 ATGATTTAGACGTACCGGCCCCGGAAGATCCCAACGAGAGGCGGTTTGGAGATTTTTC 300
DB      699 ATGATTTAGACGTACCGGCCCCGGAAGATCCCAACGAGAGGCGGTTTGGAGATTTTTC 758
QY      301 CCGAGCTGTATATGTTGGCGGTGACGAAAGGATTTGACTTACTACTTTTCCGCGCGGC 360
DB      759 CCGAGCTGTATATGTTGGCGGTGACGAAAGGATTTGACTTACTACTTTTCCGCGCGGC 818
QY      361 CCGGTTCTCCGAGCGGCTTCACTTCCCGGACCCGAGACCGGAGACGAGAGCT 420
DB      819 CCGGTTCTCCGAGCGGCTTCACTTCCCGGACCCGAGACCGGAGACGAGAGCT 878
QY      421 TGGGTCCGTTTCTATGCAAACTTGTATCCGAGGTGATGATCTTACTCTGCCAGAG 480
DB      879 TGGGTCCGTTTCTATGCAAACTTGTATCCGAGGTGATGATCTTACTCTGCCAGAG 938
QY      481 CTGGCTTTTCAACCGAGTACGAGAGATGAAAGGGTGAAGAGGTTGTGTAGATTATG 540
DB      939 CTGGCTTTTCAACCGAGTACGAGAGATGAAAGGGTGAAGAGGTTGTGTAGATTATG 998
```

```
QY      541 TGGAGACCCCGGACGAGTTGACAGTCTTGCTATATCAACCGAGGAATACGGGGAC 600
DB      999 TGGAGACCCCGGACGAGTTGACAGTCTTGCTATATCAACCGAGGAATACGGGGAC 1058
QY      601 CAGATATATATGTTGCTTGTCTATATGAGACCTTGCGATGTTGTCTACAGTAAGT 660
DB      1059 CAGATATATATGTTGCTTGTCTATATGAGACCTTGCGATGTTGTCTACAGTAAGT 1118
QY      661 GAAATTTATGGGAGGTGGTATGAGATGGTGGTGGTGGTATTTTTTTTTTAAT 720
DB      1119 GAAATTTATGGGAGGTGGTATGAGATGGTGGTGGTGGTATTTTTTTTTTAAT 1178
QY      721 TTTTACAGTTTGTGTTTAAAGATTTGTATGATTTTTTTTAAAGTCTGTGTC 780
DB      1179 TTTTACAGTTTGTGTTTAAAGATTTGTATGATTTTTTTTAAAGTCTGTGTC 1238
QY      781 TGAACCTGAGCCTGAGCCGAGCCGAGAACCGGAGCTGCAAGACTTACCCTCTTAA 840
DB      1239 TGAACCTGAGCCTGAGCCGAGCCGAGAACCGGAGCTGCAAGACTTACCCTCTTAA 1298
QY      841 AATGGCGGCTGATCTCTGAGAGCCCGACATCACTGTGCTAGAGAAATGCAATAGTAG 900
DB      1299 AATGGCGGCTGATCTCTGAGAGCCCGACATCACTGTGCTAGAGAAATGCAATAGTAG 1358
QY      901 TACGATAGCTGTGACTCCGCTCTTCTTAAACACACTCTGAGATACACCGGCTGCC 960
DB      1359 TACGATAGCTGTGACTCCGCTCTTCTTAAACACACTCTGAGATACACCGGCTGCC 1418
QY      961 GCTGTGCCCATTTAAACCACTGTCCTGTGAGAGTTGTGGGCGTCCAGGCTGTGAATG 1020
DB      1419 GCTGTGCCCATTTAAACCACTGTCCTGTGAGAGTTGTGGGCGTCCAGGCTGTGAATG 1478
QY      1021 TATCGAGACCTGCTTACACAGCCTGGGCAACCTTTGAGCTGAGCTGTAAACGCCAC 1080
DB      1479 TATCGAGACCTGCTTACACAGCCTGGGCAACCTTTGAGCTGAGCTGTAAACGCCAC 1538
QY      1081 GCCATTAAGTGTAAACCTGTGATTCGTGTGTGTGTAAACGCTTGTGTGTGATGAGT 1140
DB      1539 GCCATTAAGTGTAAACCTGTGATTCGTGTGTGTGTAAACGCTTGTGTGTGATGAGT 1598
QY      1141 TGATGTAACTTTTAAAGGTGATTAATGTTTAACTTGACATGGCTGTAAATGGGGC 1200
DB      1599 TGATGTAACTTTTAAAGGTGATTAATGTTTAACTTGACATGGCTGTAAATGGGGC 1658
QY      1201 GGGGCTTAAAGGATTAATTAAGCGCGTGGGCTAATCTTGTTTCACTGACCTATGGA 1260
DB      1659 GGGGCTTAAAGGATTAATTAAGCGCGTGGGCTAATCTTGTTTCACTGACCTATGGA 1718
QY      1261 GGGTGGAGGTGTTTGAAGATTTTCTGCTGTGCTAATCTTGCTGGAACAGAGCTTAA 1320
DB      1719 GGGTGGAGGTGTTTGAAGATTTTCTGCTGTGCTAATCTTGCTGGAACAGAGCTTAA 1778
QY      1321 CAGTACTCTTGGTTTGAAGGTTTCTGTGGGCTCATCCAGGCAAACTTATGCTGAG 1380
DB      1779 CAGTACTCTTGGTTTGAAGGTTTCTGTGGGCTCATCCAGGCAAACTTATGCTGAG 1838
QY      1381 AATTAAAGAGATTAACAAGTGGGAAATTGAAGACTTTTGAATCCTGTGTGAGCTGTT 1440
DB      1839 AATTAAAGAGATTAACAAGTGGGAAATTGAAGACTTTTGAATCCTGTGTGAGCTGTT 1898
QY      1441 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAGAGTCAACAAGCTTTGGA 1500
DB      1899 TGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAGAGAGAGTCAACAAGCTTTGGA 1958
QY      1501 TTTTTCACACCGGGGGCGGCTGCGGCTGCTGTGCTTTTGAAGTTTATAAAGATTA 1560
DB      1959 TTTTTCACACCGGGGGCGGCTGCGGCTGCTGTGCTTTTGAAGTTTATAAAGATTA 2018
QY      1561 ATGAGCGAAGAAACCATCTGAGCGGGGGTACCTGCTGGAATTTTCTGGCATGCACT 1620
DB      2019 ATGAGCGAAGAAACCATCTGAGCGGGGGTACCTGCTGGAATTTTCTGGCATGCACT 2078
QY      1621 GTGAGAGCGGTTGTGAGACACAAGATCGCTGTACTGTGTCTTCCGTCCGCCGCGC 1680
```


Db 639 TACTGGCTGATATATCTTCACCTCCTAGCCATTTTGAACACACTACCTTCACGAACTGT 698
Qy 241 ATGATTTAGAGTGAACGGCCCCCGAAGATCCCAAGAGAGCGGTTTTCCGAGATTTTTC 300
Db 699 ATGATTTAGAGTGAACGGCCCCCGAAGATCCCAAGAGAGCGGTTTTCCGAGATTTTTC 758
Qy 301 CCGACTCTGATATGTGGCGGTGACAGAAAGGATTTGACTTCACTTTTCCGCGGCGC 360
Db 759 CCGACTCTGATATGTGGCGGTGACAGAAAGGATTTGACTTCACTTTTCCGCGGCGC 818
Qy 361 CCGGTTCTCCGAGCGCCCTCACTTTTCCGCGAGCCCGAGACGCCGAGACAGAGAGCTT 420
Db 819 CCGGTTCTCCGAGCGCCCTCACTTTTCCGCGAGCCCGAGACGCCGAGAGAGAGCTT 878
Qy 421 TGGGTCGGGTTTCTATGCAACCTTGATACGAGAGTATGATCTTACCTGCGACGAGG 480
Db 879 TGGGTCGGGTTTCTATGCAACCTTGATACGAGAGTATGATCTTACCTGCGACGAGG 938
Qy 481 CTGGCTTTCAACCCAGTACGACGAGATGAAAGAGGTGAGAGTTGTGTAGATTATG 540
Db 939 CTGGCTTTCAACCCAGTACGACGAGATGAAAGAGGTGAGAGTTGTGTAGATTATG 998
Qy 541 TGGAGCACCCCGGAGCAGGTTGACAGTCTTGTCAATTACCCGAGAAATACGAGGAGCC 600
Db 999 TGGAGCACCCCGGAGCAGGTTGACAGTCTTGTCAATTACCCGAGAAATACGAGGAGCC 1058
Qy 601 CAGATATTATGTTGCTTGTGCTATATGAGGACCTGAGGCACTGTTTCTACAGTAAGT 660
Db 1059 CAGATATTATGTTGCTTGTGCTATATGAGGACCTGAGGCACTGTTTCTACAGTAAGT 1118
Qy 661 GAAATTTATGGGACAGTGGGTGATAGAGTGTGGGTTTGTGTGTAATTTTTTTTTTAT 720
Db 1119 GAAATTTATGGGACAGTGGGTGATAGAGTGTGGGTTTGTGTGTAATTTTTTTTTTAT 1178
Qy 721 TTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGTCTGTGTC 780
Db 1179 TTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATGTGATTTTTTTTAAAGTCTGTGTC 1238
Qy 781 TGAACCTGAGCTGAGCCGAGCCGAGACCGGAGCTGCAAGACCTACCCCGCTCCAA 840
Db 1239 TGAACCTGAGCTGAGCCGAGCCGAGACCGGAGCTGCAAGACCTACCCCGCTCCAA 1298
Qy 841 AATGGCGCTGCTATCTCTGAGACGCCCGACATCACTGTCTAGAGATGCAATAGTAG 900
Db 1299 AATGGCGCTGCTATCTCTGAGACGCCCGACATCACTGTCTAGAGATGCAATAGTAG 1358
Qy 901 TACGGATAGCTGTGACTCCGGTCTTTCTTAACACACTTCTTGAGATACCCGGTGTCCC 960
Db 1359 TACGGATAGCTGTGACTCCGGTCTTTCTTAACACACTTCTTGAGATACCCGGTGTCCC 1418
Qy 961 GCTGAGCCCATTTAAACAGATTGCGGTGAGAGTTGGTGGGCGTGGCCAGGCTGTGAATG 1020
Db 1419 GCTGAGCCCATTTAAACAGATTGCGGTGAGAGTTGGTGGGCGTGGCCAGGCTGTGAATG 1478
Qy 1021 TATCGAGACTTGTCTTAAAGAGCCTTGGGCAACTTTTGGACTTGGACTTAAACGCCAG 1080
Db 1479 TATCGAGACTTGTCTTAAAGAGCCTTGGGCAACTTTTGGACTTGGACTTAAACGCCAG 1538
Qy 1081 GCCATAAGGTGTAACCTGTGATTGCGTGTGTGTTAACGCCCTTTGTTGCTGAATGAGT 1140
Db 1539 GCCATAAGGTGTAACCTGTGATTGCGTGTGTGTTAACGCCCTTTGTTGCTGAATGAGT 1598
Qy 1141 TGATGTAGTTTAAATTAAGGGGTGAGATATGTTTAACTTGACATGGCGGTTAAATGGGGC 1200
Db 1599 TGATGTAGTTTAAATTAAGGGGTGAGATATGTTTAACTTGACATGGCGGTTAAATGGGGC 1658
Qy 1201 GGGGCTTAAAGGATATATATGCGCGGTGAGCTATCTTGGTTACATCTGACCTCATGGA 1260
Db 1659 GGGGCTTAAAGGATATATATGCGCGGTGAGCTATCTTGGTTACATCTGACCTCATGGA 1718
Qy 1261 GGGCTTGGAGGTGTTGGAAGATTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTCTAA 1320
Db 1719 GGGCTTGGAGGTGTTGGAAGATTTTCTGCTGTGCGTAACTTGTGGAACAGAGCTCTAA 1778

Qy 1221 CAGTACCTTTGTTTTGAGGTTTCTGTGGGCTCATCCAGGCAAAAGTTAGTCTGAG 1380
Db 1779 CAGTACCTTTGTTTTGAGGTTTCTGTGGGCTCATCCAGGCAAAAGTTAGTCTGAG 1838
Qy 1381 AATTAAAGAGATTACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1440
Db 1839 AATTAAAGAGATTACAAGTGGGAATTTGAAGACTTTTGAATCTGTGTGAGCTGTT 1898
Qy 1441 TGATTTCTTTGAATGTGGGTCAACAGCGCTTTTCCAGAGAAAGTCAACAGACTTTGGA 1500
Db 1899 TGATTTCTTTGAATGTGGGTCAACAGCGCTTTTCCAGAGAAAGTCAACAGACTTTGGA 1958
Qy 1501 TTTTTCACACCGGGGCGCGCTGCGGCTGTGCTTTTGTAGTTTATTAAGATTA 1560
Db 1959 TTTTTCACACCGGGGCGCGCTGCGGCTGTGCTTTTGTAGTTTATTAAGATTA 2018
Qy 1561 ATGAGCGAAGAAACCCATCTGAGCGGGGGTACTCTGTGATTTTCTGGCATGCACT 1620
Db 2019 ATGAGCGAAGAAACCCATCTGAGCGGGGGTACTCTGTGATTTTCTGGCATGCACT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACACAGAAATCGCTCTCTACTGTGTCTTCCGTCCGCGGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACACAGAAATCGCTCTCTACTGTGTCTTCCGTCCGCGGC 2138
Qy 1681 GATATATCCGACGAGGAGCAGCAGCAGCAGCAGAGAGAACCGAGCGCGCGCAGAGA 1740
Db 2139 GATATATCCGACGAGGAGCAGCAGCAGCAGCAGAGAGAACCGAGCGCGCGCAGAGA 2198
Qy 1741 GCAGAGCCCATGGAACCCGAGAGCCGCGCTTGACCCCTCGGAAATGAATGTTGTACAGGTG 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCCGCGCTTGACCCCTCGGAAATGAATGTTGTACAGGTG 2258
Qy 1801 GCTGAACCTGATCCAGAACTGAGACGCAATTTTGCAATTACAGAGATGGCAGGGCTTA 1860
Db 2259 GCTGAACCTGATCCAGAACTGAGACGCAATTTTGCAATTACAGAGATGGCAGGGCTTA 2318
Qy 1861 AAGGGGGTAAAGAGAGGCGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT 1920
Db 2319 AAGGGGGTAAAGAGAGGCGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT 2378
Qy 1921 TTTAGCTTAATGACACAGACCCGCTCTGAGTGTATTACTTTTCAACAGATCAAGATTAAT 1980
Db 2379 TTTAGCTTAATGACACAGACCCGCTCTGAGTGTATTACTTTTCAACAGATCAAGATTAAT 2438
Qy 1981 TGGCTTAATGAGCTTGAATCTGCTGGCGCAGAAATTTCCATAGAGCAGCTGACCACTTAC 2040
Db 2439 TGGCTTAATGAGCTTGAATCTGCTGGCGCAGAAATTTCCATAGAGCAGCTGACCACTTAC 2498
Qy 2041 TGGCTGACGCAAGGAGATGATTTTGAAGAGCTATTTAGGGTATATGCAAAAGGTGGACATT 2100
Db 2499 TGGCTGACGCAAGGAGATGATTTTGAAGAGCTATTTAGGGTATATGCAAAAGGTGGACATT 2558
Qy 2101 AGGCGAAGTTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGAAATGTGTCTACATT 2160
Db 2559 AGGCGAAGTTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGAAATGTGTCTACATT 2618
Qy 2161 TCTGGGAAACGGGCGCGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTTGAATGTAGC 2220
Db 2619 TCTGGGAAACGGGCGCGAGGTGAGATAGATACGAGAGATAGGGTGGCTTTTGAATGTAGC 2678
Qy 2221 ATGATTAATATGTGGCGGGGGTCTTGGCAATGAGCAGGGGTGTTATTAATGAATGAAG 2280
Db 2679 ATGATTAATATGTGGCGGGGGTCTTGGCAATGAGCAGGGGTGTTATTAATGAATGAAG 2738
Qy 2281 TTTACTGGCCCAATTTTAAAGCGGTTTCTGTGCAATTAACCACTTATCTTACAC 2340
Db 2739 TTTACTGGCCCAATTTTAAAGCGGTTTCTGTGCAATTAACCACTTATCTTACAC 2798
Qy 2341 GGTGTAGCTTCTATGTGGTTTAAACAATACTGTGTGGAAGCTTGACCGATGAAGGTT 2400
Db 2799 GGTGTAGCTTCTATGTGGTTTAAACAATACTGTGTGGAAGCTTGACCGATGAAGGTT 2858

Qy 2401 CGGGGCTGTGCTTTTAACTGCTGCTGGAAGGGGGTGTGTGCTGCCCCCAAGAGAGGCT 2460
Db 2859 CGGGGCTGTGCTTTTAACTGCTGCTGGAAGGGGGTGTGTGCTGCCCCCAAGAGAGGCT 2918
Qy 2461 TCAATTAAGAAATCCCTTTTGAAGAAGGTACCTTGGGTATCTGTGTGAAGGTAACTCC 2520
Db 2919 TCAATTAAGAAATCCCTTTTGAAGAAGGTACCTTGGGTATCTGTGTGAAGGTAACTCC 2978
Qy 2521 AGGGTGGCCCAATATGTCCTCCGACTGTGTGTCTTCACTAGTGAAGAAAGCTGTGCT 2580
Db 2979 AGGGTGGCCCAATATGTCCTCCGACTGTGTGTCTTCACTAGTGAAGAAAGCTGTGCT 3038
Qy 2581 GTGATTAAGCAATACTGTATGTGTGCAATGCGAGGAGAGAGGGGCTCTCAATGTGAGCC 2640
Db 3039 GTGATTAAGCAATACTGTATGTGTGCAATGCGAGGAGAGAGGGGCTCTCAATGTGAGCC 3098
Qy 2641 TGCTCGAGCGGCAACTGTCACTGTGGAAGCAATTCAGTACGAGGCACTCTCGCAAG 2700
Db 3099 TGCTCGAGCGGCAACTGTCACTGTGGAAGCAATTCAGTACGAGGCACTCTCGCAAG 3158
Qy 2701 GCGTGGCCAGTGTGTGAGCATAACTAGTACCCGCTGTCTTGCATTTGGGTAAACAG 2760
Db 3159 GCGTGGCCAGTGTGTGAGCATAACTAGTACCCGCTGTCTTGCATTTGGGTAAACAG 3218
Qy 2761 AGGGGGGTGTCTTCACTTAACTGCAATGCAATTTGATGCACTTAAGATTTGCTGAGGCC 2820
Db 3219 AGGGGGGTGTCTTCACTTAACTGCAATGCAATTTGATGCACTTAAGATTTGCTGAGGCC 3278
Qy 2821 GAGAGCATGTCTCAAGGTGAACCTGAACGGGGTGTGTGATGATGATGATGATGATGATG 2880
Db 3279 GAGAGCATGTCTCAAGGTGAACCTGAACGGGGTGTGTGATGATGATGATGATGATGATG 3338
Qy 2881 GTGTGAGGTAGTACGATGAGACCCGCAACGAGTGTGAGACCCCTGCAAGTGTGGGTAAACAT 2940
Db 3339 GTGTGAGGTAGTACGATGAGACCCGCAACGAGTGTGAGACCCCTGCAAGTGTGGGTAAACAT 3398
Qy 2941 ATTAGGAACCAAGCTGTGTGATGTGTGATGTGATGATGATGATGATGATGATGATGATG 3000
Db 3399 ATTAGGAACCAAGCTGTGTGATGTGTGATGTGATGATGATGATGATGATGATGATGATG 3458
Qy 3001 CTGGGCTGCAACCCGCGCTGATGATTTGGCTCTAGCGATGAAGATGATGATGATGATG 3052
Db 3459 CTGGGCTGCAACCCGCGCTGATGATTTGGCTCTAGCGATGAAGATGATGATGATGATG 3510

RESULT 13
US-10-433-681-1
; Sequence 1, Application US/10433681
; Publication No. US20040146856A1
; GENERAL INFORMATION:
; APPLICANT: IGGO, RICHARD
; APPLICANT: HOMICKO, KRISTIAN
; APPLICANT: FUERER, KRISTOPHE
; TITLE OF INVENTION: ANTI-NEOPLASTIC AGENTS
; FILE REFERENCE: 604-687
; CURRENT APPLICATION NUMBER: US/10/433, 681
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: PCT/GB02/03211
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: GB 0117198.2
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: Adenovirus type 5
US-10-433-681-1

Query Match 100.0%; Score 3052; DB 24; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTGTAGTATTTTAACTCCGCTGATGTTCTCAAGAGGCCACTTTGATGCTCAGCGAGT 60
Db 459 CGTGTAGTATTTTAACTCCGCTGATGTTCTCAAGAGGCCACTTTGATGCTCAGCGAGT 518
Qy 61 AGAGTTTCTCTCCGAGCGGCTCCGACACCGGGAGTGAATAAGACATATTAATCTGCC 120
Db 519 AGAGTTTCTCTCCGAGCGGCTCCGACACCGGGAGTGAATAAGACATATTAATCTGCC 578
Qy 121 ACGAGGTGTATTAACGAAGAAATGACCGGCACTCTTTTGGACAGCTGATGCAAGAG 180
Db 579 ACGAGGTGTATTAACGAAGAAATGACCGGCACTCTTTTGGACAGCTGATGCAAGAG 638
Qy 181 TACTGGCTGATTAATCTTCACTCTTACCTTTTGAACCACTTACCTTACGAACGT 240
Db 639 TACTGGCTGATTAATCTTCACTCTTACCTTTTGAACCACTTACCTTACGAACGT 698
Qy 241 ATGATTTAGACGTACGAGGCCCGGAGATCCCAACGAGAGAGGGTGTGAGATTTTTC 300
Db 699 ATGATTTAGACGTACGAGGCCCGGAGATCCCAACGAGAGAGGGTGTGAGATTTTTC 758
Qy 301 CCGACTGTATATGTGGCGGTGAGAGAGGATTAATTAATCACTTTTCGCGCGGC 360
Db 759 CCGACTGTATATGTGGCGGTGAGAGAGGATTAATTAATCACTTTTCGCGCGGC 818
Qy 361 CCGGTCTCCGAGACCGCTTCACTTTCCGAGACCGGAGACCGGAGAGAGGCT 420
Db 819 CCGGTCTCCGAGACCGCTTCACTTTCCGAGACCGGAGACCGGAGAGAGGCT 878
Qy 421 TGGGTCCGGTTTCTATGACCAACCTTGAACGAGGTGATGATCTTAACCTGCAACAG 480
Db 879 TGGGTCCGGTTTCTATGACCAACCTTGAACGAGGTGATGATCTTAACCTGCAACAG 938
Qy 481 CTGGCTTTTCAACCGAGTACGACGAGATGAAGAGGTGAGAGTGTGTATTAATATG 540
Db 939 CTGGCTTTTCAACCGAGTACGACGAGATGAAGAGGTGAGAGTGTGTATTAATATG 998
Qy 541 TGAAGCACCCCGGAGACGAGTGTGAGTGTGTATTAATCAACCGAGAAATACGGGGAGC 600
Db 999 TGAAGCACCCCGGAGACGAGTGTGAGTGTGTATTAATCAACCGAGAAATACGGGGAGC 1058
Qy 601 CAGATTAATATGTGTGCTTGTGATTAAGAGACCTGAGGATGTTGTCTACAGTATG 660
Db 1059 CAGATTAATATGTGTGCTTGTGATTAAGAGACCTGAGGATGTTGTCTACAGTATG 1118
Qy 661 GAAATTAATGAGGAGGTGATAGTGTGTGTGTGTGTATTTTATTTTAT 720
Db 1119 GAAATTAATGAGGAGGTGATAGTGTGTGTGTGTGTATTTTATTTTAT 1178
Qy 721 TTTTACGTTTGTGTGTAAAGATTTTGTATGTGATTTTAAAGGTCTGTGTC 780
Db 1179 TTTTACGTTTGTGTGTAAAGATTTTGTATGTATTTTAAAGGTCTGTGTC 1238
Qy 781 TGAACCTGAGGCTGAGGCCGAGAGACCGGAGACCTGCAAGACCTTCCGCTCTAA 840
Db 1239 TGAACCTGAGGCTGAGGCCGAGAGACCGGAGACCTTCCGCTCTAA 1298
Qy 841 AATGGCCCTGTATCTTGAAGCGCCGACATCACTGTGTCTAGAGATGCAATAGTAG 900
Db 1299 AATGGCCCTGTATCTTGAAGCGCCGACATCACTGTGTCTAGAGATGCAATAGTAG 1358
Qy 901 TACGATAGCTGATCTCCGCTCTTTTAAACACCTTCTGAGATCAACCGGTGTGCC 960
Db 1359 TACGATAGCTGATCTCCGCTCTTTTAAACACCTTCTGAGATCAACCGGTGTGCC 1418
Qy 961 GCTGTGCCCATTAACAGATGCGGTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
Db 1419 GCTGTGCCCATTAACAGATGCGGTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1478
Qy 1021 TATCGAGACTGTGTAAACGAGCTGAGCAACCTTTGAGACTGTAAACGCCCCAG 1080
Db 1479 TATCGAGACTGTGTAAACGAGCTGAGCAACCTTTGAGACTGTAAACGCCCCAG 1538
Qy 1081 GCCATTAAGGTATAACCTGTGATTTGCTGTGTGTAAACGCTTTTGTGTCTGATGAGT 1140

Db 1539 GCCATTAAGGTGTAACCTGTGATTCGCTGTGTGTGAACGCTTTGTTGCTGATAGT 1598
Qy 1141 TGATGTAACTTTAAATAAAGGTGAGATATATGTTAACTTGACATGCGCTGTTAAATGGGC 1200
Db 1599 TGATGTAACTTTAAATAAAGGTGAGATATATGTTAACTTGACATGCGCTGTTAAATGGGC 1658
Qy 1201 GGGGCTTAAAGGTATATAAATGCGCGGTGGGCTAATCTTGATTCATCTGACCTCATAAG 1260
Db 1659 GGGGCTTAAAGGTATATAAATGCGCGGTGGGCTAATCTTGATTCATCTGACCTCATAAG 1718
Qy 1261 GGGGCTTAAAGGTATATAAATGCGCGGTGGGCTAATCTTGATTCATCTGACCTCATAAG 1320
Db 1719 GGGGCTTAAAGGTATATAAATGCGCGGTGGGCTAATCTTGATTCATCTGACCTCATAAG 1778
Qy 1321 CAGTACCTCTGTTGTTGAGAGTTTCTGTGGGCTCATCCAGGCAAGTTAGTTCAG 1380
Db 1779 CAGTACCTCTGTTGTTGAGAGTTTCTGTGGGCTCATCCAGGCAAGTTAGTTCAG 1838
Qy 1381 AATTAAAGGAGATTACAAAGTGGAAATTGAAAGCTTTGAAATCTGTGGTGAAGTCT 1440
Db 1839 AATTAAAGGAGATTACAAAGTGGAAATTGAAAGCTTTGAAATCTGTGGTGAAGTCT 1898
Qy 1441 TGATTCCTTTGATCTGAGTCAACAGCGCTTTTCCAAAGAGAGTCAACAAGCTTTGGA 1500
Db 1899 TGATTCCTTTGATCTGAGTCAACAGCGCTTTTCCAAAGAGAGTCAACAAGCTTTGGA 1958
Qy 1501 TTTTTCACACCGGGGGCGGCTGCGGCTGCTGTTGCTTTTGAAGTTTAAAGATTA 1560
Db 1959 TTTTTCACACCGGGGGCGGCTGCGGCTGCTGTTGCTTTTGAAGTTTAAAGATTA 2018
Qy 1561 ATGGAGCAAGAAACCCATCTGAAGCGGGGGTACCTGTGATTTTCTGGCATGCACT 1620
Db 2019 ATGGAGCAAGAAACCCATCTGAAGCGGGGGTACCTGTGATTTTCTGGCATGCACT 2078
Qy 1621 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGTGCTGCTTCCGTCGCGCGGC 1680
Db 2079 GTGAGAGCGGTTGTGAGACACAAGAAATCGCTGTGCTGCTTCCGTCGCGCGGC 2138
Qy 1681 GATTAATACCAACGAGAGACAGCAGCAGCAGCAGAGAGAACCGCGCGCGCAGGA 1740
Db 2139 GATTAATACCAACGAGAGACAGCAGCAGCAGCAGAGAGAACCGCGCGCGCAGGA 2198
Qy 1741 GCAGAGCCCATGGAACCCGAGAGCGGCTGGAACCTCGGGAAATGAATGTTGACAGGT 1800
Db 2199 GCAGAGCCCATGGAACCCGAGAGCGGCTGGAACCTCGGGAAATGAATGTTGACAGGT 2258
Qy 1801 GCTGAACGTATCCAGAACTGAGACGCAATTTTGAACAATTACAGAGATGGCAGGGCTA 1860
Db 2259 GCTGAACGTATCCAGAACTGAGACGCAATTTTGAACAATTACAGAGATGGCAGGGCTA 2318
Qy 1861 AAGGGGTTAAAGAGAGAGCGGGGCTTGTAGGCTACAGAGAGCTAGAAATCTAGCT 1920
Db 2319 AAGGGGTTAAAGAGAGAGCGGGGCTTGTAGGCTACAGAGAGCTAGAAATCTAGCT 2378
Qy 1921 TTTAGCTTAATGACACAGACCGTCTGAGTGTATTACTTTTCAACAGATCAAGGATAT 1980
Db 2379 TTTAGCTTAATGACACAGACCGTCTGAGTGTATTACTTTTCAACAGATCAAGGATAT 2438
Qy 1981 TGGCTTAATGAGCTTGATCTGCTGGCGGAGAAATTCATATAGCAGCTGACCACTTAC 2040
Db 2439 TGGCTTAATGAGCTTGATCTGCTGGCGGAGAAATTCATATAGCAGCTGACCACTTAC 2498
Qy 2041 TGGCTGACGCAAGGGGATGATTTTGAAGAGCTATATAGGATATGCAAAAGTGCACCT 2100
Db 2499 TGGCTGACGCAAGGGGATGATTTTGAAGAGCTATATAGGATATGCAAAAGTGCACCT 2558
Qy 2101 AGGCAAGATTCAAGTACAAAGTCAAGAACTTGTAAATATCAGAAATGTTGCTACATT 2160
Db 2559 AGGCAAGATTCAAGTACAAAGTCAAGAACTTGTAAATATCAGAAATGTTGCTACATT 2618
Qy 2161 TCTGGGAAACGGGGCCGAGGTGGAATGATACGAGATAGGCTTTAGATGAGC 2220

Db 2619 TCTGGGAAACGGGGCCGAGGTGGAATGATACGAGATAGGCTTGTAGATGAGC 2678
Qy 2221 ATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAACGGGGTGTATATATGATTAAG 2280
Db 2679 ATGATTAATATGTGGCCGGGGGTGCTTGGCATGGAACGGGGTGTATATATGATTAAG 2738
Qy 2281 TTTACTGGCCCAATTTTAAAGGATGAGGTTTCTGTGGCAATACCACTTATCTTACAC 2340
Db 2739 TTTACTGGCCCAATTTTAAAGGATGAGGTTTCTGTGGCAATACCACTTATCTTACAC 2798
Qy 2341 GGTGTAAGCTTATATGAGTTTAAACAATACCTGTGTGGAAGCTGAGACGATGAAGGTT 2400
Db 2799 GGTGTAAGCTTATATGAGTTTAAACAATACCTGTGTGGAAGCTGAGACGATGAAGGTT 2858
Qy 2401 CCGGGCTGTGCTTTTACTGCTGCTGGAAGGGGTGTGTGTGCGCCCAAAAGCAGGCT 2460
Db 2859 CCGGGCTGTGCTTTTACTGCTGCTGGAAGGGGTGTGTGTGCGCCCAAAAGCAGGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTTGAAAGGTTACCTTGGGATCCTGTGAGGGTAACTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTTGAAAGGTTACCTTGGGATCCTGTGTGAGGGTAACTCC 2978
Qy 2521 AGGGTGGCCCAAAATGTGGCTCCGACTGTGTGCTTCAATGCTAATGAAAAAGGTGCT 2580
Db 2979 AGGGTGGCCCAAAATGTGGCTCCGACTGTGTGCTTCAATGCTAATGAAAAAGGTGCT 3038
Qy 2581 GTATTAAGCATTAACATGTATGTGCAATGCGAGAGACAGGGCTCTCAATGTCTGACC 2640
Db 3039 GTATTAAGCATTAACATGTATGTGCAATGCGAGACAGGGCTCTCAATGTCTGACC 3098
Qy 2641 TGCTCGAGCGCACTGCACTGCTGAAAGCACTTACAGTACAGCAGCAGCACTTCGCAAG 2700
Db 3099 TGCTCGAGCGCACTGCACTGCTGAAAGCACTTACAGTACAGCAGCAGCACTTCGCAAG 3158
Qy 2701 GCTGGCCAGTGTGAGCATTAACATGACCCGCTGTTCCTTGCATTTGGTAAACAG 2760
Db 3159 GCTGGCCAGTGTGAGCATTAACATGACCCGCTGTTCCTTGCATTTGGTAAACAG 3218
Qy 2761 AGGGGGTGTTCCTTACCTTACCAATGCAATTTGATGACACCTAATGATTTGCTGAGCC 2820
Db 3219 AGGGGGTGTTCCTTACCTTACCAATGCAATTTGATGACACCTAATGATTTGCTGAGCC 3278
Qy 2821 GAGAGCATGTCCAAAGTGAACCTGAACGGGGTGTGATGATGACATGAAATCTGGAAG 2880
Db 3279 GAGAGCATGTCCAAAGTGAACCTGAACGGGGTGTGATGATGACATGAAATCTGGAAG 3338
Qy 2881 GTGCTGAGTACGATGAGACCCGACCAAGGTGCAGACCTGCGAGTGTGGCGTAAACAT 2940
Db 3339 GTGCTGAGTACGATGAGACCCGACCAAGGTGCAGACCTGCGAGTGTGGCGTAAACAT 3398
Qy 2941 ATTAGGAACCAAGCTGTGATGCTGGAATGTGACCGAGAGAGCTGAAGCCGATCACTGGTG 3000
Db 3399 ATTAGGAACCAAGCTGTGATGCTGGAATGTGACCGAGAGAGCTGAAGCCGATCACTGGTG 3458
Qy 3001 CTGGCTGCAACCCGCTGATTTGGCTTACGATGAAGATACAGATTGAG 3052
Db 3459 CTGGCTGCAACCCGCTGATTTGGCTTACGATGAAGATACAGATTGAG 3510

RESULT 14
US-10-612-285-1
; Sequence 1, Application US/10612285
; Publication No. US20050175589A1
; GENERAL INFORMATION:
; APPLICANT: IGGO, RICHARD DEREK
; APPLICANT: FUEHER, CHRISTOPHE
; APPLICANT: HOMICKO, KRISTIAN GYULA
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILE REFERENCE: 604-689
; CURRENT APPLICATION NUMBER: US/10/612,285
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10/433,681
; PRIOR FILING DATE: 2003-06-04

Db 2379 TTATAGTTAATGACAGACCGTCTGATGTATTAATCTTTCAACAGATCAAGATATAT 2438
Qy 1981 TGGCCTAATGAGCTTGTATCTGCTGGCCGAGAAAGTATTCATAGAGCAGCTGACCATTTAC 2040
Db 2439 TGCCCTAATGAGCTTGTATCTGCTGGCCGAGAAAGTATTCATAGAGCAGCTGACCATTTAC 2498
Qy 2041 TGGCTGACGACGAGGAGATGATTTTGAAGAGGCTATTAGGATATATGCAAGAGTGCACTT 2100
Db 2499 TGGCTGACGACGAGGAGATGATTTTGAAGAGGCTATTAGGATATATGCAAGAGTGCACTT 2558
Qy 2101 AGGCCAAGTTCAGATACAGATACAGAACTTGTAAATATACAGAAATTTGTTCTACATT 2160
Db 2559 AGGCCAAGTTCAGATACAGATACAGAACTTGTAAATATACAGAAATTTGTTCTACATT 2618
Qy 2161 TCTGGGAAACGGGGCCGAGGTGAGATAGATACGAGATAGAGGTGGCTTAAAGATAGAC 2220
Db 2619 TCTGGGAAACGGGGCCGAGGTGAGATAGATACGAGATAGAGGTGGCTTAAAGATAGAC 2678
Qy 2221 ATGATAAATATGTGGCCGAGGTGCTTGGCATGACGAGGTGTTATTAATGATGTAAG 2280
Db 2679 ATGATAAATATGTGGCCGAGGTGCTTGGCATGACGAGGTGTTATTAATGATGTAAG 2738
Qy 2281 TTTAAGTGGCCCAATTTTAAAGCGGTATTCCTGGCCAAATACCAACTTATCTTACAC 2340
Db 2739 TTTAAGTGGCCCAATTTTAAAGCGGTATTCCTGGCCAAATACCAACTTATCTTACAC 2798
Qy 2341 GGTTAAGCTTCTAATGAGTTTAAACAATACCTGTGTGAGAGCTGAGACGATGTAAGGTT 2400
Db 2799 GGTTAAGCTTCTAATGAGTTTAAACAATACCTGTGTGAGAGCTGAGACGATGTAAGGTT 2858
Qy 2401 CGGGGCTGTGCTTTTAACTGCTGTGAGAGGGGTGTGTGCTGCCCCCAAAAGAGGAGCT 2460
Db 2859 CGGGGCTGTGCTTTTAACTGCTGTGAGAGGGGTGTGTGCTGCCCCCAAAAGAGGAGCT 2918
Qy 2461 TCAATTAAGAAATGCTCTTTGAAAGGTGATCTTGGGTATCTGTGTGAGGATTAAGCTCC 2520
Db 2919 TCAATTAAGAAATGCTCTTTGAAAGGTGATCTTGGGTATCTGTGTGAGGATTAAGCTCC 2978
Qy 2521 AGGGTGGCCCAATGAGTGGCTCCGACGTGTGTTGCTTCAATGATGTAAGAGGAGGCT 2580
Db 2979 AGGGTGGCCCAATGAGTGGCTCCGACGTGTGTTGCTTCAATGATGTAAGAGGAGGCT 3038
Qy 2581 GTGATTAAGCATTAATGATGTGTGCAACTGCGAGACAGAGGCTCTCAGATCTGAC 2640
Db 3039 GTGATTAAGCATTAATGATGTGTGCAACTGCGAGACAGAGGCTCTCAGATCTGAC 3098
Qy 2641 TGCTCGAGCGGCACTGTCACTGTGTAAGACCAATTCAGTACGACGACCTCTTCGCAAG 2700
Db 3099 TGCTCGAGCGGCACTGTCACTGTGTAAGACCAATTCAGTACGACGACCTCTTCGCAAG 3158
Qy 2701 GCGTGGCCAGTGTGAGCATTAATGATGACCGGCTGCTTGGCATTTGGGATTAACAG 2760
Db 3159 GCGTGGCCAGTGTGAGCATTAATGATGACCGGCTGCTTGGCATTTGGGATTAACAG 3218
Qy 2761 AGGGGGGTGTCTTAACCTTAACCAATGCAATTTGAGTCACTAAGATATTTCTTGAAGCC 2820
Db 3219 AGGGGGGTGTCTTAACCTTAACCAATGCAATTTGAGTCACTAAGATATTTCTTGAAGCC 3278
Qy 2821 GAGAGCATGTCAAGAGTGAACCTGAACGGGGTGTGTCATGACATGACATGAAAGATCTGGAAG 2880
Db 3279 GAGAGCATGTCAAGAGTGAACCTGAACGGGGTGTGTCATGACATGAAAGATCTGGAAG 3338
Qy 2881 GTGCTGAGGTGAGTGAACCGGACCGAGTGAAGACCTGTGAGTGTGGGATTAACAT 2940
Db 3339 GTGCTGAGGTGAGTGAACCGGACCGAGTGAAGACCTGTGAGTGTGGGATTAACAT 3398
Qy 2941 ATTAGGAACCAAGCTGTGATCTGATGTGACCGAGAGCTGAGGCCGATCACTTGGTGT 3000
Db 3399 ATTAGGAACCAAGCTGTGATCTGATGTGACCGAGAGCTGAGGCCGATCACTTGGTGT 3458
Qy 3001 CTGGCCCTGACACCGCGCTGAGTTGGCTTAAGCATGAAATTAACATTTGAG 3052
Db 3459 CTGGCCCTGACACCGCGCTGAGTTGGCTTAAGCATGAAATTAACATTTGAG 3510

RESULT 15
US-10-794-514A-732
; Sequence 732, Application US/10794514A
; Publication No. US20050112134A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas
; APPLICANT: Laus, Reiner
; APPLICANT: Diegel, Michael
; TITLE OF INVENTION: Compositions and Methods Employing Alternative of
; TITLE OF INVENTION: Reading Frame Polypeptides for the Treatment of
; FILE REFERENCE: 11311.1003U
; CURRENT APPLICATION NUMBER: US/10/794,514A
; NUMBER OF SEQ ID NOS: 733
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 732
; LENGTH: 35938
; TYPE: DNA
; ORGANISM: Adeno Virus
US-10-794-514A-732
Query Match 100.0%; Score 3052; DB 22; Length 35938;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTGTAGTATTAATTAACCCGGTGAAGTTCCTCAAGAGGCCACTTGTAGTCCAGAGT 60
Db 459 CGTGTAGTATTAATTAACCCGGTGAAGTTCCTCAAGAGGCCACTTGTAGTCCAGAGT 518
Qy 61 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAATATGACATTTATCTGCC 120
Db 519 AGAGTTTCTCTCCGAGCCGCTCCGACACCGGAGCTGAAATATGACATTTATCTGCC 578
Qy 121 ACGAGGTGTTATTAACGGAAGAAATGCGCGCAGTCTTTTGAACAGCTGATCGAAGG 180
Db 579 ACGAGGTGTTATTAACGGAAGAAATGCGCGCAGTCTTTTGAACAGCTGATCGAAGG 638
Qy 181 TACTGCTGATTAATCTTCAACTCTTCAAGCAATTTGAACCACTTACCGAAGCTGT 240
Db 639 TACTGCTGATTAATCTTCAACTCTTCAAGCAATTTGAACCACTTACCGAAGCTGT 698
Qy 241 ATGATTTAGACGTGACGCGCCCGGAAGATCCCAACGAGAGGCGGTTTGGAGATTTTC 300
Db 699 ATGATTTAGACGTGACGCGCCCGGAAGATCCCAACGAGAGGCGGTTTGGAGATTTTC 758
Qy 301 CCGACTCTGTATGTGGCGGTGACGAGAGGATTAAGTCACTTTTCCGCGGCGC 360
Db 759 CCGACTCTGTATGTGGCGGTGACGAGAGGATTAAGTCACTTTTCCGCGGCGC 818
Qy 361 CCGGTTCTCCGAGCCGCTCACTTTTCCGCGAGCCCGAGACCGGAGAGAGGCT 420
Db 819 CCGGTTCTCCGAGCCGCTCACTTTTCCGCGAGCCCGAGAGCGGAGAGGCT 878
Qy 421 TGGGTCCGTTTCTATGACCAAACTTGTACCGGAGGTGATGATCTTACCTGCCACGAG 480
Db 879 TGGGTCCGTTTCTATGACCAAACTTGTACCGGAGGTGATGATCTTACCTGCCACGAG 938
Qy 481 CTGGCTTTCACCAAGTGAAGAGGATGAGAGGATGAGAGTGTGTGATTAATG 540
Db 939 CTGGCTTTCACCAAGTGAAGAGGATGAGAGGATGAGAGTGTGTGATTAATG 998
Qy 541 TGGAGACCCCGGAGCAGGTTGACAGTCTTGTCAATTAACCGAGAGAAATACGGGGAGC 600
Db 999 TGGAGACCCCGGAGCAGGTTGACAGTCTTGTCAATTAACCGAGAGAAATACGGGGAGC 1058
Qy 601 CAGATATTATGTGTGCTTGTCTATATGAGACCTGTGGCATTTGTCTACAGTAACT 660
Db 1059 CAGATATTATGTGTGCTTGTCTATATGAGACCTGTGGCATTTGTCTACAGTAACT 1118

QY 661 GAAATTTATGGGCACTGAGTATAGAGTGTGGTTTGGTGGTAATTTTTTTTAAAT 720
Db 1119 GAAATTTATGGGCACTGAGTATAGAGTGTGGTTTGGTGGTAATTTTTTTTAAAT 1178
QY 721 TTTTACAGTTTTTGAGTTTAAAGAAATTTTGTATTGTGATTTTTTTTAAAGGTCGTC 780
Db 1179 TTTTACAGTTTTTGAGTTTAAAGAAATTTTGTATTGTGATTTTTTTTAAAGGTCGTC 1238
QY 781 TGAACCTGAGCTTGAAGCCGAGCCAGAAACCGAGCCTGCAAGACTACCCGCGCTCTAA 840
Db 1239 TGAACCTGAGCTTGAAGCCGAGCCAGAAACCGAGCCTGCAAGACTACCCGCGCTCTAA 1298
QY 841 AATGGCCCGCTGCTATCCTGAGAACGCCGCAATCACTGTGTCTAGAGAAATGCAATAGTAG 900
Db 1299 AATGGCCCGCTGCTATCCTGAGAACGCCGCAATCACTGTGTCTAGAGAAATGCAATAGTAG 1358
QY 901 TACGATAGCTGTGACTCCGGCTCTTCTAACACACTCTGAGATACACCCGGTGTCTCC 960
Db 1359 TACGATAGCTGTGACTCCGGCTCTTCTAACACACTCTGAGATACACCCGGTGTCTCC 1418
QY 961 GCTGTGCCCATTTAAACCAAGTTCGCTGAGAGTGTGTGGCGCTGCGCAAGCTGTGAAATG 1020
Db 1419 GCTGTGCCCATTTAAACCAAGTTCGCTGAGAGTGTGTGGCGCTGCGCAAGCTGTGAAATG 1478
QY 1021 TATCGAGAGACTTGTCTTAAACGAGCCTGGGCAACCTTTGGAATTGAGCTTAAACGCCCTAG 1080
Db 1479 TATCGAGAGACTTGTCTTAAACGAGCCTGGGCAACCTTTGGAATTGAGCTTAAACGCCCTAG 1538
QY 1081 GGCATTAAGGTAAACCTGTGATTGCGTGTGTGTGTTAACGCTTTGTTGTGATGATAGT 1140
Db 1539 GGCATTAAGGTAAACCTGTGATTGCGTGTGTGTGTTAACGCTTTGTTGTGATGATAGT 1598
QY 1141 TGAATGTAAGTTTAAATAAGGTGAGATATATGTTTAACTTGATGGCGTGTAAATGGGGC 1200
Db 1599 TGAATGTAAGTTTAAATAAGGTGAGATATATGTTTAACTTGATGGCGTGTAAATGGGGC 1658
QY 1201 GGGGCTTAAAGGTAATATATATGCGCCGTGGGCTAATCTTGGTTACATGTGACTGATGGA 1260
Db 1659 GGGGCTTAAAGGTAATATATATGCGCCGTGGGCTAATCTTGGTTACATGTGACTGATGGA 1718
QY 1261 GGGTGGGAGTGTGGAAGATTTTTTCTGTGTGGGTAACTTGCTGGAACAGAGCTCTAA 1320
Db 1719 GGGTGGGAGTGTGGAAGATTTTTTCTGTGTGGGTAACTTGCTGGAACAGAGCTCTAA 1778
QY 1321 CAGTACCTTGTGTTTGTGAGAGTTCGTGTGGGCTCATCCAGGCAAAAGTTAGTCTGAG 1380
Db 1779 CAGTACCTTGTGTTTGTGAGAGTTCGTGTGGGCTCATCCAGGCAAAAGTTAGTCTGAG 1838
QY 1381 AATTAAAGAGATTTACAAAGTGGGAATTTGAAGAGCTTTTGAATTCCTGTGTGAGCTGTT 1440
Db 1839 AATTAAAGAGATTTACAAAGTGGGAATTTGAAGAGCTTTTGAATTCCTGTGTGAGCTGTT 1898
QY 1441 TGATTTCTTTGAATCTGGGTCAACAGCGCTTTTCCAAAGAAAGTCAATCAAGACTTTGGA 1500
Db 1899 TGATTTCTTTGAATCTGGGTCAACAGCGCTTTTCCAAAGAAAGTCAATCAAGACTTTGGA 1958
QY 1501 TTTTTCACACACCGGGGGCGGTGCGGCTGTGTTGCTTTTGAAGTTTATTAAGGAATA 1560
Db 1959 TTTTTCACACACCGGGGGCGGTGCGGCTGTGTTGCTTTTGAAGTTTATTAAGGAATA 2018
QY 1561 ATGAGAGGAAGAAACCCATCTGAGAGGGGGGTAATCTGCTGGAATTTTCTGGGCAATGATCT 1620
Db 2019 ATGAGAGGAAGAAACCCATCTGAGAGGGGGGTAATCTGCTGGAATTTTCTGGGCAATGATCT 2078
QY 1621 GTGAGAGCGGTTGTGAGACAACAAGATCGGCTGTACTGTGTCTTCCGTCGCCCGGCG 1680
Db 2079 GTGAGAGCGGTTGTGAGACAACAAGATCGGCTGTACTGTGTCTTCCGTCGCCCGGCG 2138
QY 1681 GATTAATACCGACGAGAGACAGACAGACAGAGAGAGCCAGCGCGGCGGACAGGA 1740
Db 2139 GATTAATACCGACGAGAGACAGACAGACAGAGAGAGCCAGCGCGGCGGACAGGA 2198
QY 1741 GCAAGGCCCATGGAACCGGAGAGCGGCTGGAACCTCGGGAATGAATGTTGTACAGGTG 1800

Db 2199 GCAAGGCCCATGGAACCGGAGAGCGGCTGTGACCTCGGGAATGAATGTTGTACAGGTG 2258
QY 1801 GCTGAACGTATCCAGAACTGAGACGATTTTGAACAATTAACAGAGATGGGACAGGGCTTA 1860
Db 2259 GCTGAACGTATCCAGAACTGAGACGATTTTGAACAATTAACAGAGATGGGACAGGGCTTA 2318
QY 1861 AAGGGGGTAAAGAGAGACCGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT 1920
Db 2319 AAGGGGGTAAAGAGAGACCGGGGGCTTGTGAGGCTACAGAGAGGCTAGGAATCTAGCT 2378
QY 1921 TTTAGCTTAATGACACAGACCCGCTGAGGTATTTCTTTCAACAGATCAAGGAATAT 1980
Db 2379 TTTAGCTTAATGACACAGACCCGCTGAGGTATTTCTTTCAACAGATCAAGGAATAT 2438
QY 1981 TGGCCTAATGAGCTTGAATCTGCTGGCGAGAAATTTCCATAGAGACGCTGACACTTAC 2040
Db 2439 TGGCCTAATGAGCTTGAATCTGCTGGCGAGAAATTTCCATAGAGACGCTGACACTTAC 2498
QY 2041 TGGCTGACCCAGGGGATGATTTTGAAGAGCTATTTAGGTAATTCGAAAGGTGCACTT 2100
Db 2499 TGGCTGACCCAGGGGATGATTTTGAAGAGCTATTTAGGTAATTCGAAAGGTGCACTT 2558
QY 2101 AGGCAAGTTGCAAGTACAGAACTGTAAATATCAGGAATGTTGCTACATT 2160
Db 2559 AGGCAAGTTGCAAGTACAGAACTGTAAATATCAGGAATGTTGCTACATT 2618
QY 2161 TCTGGAAACGGGGCGGAGGTGAGATAGATACGAGAGTAAAGGTGAGCTTTAGATAGTAC 2220
Db 2619 TCTGGAAACGGGGCGGAGGTGAGATAGATACGAGAGTAAAGGTGAGCTTTAGATAGTAC 2678
QY 2221 ATGATTAATATGTGACCGGGGGTCTTGGCATGGAACGGGGTGTATTATGAATGTAAG 2280
Db 2679 ATGATTAATATGTGACCGGGGGTCTTGGCATGGAACGGGGTGTATTATGAATGTAAG 2738
QY 2281 TTTTATGGCCCCCAATTTTAAAGGTAACGGTTTCCGTGGCAATACCAACCTTATGCTAAC 2340
Db 2739 TTTTATGGCCCCCAATTTTAAAGGTAACGGTTTCCGTGGCAATACCAACCTTATGCTAAC 2798
QY 2341 GGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGTGAAAGCTGGAACGATGAAGGTT 2400
Db 2799 GGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGTGAAAGCTGGAACGATGAAGGTT 2858
QY 2401 CGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGTGTCCGCCCAAAAGCAGGCT 2460
Db 2859 CGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGTGTGTCCGCCCAAAAGCAGGCT 2918
QY 2461 TCAATTTAAAGAAATGCTCTTTGAAGAGGTACCTTGGGTATCCTGTGAGGGTAACTCC 2520
Db 2919 TCAATTTAAAGAAATGCTCTTTGAAGAGGTACCTTGGGTATCCTGTGAGGGTAACTCC 2978
QY 2521 AGGGTGGCCCAATATGTGGCTCCGACTGTGTGTTGCTTCAATGATGTAAGAAAGCTGCT 2580
Db 2979 AGGGTGGCCCAATATGTGGCTCCGACTGTGTGTTGCTTCAATGATGTAAGAAAGCTGCT 3038
QY 2581 GTGATTAAGCATTAACATGTGTGGAATGTGGAATGTGGAAGACAGGGCTCTCAATGTCTAAC 2640
Db 3039 GTGATTAAGCATTAACATGTGTGGAATGTGGAATGTGGAAGACAGGGCTCTCAATGTCTAAC 3098
QY 2641 TGGCTGGAACGGCACTGTCACTGTGGAAGACATTCACGTAGGCAAGCACTCTGCAAG 2700
Db 3099 TGGCTGGAACGGCACTGTCACTGTGGAAGACATTCACGTAGGCAAGCACTCTGCAAG 3158
QY 2701 GCTGTGGCCAGTGTTTGAGCATTAATATCTGACCCGCTGTCTTGTGAGTTGGGTAAACAG 2760
Db 3159 GCTGTGGCCAGTGTTTGAGCATTAATATCTGACCCGCTGTCTTGTGAGTTGGGTAAACAG 3218
QY 2761 AGGGGGGTGTTCTTACTTACATTCGAATTTGAGTCACTTAAGATTTGCTTGAAGCCC 2820
Db 3219 AGGGGGGTGTTCTTACTTACATTCGAATTTGAGTCACTTAAGATTTGCTTGAAGCCC 3278
QY 2821 GAGAGCATGTCCAGAGGTGAACCTGAACGGGGGTGTTTGAATGATCAATGAAGATCTGGAAG 2880

```
Db      3279 GAGAGCATGTCCAAGTGAACCTGAACGGGGTGTTTGACATGACCATGAAGATCTGGAG 3338
Qy      2881 |G|G|C|T|G|A|G|T|A|C|G|A|T|G|A|G|A|C|C|C|G|A|C|C|G|A|G|T|G|C|G|A|G|T|G|G|G|G|T|A|A|C|A|T| 2940
Db      3339 |G|T|G|C|T|G|A|G|T|A|C|G|A|T|G|A|G|A|C|C|G|A|C|C|G|A|G|T|G|C|G|A|G|T|G|G|G|G|T|A|A|C|A|T| 3398
Qy      2941 |A|T|T|A|G|A|A|C|C|A|G|C|C|T|G|A|T|G|C|T|G|A|T|G|T|G|A|C|C|G|A|G|A|G|C|T|G|A|G|G|C|C|G|A|T|C|A|C|T|T|G|G|T|G| 3000
Db      3399 |A|T|T|A|G|A|A|C|C|A|G|C|C|T|G|A|T|G|C|T|G|A|T|G|T|G|A|C|C|G|A|G|A|G|C|T|G|A|G|G|C|C|G|A|T|C|A|C|T|T|G|G|T|G| 3458
Qy      3001 |C|T|G|G|C|C|T|G|C|A|C|C|C|G|C|G|C|T|G|A|G|T|T|G|G|C|T|T|A|G|C|G|A|T|G|A|G|T|A|C|A|G|A|T|T|G|A|G| 3052
Db      3459 |C|T|G|G|C|C|T|G|C|A|C|C|C|G|C|G|C|T|G|A|G|T|T|G|G|C|T|T|A|G|C|G|A|T|G|A|G|T|A|C|A|G|A|T|T|G|A|G| 3510
```

Search completed: October 28, 2005, 11:35:22
Job time : 8988 secs

QY	1	A	T	C	G	A	T	C	T	T	A	C	T	G	C	A	G	A	G	G	T	T	T	C	A	C	C	A	C	T	A	G	A	G	G	T	A	A	G	G	T		60
Db	401	A	T	C	G	A	T	C	T	T	A	C	T	G	C	A	G	A	G	G	T	T	T	C	A	C	C	A	C	T	A	G	A	G	G	T	A	A	G	G	T	460	

QY 61 GAGAGTTTGTAGATTATGTGAGGACCCCGGCGACGGTTCAGGTCCTTGTCATTAT 120
| | | | |
Db 461 GAGAGTTTGTGTAGATTATGTGAGGACCCCGGCGACGGTTCAGGTCCTTGTCATTAT 520
| | | | |
QY 121 CACCGAGGAATACGGGGGACCCAGATATATGTGTGCTTTGCTATATAGAGACCTGT 180
| | | | |
Db 521 CACCGAGGAATACGGGGGACCCAGATATATGTGTGCTTTGCTATATAGAGACCTGT 580
| | | | |
QY 181 GGCAGTTTGTCTACAGTAAGTGAATAATATGAGGAGTGTATAGATGTGTGTG 240
| | | | |
Db 581 GGCAGTTTGTCTACAGTAAGTGAATAATATGAGGAGTGTATAGATGTGTGTG 640
| | | | |
QY 241 GTGTGTATATTTTATTTTATTTTACAGTTTGTGTGTTAAAGAAATTTGTATTTGA 300
| | | | |
Db 641 GTGTGTATATTTTATTTTATTTTACAGTTTGTGTGTTAAAGAAATTTGTATTTGA 700
| | | | |
QY 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGAGCCTG 360
| | | | |
Db 701 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGAGCCTG 760
| | | | |
QY 361 CAAGACCTACCCGCGCTCTAAATATGAGGCGCTGCTATCTGAGACGCCGACATCACTG 420
| | | | |
Db 761 CAAGACCTACCCGCGCTCTAAATATGAGGCGCTGCTATCTGAGACGCCGACATCACTG 820
| | | | |
QY 421 TGTCTAGAAATGCAATAGTAGTACGATAGCTGTGACTCCGTCCTTCTAACACACTC 480
| | | | |
Db 821 TGTCTAGAAATGCAATAGTAGTACGATAGCTGTGACTCCGTCCTTCTAACACACTC 880
| | | | |
QY 481 CTGAGATACACCCGGTGTCCCGCTGTGTCCTCAATTAACAGTTGCCGTGAGAGTTG 540
| | | | |
Db 881 CTGAGATACACCCGGTGTCCCGCTGTGTCCTCAATTAACAGTTGCCGTGAGAGTTG 940
| | | | |
QY 541 GGGCGCGCAGGCTGTGGAATGTATCGAGGACTTGCTTAAGAGCTGGGACACTTTGG 600
| | | | |
Db 941 GGGCGCGCAGGCTGTGGAATGTATCGAGGACTTGCTTAAGAGCTGGGACACTTTGG 1000
| | | | |
QY 601 ACTTGAGCTGTAAACGCCCGACAGCCATAGAGTGTAAACCTGTGATGGCTGTGTGTTAA 660
| | | | |
Db 1001 ACTTGAGCTGTAAACGCCCGACAGCCATAGAGTGTAAACCTGTGATGGCTGTGTGTTAA 1060
| | | | |
QY 661 CGCCTTTGTTTGTGGAATGAGTTGATGTAACTTTAATAAGGCTGAGATTAATGTTTAACT 720
| | | | |
Db 1061 CGCCTTTGTTTGTGGAATGAGTTGATGTAACTTTAATAAGGCTGAGATTAATGTTTAACT 1120
| | | | |
QY 721 TGCATGCGGTGTAAATGGGCGGGGCTTAAAGGATATATATGCGCGTGGCTAATCT 780
| | | | |
Db 1121 TGCATGCGGTGTAAATGGGCGGGGCTTAAAGGATATATATGCGCGCTAATCT 1180
| | | | |
QY 781 TGTGTTACATCTGACCTCATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGCTA 840
| | | | |
Db 1181 TGTGTTACATCTGACCTCATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGCTA 1240
| | | | |
QY 841 ACTTGCTGGAACAGAGCTTAAACGATACCTCTGTGTTTGGAGGTTTCTGTGGGCTCAT 900
| | | | |
Db 1241 ACTTGCTGGAACAGAGCTTAAACGATACCTCTGTGTTTGGAGGTTTCTGTGGGCTCAT 1300
| | | | |
QY 901 CCCAGGCAAGTGTGTGCAAGATTAAGAGGATTAAGAAGGGAATTTGAAGAGCTTT 960
| | | | |
Db 1301 CCCAGGCAAGTGTGTGCAAGATTAAGAGGATTAAGAAGGGAATTTGAAGAGCTTT 1360
| | | | |
QY 961 TGAATCCTGTGTGAGCTGTGTTGATCTTTGAACTGTGGTCAACAGGCGCTTTTCCAAAG 1020
| | | | |
Db 1361 TGAATCCTGTGTGTGAGCTGTGTTGATCTTTGAACTGTGGTCAACAGGCGCTTTTCCAAAG 1420
| | | | |
QY 1021 AGAAGGTATCAAGACTTTGGATTTTTCACACCGGGGCGGCTGCGGCTGTGTTGCTT 1080
| | | | |
Db 1421 AGAAGGTATCAAGACTTTGGATTTTTCACACCGGGGCGGCTGCGGCTGTGTTGCTT 1480
| | | | |
QY 1081 TTTTGAAGTTTATAAAGATTAATGAGGAGAAACCATCTGAGCGGGGGGTAACTGCG 1140
| | | | |
Db 1481 TTTTGAAGTTTATAAAGATTAATGAGGAGAAACCATCTGAGCGGGGGGTAACTGCG 1540
| | | | |
QY 1141 TGGATTTTCTGCGCATGCTGTGTGAGAGCGGTTGTGAGACACAAGAACTGCCCTGTAC 1200
| | | | |

Db 1541 TGGATTTTCTGCGCATGCTGTGTGAGAGCGGTTGTGAGACACAAGAACTGCCCTGTAC 1600
| | | | |
QY 1201 TGTGTCTTCCTCGCTCCGCCGCGCATATATCCGACGAGAGACAGACAGCAGAGAGG 1260
| | | | |
Db 1601 TGTGTCTTCCTCGCTCCGCCGCGCATATATCCGACGAGAGACAGACAGCAGAGAGG 1660
| | | | |
QY 1261 AAGCAGGCGGCGGCGCAGAGAGAGCCCATGGAACCCGAGAGCGGGCTGTGACCTC 1320
| | | | |
Db 1661 AAGCAGGCGGCGGCGCAGAGAGAGCCCATGGAACCCGAGAGCGGGCTGTGACCTC 1720
| | | | |
QY 1321 GGGATGAATGTTGTATACAGGTGTGTAACCTGTATCCAGAACTGAGACGATTTTGACAA 1380
| | | | |
Db 1721 GGGATGAATGTTGTATACAGGTGTGTAACCTGTATCCAGAACTGAGACGATTTTGACAA 1780
| | | | |
QY 1381 TACAGAGATGGGCGAGGGGCTAAAGGGGTAAAGAGGAGCGGGGGCTGTGAGGCTAC 1440
| | | | |
Db 1781 TACAGAGATGGGCGAGGGGCTAAAGGGGTAAAGAGGAGCGGGGGCTGTGTGAGGCTAC 1840
| | | | |
QY 1441 AGAGAGGCTTAGGAATCTAGCTTTTACCTTAATGACAGACACCGCTGTGATTTAC 1500
| | | | |
Db 1841 AGAGAGGCTTAGGAATCTAGCTTTTACCTTAATGACAGACACCGCTGTGATTTAC 1900
| | | | |
QY 1501 TTTTCAACAGATCAAGGATATATGCGCTAATGAGCTTGAATCTGTGCGCAGAAATTC 1560
| | | | |
Db 1901 TTTTCAACAGATCAAGGATATATGCGCTAATGAGCTTGAATCTGTGCGCAGAAATTC 1960
| | | | |
QY 1561 CATAGACAGCTGACCACTTAATGCTGTGACGCCAGGGAGATGATTTTGAAGGCTATTTAG 1620
| | | | |
Db 1961 CATAGACAGCTGACCACTTAATGCTGTGACGCCAGGGAGATGATTTTGAAGGCTATTTAG 2020
| | | | |
QY 1621 GGTATATGCAAGAGTGCACCTTAGAGCCAGATTGCAATGATCAAGATCAGCAACTTGTAAA 1680
| | | | |
Db 2021 GGTATATGCAAGAGTGCACCTTAGAGCCAGATTGCAATGATCAAGATCAGCAACTTGTAAA 2080
| | | | |
QY 1681 TATCAGGAATGTTGTTCTACATTTCTGGGAAACGGGCGCAGGTGAGATAGATACGAGGA 1740
| | | | |
Db 2081 TATCAGGAATGTTGTTCTACATTTCTGGGAAACGGGCGCAGGTGAGATAGATACGAGGA 2140
| | | | |
QY 1741 TAGGATGGCTTTAGATGATGATGATTAATATGTGGCCGGGGGTGCTTGTGCAATGACG 1800
| | | | |
Db 2141 TAGGATGGCTTTAGATGATGATGATTAATATGTGGCCGGGGGTGCTTGTGCAATGACG 2200
| | | | |
QY 1801 GGTGTTATATGATGATGATGATTTAATGAGGCTTAACTGAGGCTTAACTGAGGCTTAACT 1860
| | | | |
Db 2201 GGTGTTATATGATGATGATGATTTAATGAGGCTTAACTGAGGCTTAACTGAGGCTTAACT 2260
| | | | |
QY 1861 CAATACCAACCTTAATCTTACACGCTGTAGCTTCTATGAGGTTTAACAATACCTGTGTGA 1920
| | | | |
Db 2261 CAATACCAACCTTAATCTTACACGCTGTAGCTTCTATGAGGTTTAACAATACCTGTGTGA 2320
| | | | |
QY 1921 AGCTGGAACCGATGTAAAGGCTTGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGT 1980
| | | | |
Db 2321 AGCTGGAACCGATGTAAAGGCTTGGGGCTGTGCTTTTATCTGCTGTGGAAGGGGGTGT 2380
| | | | |
QY 1981 GTGTGCGCCCAAAAACGAGGCTTCAATTTAAGAAATGCTCTTTTGAAGGTGTACCTTGGG 2040
| | | | |
Db 2381 GTGTGCGCCCAAAAACGAGGCTTCAATTTAAGAAATGCTCTTTTGAAGGTGTACCTTGGG 2440
| | | | |
QY 2041 TATCTGTGTGAGGTTAATCTCAAGGTGCGCACAAATGTGGCTCCGACGTGTGTTGCTT 2100
| | | | |
Db 2441 TATCTGTGTGAGGTTAATCTCAAGGTGCGCACAAATGTGGCTCCGACGTGTGTTGCTT 2500
| | | | |
QY 2101 CATGCTAGTGAATAAGGCTGTGATGATTAAGCATTAATGTGTATGTGTGCAATCTGCGAGA 2160
| | | | |
Db 2501 CATGCTAGTGAATAAGGCTGTGATGATTAAGCATTAATGTGTATGTGTGCAATCTGCGAGA 2560
| | | | |
QY 2161 CAGGGCTCTCAAGTGTGACTGCTCGAGCGGCAACTGTCACTGCTGGAAGACCAATTCA 2220
| | | | |
Db 2561 CAGGGCTCTCAAGTGTGACTGCTCGAGCGGCAACTGTCACTGCTGGAAGACCAATTCA 2620
| | | | |
QY 2221 CGTAGCAGGCACTCTGCAAGGCTGTGGCAATGTTTGTGACATTAACATGACCCGCTG 2280
| | | | |

Db 2621 CGTAGCCAGCACTCTGCGAAGGCTGCGCAGTGTGTTGAGCATATACATCTGACCCGCTG 2680
Qy 2281 TTCTTGATTTGGGTAAACAGAGAGGGGGTGTCTTACCTTAACAAATGCAATTTGAGTCA 2340
Db 2681 TTCTTGATTTGGGTAAACAGAGAGGGGGTGTCTTACCTTAACAAATGCAATTTGAGTCA 2740
Qy 2341 CACTAAGATATTGCTTGAGCCCGAGAGAGATGTCACAGGTGAACCTGAAACGGGGTGTGGA 2400
Db 2741 CACTAAGATATTGCTTGAGCCCGAGAGAGATGTCACAGGTGAACCTGAAACGGGGTGTGGA 2800
Qy 2401 CATACACATGAAGATCTGGAAGTGTCTGAGGTACGATGAGACCCGACACAGGTGAGACC 2460
Db 2801 CATACACATGAAGATCTGGAAGTGTCTGAGGTACGATGAGACCCGACACAGGTGAGACC 2860
Qy 2461 CTGGAAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGCTGATGTGACCGAGGA 2520
Db 2861 CTGGAAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGCTGATGTGACCGAGGA 2920
Qy 2521 GCTAGAGCCCGATCATCTGTGTCCTGCGCTGACACCCGCGCTGATTTGGCTCTAGCGATGA 2580
Db 2921 GCTAGAGCCCGATCATCTGTGTCCTGCGCTGACACCCGCGCTGATTTGGCTCTAGCGATGA 2980
Qy 2581 AGATACAGATTGAG 2594
Db 2981 AGATACAGATTGAG 2994

RESULT 2
AR310582
LOCUS AR310582 7090 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 18 from patent US 6558948.
ACCESSION AR310582
VERSION AR310582.1 GI:31703596
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7090)
AUTHORS Kochanek,S. and Schledner,G.
TITLE Permanent amniocytic cell line, its production and use for the
JOURNAL Patent: US 6558948-A 18 06-MAY-2003;
FEATURES
source Location/Qualifiers
1..7090
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 2594; DB 6; Length 7090;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCATCTTACCTGCAAGAGCTGGCTTTCACCCAGTGACGAGAGATGAAGAGGT 60
Db 3165 ATCATCTTACCTGCAAGAGCTGGCTTTCACCCAGTGACGAGAGATGAAGAGGT 3224
Qy 61 GAGAGTTTGTGTAGATTATGTGAGACACCCCGGACGAGTTCAGGTCCTTTCATTAT 120
Db 3225 GAGAGTTTGTGTAGATTATGTGAGACACCCCGGACGAGTTCAGGTCCTTTCATTAT 3284
Qy 121 CACCGGAGGAATAGGGGGGACCCAGATTTATGTGTTGCTTTGCTATATAGACCTGT 180
Db 3285 CACCGGAGGAATAGGGGGGACCCAGATTTATGTGTTGCTTTGCTATATAGACCTGT 3344
Qy 181 GGCATGTTTGTCTACATGAGTGAATAATTATGGGAGTGGGTATAGAGTGGGGTTTG 240
Db 3345 GGCATGTTTGTCTACATGAGTGAATAATTATGGGAGTGGGTATAGAGTGGGGTTTG 3404
Qy 241 GTGTGTAATTTTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGAAATTTTGAATTGGA 300
Db 3405 GTGTGTAATTTTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGAAATTTTGAATTGGA 3464
Qy 301 TTTTAAAAAGGTCCTGTCTGTCTGAACCTGAGCCTGAGCCGAGACCGAGAGCCTG 360

Db 3465 TTTTAAAAAGGTCCTGTCTGTCTGAACCTGAGCCTGAGCCGAGACCGAGAGCCTG 3524
Qy 361 CAAGACCTACCCGCGCTCTTAAATGGCGCTGTATCTGAGAGCGCCGACATCACTG 420
Db 3525 CAAGACCTACCCGCGCTCTTAAATGGCGCTGTATCTGAGAGCGCCGACATCACTG 3584
Qy 421 TGTCTAAGAAATGCAATAGTATGTAACGATAGCTGTGATCTCGGTCTTTTACACACCTC 480
Db 3585 TGTCTAAGAAATGCAATAGTATGTAACGATAGCTGTGATCTCGGTCTTTTACACACCTC 3644
Qy 481 CTGAGATACACCCGCTGTCCCGTGTGCCCCATTAAACCAAGTTGCCGTGAGATTGTTG 540
Db 3645 CTGAGATACACCCGCTGTCCCGTGTGCCCCATTAAACCAAGTTGCCGTGAGATTGTTG 3704
Qy 541 GGCCTCCGACAGCTGTGGAATGTATCGAGAGACTTGTAAACGAGCTGGGCAACTTTGG 600
Db 3705 GGCCTCCGACAGCTGTGGAATGTATCGAGAGACTTGTAAACGAGCTGGGCAACTTTGG 3764
Qy 601 ACTTGAAGTGTAAACGCCCAAGCCATPAGGTGTAACCTGTGATTTGCTGTGTTAA 660
Db 3765 ACTTGAAGTGTAAACGCCCAAGCCATPAGGTGTAACCTGTGATTTGCTGTGTTAA 3824
Qy 661 CGCCTTTGTTTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Db 3825 CGCCTTTGTTTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3884
Qy 721 TGCAATGCGCTGTAAATGGGCGGGGCTTAAAGGGTATATATGCGCGGTAACTCT 780
Db 3885 TGCAATGCGCTGTAAATGGGCGGGGCTTAAAGGGTATATATGCGCGGTAACTCT 3944
Qy 781 TGTTCATCTGACCTCATGAGAGCTTGGAGTGTGGAAGATTTTTCGTGTGCGTA 840
Db 3945 TGTTCATCTGACCTCATGAGAGCTTGGAGTGTGGAAGATTTTTCGTGTGCGTA 4004
Qy 841 ACTTGCAGAAACAGAGCTTAAACAGTACCTTGTGTTTGAAGTTTCTGTGGGCTCAT 900
Db 4005 ACTTGCAGAAACAGAGCTTAAACAGTACCTTGTGTTTGAAGTTTCTGTGGGCTCAT 4064
Qy 901 CCCAGCAAGTATGATGTGCAAGATTAAGAGAGATTCAAGTGGAAATTTGAAGAGCTTT 960
Db 4065 CCCAGCAAGTATGATGTGCAAGATTAAGAGAGATTCAAGTGGAAATTTGAAGAGCTTT 4124
Qy 961 TGAATCTGTGTGAGCTGTGTTGATTTCTTGAATCTGTGCTACAGAGCGCTTTTCAAG 1020
Db 4125 TGAATCTGTGTGAGCTGTGTTGATTTCTTGAATCTGTGCTACAGAGCGCTTTTCAAG 4184
Qy 1021 AGAAGTTCATCAAGACTTTGATTTTCCACACCGGGGCGCGCTGCGCTGTGCTT 1080
Db 4185 AGAAGTTCATCAAGACTTTGATTTTCCACACCGGGGCGCGCTGCGCTGTGCTT 4244
Qy 1081 TTTTGAATTTTAAAGATTAATGAGAGCAAGAAACCATCTTGAAGCGGGGGGTAACTGC 1140
Db 4245 TTTTGAATTTTAAAGATTAATGAGAGCAAGAAACCATCTTGAAGCGGGGGGTAACTGC 4304
Qy 1141 TGAATTTTTCGCCATCATCTGTGAGAGCGTGTGAGACACAAAGATTCGCTGTAC 1200
Db 4305 TGAATTTTTCGCCATCATCTGTGAGAGCGTGTGAGACACAAAGATTCGCTGTAC 4364
Qy 1201 TGTGTCTTCCGTCCGCGCGCGGCAATATACCGAGAGAGACAGACAGACAGAGAGG 1260
Db 4365 TGTGTCTTCCGTCCGCGCGCGGCAATATACCGAGAGAGACAGACAGACAGAGAGG 4424
Qy 1261 AAGCCAGGCGGCGGCGGCAAGAGAGAGCCATGGAACCGAGAGCGGCGTGAACCTC 1320
Db 4425 AAGCCAGGCGGCGGCGGCAAGAGAGAGCCATGGAACCGAGAGCGGCGTGAACCTC 4484
Qy 1321 GGAATGAATGTTGTACAGGTGTGAACTGTATCCAGAACTGAGACGCAATTTGCAAT 1380
Db 4485 GGAATGAATGTTGTACAGGTGTGAACTGTATCCAGAACTGAGACGCAATTTGCAAT 4544
Qy 1381 TACAGAGATGGGCAAGGGGTTAAAGGGGTAAAGAGGAGACGGGGGCTGTGAGGCTAC 1440

D 4545 TACAGAGATGGGACGAGGGCTAAAGGGGTAAGAGGAGCGGGGGCTTGTGAGCTAC 4604
Q 1441 AGAGAGGCTAGAGATCTAGCTTTTAACTTAATGACACAGACCGTCTGTGATTTAC 1500
D 4605 AGAGAGGCTAGAGATCTAGCTTTTAACTTAATGACACAGACCGTCTGTGATTTAC 4664
Q 1501 TTTTCAACAGATCAAGGTAATTTGGCTAATGAGCTTGAATCTGCTGGGCGGAAGTATTC 1560
D 4665 TTTTCAACAGATCAAGGTAATTTGGCTAATGAGCTTGAATCTGCTGGGCGGAAGTATTC 4724
Q 1561 CATAGAGAGCTGACCACTTACTGGCTGACACGAGGGGATGTTTGAAGAGCTATTAG 1620
D 4725 CATAGAGAGCTGACCACTTACTGGCTGACACGAGGGGATGTTTGAAGAGCTATTAG 4784
Q 1621 GGTATATGCAAAAGGTGGCACTTAAGCCAGATTGCAAGTACAAATCAGCAAACTTTGAAA 1680
D 4785 GGTATATGCAAAAGGTGGCACTTAAGCCAGATTGCAAGTACAAATCAGCAAACTTTGAAA 4844
Q 1681 TATCAGGAATTTGTGCTACATTTCTGGGAAAGGGGCGAGGATAGATAGAGAGGA 1740
D 4845 TATCAGGAATTTGTGCTACATTTCTGGGAAAGGGGCGAGGATAGATAGAGAGGA 4904
Q 1741 TAGGCTGCTTTAGATGTACATGATTAATATGTGCGGGGCTGCTTGGCATGACG 1800
D 4905 TAGGCTGCTTTAGATGTACATGATTAATATGTGCGGGGCTGCTTGGCATGACG 4964
Q 1801 GGTGTTATTTATGAAATGATGATTACTGCGCCCAATTTTACCGGTACGGTTTCTGCGC 1860
D 4965 GGTGTTATTTATGAAATGATGATTACTGCGCCCAATTTTACCGGTACGGTTTCTGCGC 5024
Q 1861 CAATACCAACCTTTATCCACACGAGGTAAAGCTTCATGGGTTTAAACAATACCTGATGGA 1920
D 5025 CAATACCAACCTTTATCCACACGAGGTAAAGCTTCATGGGTTTAAACAATACCTGATGGA 5084
Q 1921 AGCCTGGAACCGATGAAGGTTGCGGGCTGTGCTTTTACTGCTGTGGAAGGGGATGCT 1980
D 5085 AGCCTGGAACCGATGAAGGTTGCGGGCTGTGCTTTTACTGCTGTGGAAGGGGATGCT 5144
Q 1981 GTGTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATCTTGGG 2040
D 5145 GTGTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATCTTGGG 5204
Q 2041 TATCTGTCTAAGGGTAACTCAAGGGTGGCAACAATGTGCTCCGACTGGTGGTCTT 2100
D 5205 TATCTGTCTAAGGGTAACTCAAGGGTGGCAACAATGTGCTCCGACTGGTGGTCTT 5264
Q 2101 CATGCTAGTGAAGGCGTGTGCTGATTAAGCATTAACATGATGTGCAACTGCGAGA 2160
D 5265 CATGCTAGTGAAGGCGTGTGCTGATTAAGCATTAACATGATGTGCAACTGCGAGA 5324
Q 2161 CAGGGCTCTCAATGCTGACCTGTGCGACGGCACTGTCACTGTGGAAGCACTTCA 2220
D 5325 CAGGGCTCTCAATGCTGACCTGTGCGACGGCACTGTCACTGTGGAAGCACTTCA 5384
Q 2221 CGTAGCCAGCACTCTGCGAAGGCTGCGCAAGTGTGTAAGCATTAACAATGACCCGCTG 2280
D 5385 CGTAGCCAGCACTCTGCGAAGGCTGCGCAAGTGTGTAAGCATTAACAATGACCCGCTG 5444
Q 2281 TTCTTGTGATTTGGGTAAACAGAGAGGGGATGTTCTTACCTTAACCAATGCAATTTGAGTCA 2340
D 5445 TTCTTGTGATTTGGGTAAACAGAGAGGGGATGTTCTTACCTTAACCAATGCAATTTGAGTCA 5504
Q 2341 CACTTAAGATTTGCTTGAAGCCGAGAGACATGTCAGAGTGAACCTGAACGGGGTGTGGA 2400
D 5505 CACTTAAGATTTGCTTGAAGCCGAGAGACATGTCAGAGTGAACCTGAACGGGGTGTGGA 5564
Q 2401 CATGACCAATGAAGATCTGGAAGGTGCTGAGATGAGATGAGACCCGCAACAGGTGAGACC 2460
D 5565 CATGACCAATGAAGATCTGGAAGGTGCTGAGATGAGATGAGACCCGCAACAGGTGAGACC 5624
Q 2461 CTGCGAGTGTGGCGGTAAACATATTAGAACACAGCTGTGATGTGATGTGACCGAGGA 2520
D 5625 CTGCGAGTGTGGCGGTAAACATATTAGAACACAGCTGTGATGTGATGTGACCGAGGA 5684

Q 2521 GCTGAGGCCGATACCTTGGTGTGCTGCTGACACCCGGCTGAGTTGGCTTACGAGTGA 2580
D 5685 GCTGAGGCCGATACCTTGGTGTGCTGCTGACACCCGGCTGAGTTGGCTTACGAGTGA 5744
Q 2581 AGATACAGATTGAG 2594
D 5745 AGATACAGATTGAG 5758

RESULT 3
AX150263
LOCUS AX150263 7090 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 18 from Patent WO0136615.
ACCESSION AX150263
VERSION AX150263.1 GI:14348283
KEYWORDS
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.

REFERENCE
1
AUTHORS KoehaneK,S. and Schiedner,G.
TITLE Permanent amniocyte cell line, the production thereof and its use
for producing gene transfer vectors
JOURNAL Patent: WO 0136615-A 18 25-MAY-2001,
KoehaneK, Stefan (DE)
FEATURES
Location/Qualifiers
source
1..7090
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Plasmid STK146"

ORIGIN
Query Match 100.0%; Score 2594; DB 6; Length 7090;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q 1 ATCATCTTACCTGCGCACGAGGCTGGCTTTCCACCCGATGACGAGATGAAGAGGCT 60
D 3165 ATCATCTTACCTGCGCACGAGGCTGGCTTTCCACCCGATGACGAGATGAAGAGGCT 3224
Q 61 GAGGAGTTTGTTAGTATGATTAATGAGAGACCCCGGAGCAGGTTGACAGTCTTGCATTAT 120
D 3225 GAGGAGTTTGTTAGTATGATTAATGAGAGACCCCGGAGCAGGTTGACAGTCTTGCATTAT 3284
Q 121 CACCGAGGAATACGGGGGACCCAGATATTATGTTGCTTTGCTATATGAGGACCTGT 180
D 3285 CACCGAGGAATACGGGGGACCCAGATATTATGTTGCTTTGCTATATGAGGACCTGT 3344
Q 181 GGCATGTTTGTCTACAGTAAAGTAAATTAATGGCAATGGGTGATTAAGTGTGGTTTG 240
D 3345 GGCATGTTTGTCTACAGTAAAGTAAATTAATGGCAATGGGTGATTAAGTGTGGTTTG 3404
Q 241 GTGTGTAATTTTTTTTTTAAATTTTACAGTTTGTGTTTAAAGAAATTTGTAATGGA 300
D 3405 GTGTGTAATTTTTTTTTTAAATTTTACAGTTTGTGTTTAAAGAAATTTGTAATGGA 3464
Q 301 TTTTAAAAAGGCTCTGTGCTGTAACCTGAGCCTGAGCCGAGCCGAACCGGAGCCTG 360
D 3465 TTTTAAAAAGGCTCTGTGCTGTAACCTGAGCCTGAGCCGAGCCGAACCGGAGCCTG 3524
Q 361 CAGAGCTACCCCGCGTCTTAAATGCGGCTGTATTCCTGAAGACGGCCGACATCACTG 420
D 3525 CAGAGCTACCCCGCGTCTTAAATGCGGCTGTATTCCTGAAGACGGCCGACATCACTG 3584
Q 421 TGTTTAGAGATGCAATAGTATGATGCGGATGCTGTGACTCGCGGCTTCTTAAACACACTC 480
D 3585 TGTTTAGAGATGCAATAGTATGATGCGGATGCTGTGACTCGCGGCTTCTTAAACACACTC 3644
Q 481 CTGAGATACACCCGGTGTGCTCGGCTGTGCCCATTTAAACAGATGCGGTGAGAGTGGTG 540
D 3645 CTGAGATACACCCGGTGTGCTCGGCTGTGCCCATTTAAACAGATGCGGTGAGAGTGGTG 3704

QY 541 GGCCTGCCAGGCTGTGAAATGATCGAGAACTTGCTTACGAGCTCGGCAACTTTGG 600
Db 3705 GCGCGTCGACAGGCTGTGAAATGATCGAGAACTTGCTTACGAGCTCGGCAACTTTGG 3764
QY 601 ACTGAGCTGTAAAGCCCGCAGGCAATAGGTAAAGCTGTGATGCTGTGTGTAA 660
Db 3765 ACTTACGCTGTAAAGCCCGCAGGCAATAGGTAAAGCTGTGATGCTGTGTGTAA 3824
QY 661 GCGCTTTGTGTGCTGAATGAGTGTGATGATTAATAAAGGAGATTAATGTTAACT 720
Db 3825 GCGCTTTGTGTGCTGAATGAGTGTGATGATTAATAAAGGAGATTAATGTTAACT 3884
QY 721 TGCATGGGCTGTAAATGAGGCGGCGCTTAAAGGATTAATGCGCGCTGTAACT 780
Db 3885 TGCATGGGCTGTAAATGAGGCGGCGCTTAAAGGATTAATGCGCGCTGTAACT 3944
QY 781 TGGTACATCTGACCTCATGAGAGCTGGAGTGTGGAGATTTTCTGCTGTGCGTA 840
Db 3945 TGGTACATCTGACCTCATGAGAGCTGGAGTGTGGAGATTTTCTGCTGTGCGTA 4004
QY 841 ACTTCTGGAACAGAGCTCTAACAGTACCTCTGTGTTTGTGAGTTTCTGTGCGCTCAT 900
Db 4005 ACTTCTGGAACAGAGCTCTAACAGTACCTCTGTGTTTGTGAGTTTCTGTGCGCTCAT 4064
QY 901 CCCAGGCAAGTTAGTCTGCAAGATTAAGAGAGATTAACAAGGGAATTTGAAGCTTT 960
Db 4065 CCCAGGCAAGTTAGTCTGCAAGATTAAGAGAGATTAACAAGGGAATTTGAAGCTTT 4124
QY 961 TGAATTCCTGTGTGAGCTGTGATTTCTTGAATCTGGGTACAGGCGCTTTCCAG 1020
Db 4125 TGAATTCCTGTGTGAGCTGTGATTTCTTGAATCTGGGTACAGGCGCTTTCCAG 4184
QY 1021 AGAAGTCATCAAGACTTTGATTTTTCACACCGGCGCGCTGCTGTGTGCTT 1080
Db 4185 AGAAGTCATCAAGACTTTGATTTTTCACACCGGCGCGCTGCTGTGTGCTT 4244
QY 1081 TTTTGAAGTTTAAAGATTAATGAGAGCAAGAAACCATTTGACGCGGCTTACCTGC 1140
Db 4245 TTTTGAAGTTTAAAGATTAATGAGAGCAAGAAACCATTTGACGCGGCTTACCTGC 4304
QY 1141 TGGATTTTCTGAGCATCTGTGAGAGCGTGTGAGACACAAGATGCGCTGTAC 1200
Db 4305 TGGATTTTCTGAGCATCTGTGAGAGCGTGTGAGAGCGTGTGAGAGCGTGTAC 4364
QY 1201 TGTGTCTTCCGTCGCGCCGCGGATTAATCCGACGAGAGAGCAGCAGCAGAGAG 1260
Db 4365 TGTGTCTTCCGTCGCGCCGCGGATTAATCCGACGAGAGAGCAGCAGCAGAGAG 4424
QY 1261 AAGCCAGCGCGCGCGGAGAGAGAGCCCATGGAACCCGAGAGCCGCTGTGACCTTC 1320
Db 4425 AAGCCAGCGCGCGCGGAGAGAGAGCCCATGGAACCCGAGAGCCGCTGTGACCTTC 4484
QY 1321 GGGATGAAATGTTGTGACAGTGTGCTGAATCTGATCAGAACTGAGACGATTTTGACAT 1380
Db 4485 GGGATGAAATGTTGTGACAGTGTGCTGAATCTGATCAGAACTGAGACGATTTTGACAT 4544
QY 1381 TACAGAGATGAGCAGGAGCTAAAGGGGTAAAGAGAGCGGCGGCTGTGAGGCTAC 1440
Db 4545 TACAGAGATGAGCAGGAGCTAAAGGGGTAAAGAGAGCGGCGGCTGTGAGGCTAC 4604
QY 1441 AGAGAGGCTGTGAATCTAGCTTTAGCTTAATGACAGACCGCTCTGAGTGTATAC 1500
Db 4605 AGAGAGGCTGTGAATCTAGCTTTAGCTTAATGACAGACCGCTCTGAGTGTATAC 4664
QY 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTATCTGCTGCGCGCAAGATATTC 1560
Db 4665 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTATCTGCTGCGCGCAAGATATTC 4724
QY 1561 CATGAGAGAGCTGACCACTTACTGCTGACAGCAGGAGATGATTTTGAAGAGCTATTAG 1620
Db 4725 CATGAGAGAGCTGACCACTTACTGCTGACAGCAGGAGATGATTTTGAAGAGCTATTAG 4784

QY 1621 GGTATATCCAAAGGTGCGACTTTAGGCCAGATTGCCAGTACAAAGATCAGCAAACTTTTAA 1680
Db 4785 GGTATATCCAAAGGTGCGACTTTAGGCCAGATTGCCAGTACAAAGATCAGCAAACTTTTAA 4844
QY 1681 TATCAGAAATTTGTTCTCATTTTCTGAGGAGCGGCGCGAGGTGAGATGATPACGAGAGA 1740
Db 4845 TATCAGAAATTTGTTCTCATTTTCTGAGGAGCGGCGCGAGGTGAGATGATPACGAGAGA 4904
QY 1741 TAGGCTGACCTTTAGATGATGATGATTAATATGATGATGATGATGATGATGATGATGAT 1800
Db 4905 TAGGCTGACCTTTAGATGATGATGATTAATATGATGATGATGATGATGATGATGATGAT 4964
QY 1801 GGTGTTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Db 4965 GGTGTTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5024
QY 1861 CAATPACCAACCTTTATCCPACACGAGTGAAGCTTCTATGAGGTTTAACAATPACCTGATGGA 1920
Db 5025 CAATPACCAACCTTTATCCPACACGAGTGAAGCTTCTATGAGGTTTAACAATPACCTGATGGA 5084
QY 1921 AGCTGACCCGATGTAAGGCTTGGGCGCTGTGCTTTTACTGTCTGTGAAAGGGGCTGT 1980
Db 5085 AGCTGACCCGATGTAAGGCTTGGGCGCTGTGCTTTTACTGTCTGTGAAAGGGGCTGT 5144
QY 1981 GTGTGCGCCCAAAAGCAGGCGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTACTTGTGG 2040
Db 5145 GTGTGCGCCCAAAAGCAGGCGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTACTTGTGG 5204
QY 2041 TATCTGTCTGAGGTTATCTCAGGAGTGCACAAATGAGCTCCGACTGTGTGTGCTT 2100
Db 5205 TATCTGTCTGAGGTTATCTCAGGAGTGCACAAATGAGCTCCGACTGTGTGTGCTT 5264
QY 2101 CATCTAGTGAAGAAAGCTGTGTGATTAAGCATPACATGATGTGTGCAACTGTGAGAGA 2160
Db 5265 CATCTAGTGAAGAAAGCTGTGTGATTAAGCATPACATGATGTGTGCAACTGTGAGAGA 5324
QY 2161 CAGGCGCTCTGAGATGCTGATCTGTGTGAGAGGCACTGTCACTGTGAGAGCACTTCA 2220
Db 5325 CAGGCGCTCTGAGATGCTGATCTGTGTGAGAGGCACTGTCACTGTGAGAGCACTTCA 5384
QY 2221 CGTACGACGACCTCTGCAAGGCTGTGCTGATTAAGCATPACATGATGTGTGCAACTGTGAG 2280
Db 5385 CGTACGACGACCTCTGCAAGGCTGTGCTGATTAAGCATPACATGATGTGTGCAACTGTGAG 5444
QY 2281 TTCCTGTGATTTGGGTAAACAGAGAGGGGTGTTCTTACCTTACCAATGCAATTTGATCA 2340
Db 5445 TTCCTGTGATTTGGGTAAACAGAGAGGGGTGTTCTTACCTTACCAATGCAATTTGATCA 5504
QY 2341 CACTTAAGTATTTGCTTGAAGCCCGAGAGCATTTCCAAAGTGAACCTGAACCGGGTGTGGA 2400
Db 5505 CACTTAAGTATTTGCTTGAAGCCCGAGAGCATTTCCAAAGTGAACCTGAACCGGGTGTGGA 5564
QY 2401 CATGACCATGAAGATCTGGAAGTGTGAGGATGATGATGATGATGATGATGATGATGATGAT 2460
Db 5565 CATGACCATGAAGATCTGGAAGTGTGAGGATGATGATGATGATGATGATGATGATGATGAT 5624
QY 2461 CTGCGAGTGTGCGGTAAACATATTAGGAACCAAGCTGTGTGATGATGATGATGATGATGAT 2520
Db 5625 CTGCGAGTGTGCGGTAAACATATTAGGAACCAAGCTGTGTGATGATGATGATGATGATGATGAT 5684
QY 2521 GCTGAGGCGCGATCACTTTGT 2580
Db 5685 GCTGAGGCGCGATCACTTTGT 5744
QY 2581 AGATACAGATTGAG 2594
Db 5745 AGATACAGATTGAG 5758

RESULT 4
BD268237 7607 bp DNA linear PAT 17-JUL-2003
LOCUS Adenovirus vector, packaging cell line, composition and method for

ACCESSION BD268237.1 GI:33078005
VERSION BD268237.1
KEYWORDS JP 2002534130-A/41.
SOURCE Synthetic construct
ORGANISM Synthetic construct
REFERENCE 1 (bases 1 to 7607)
AUTHORS Nemerow,G.R., Seggern,D.J.V., Hallenbeck,P.L., Stevenson,S.C. and Skripchenko,Y.
TITLE Adenovirus vector, packaging cell line, composition and method for production and use
JOURNAL Patent: JP 2002534130-A 41 15-OCT-2002;
NOVARTIS AG,THE SCRIPPS RESEARCH INSTITUTE
COMMENT OS Artificial Sequence
PN JP 2002534130-A/41
PD 15-OCT-2002
PF 14-JAN-2000 JP 2000593765
PI 14-JAN-1999 US 60/115920
PI GLEN ROBERT NEMEROW,DANIEL J VON SEGGERN,PAUL L HALLENBECK,PI SUSAN C STEVENSON,YELENA SKRIPCHENKO
PC C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00,A61P43/00,PC C12N5/10,
PC C12N7/00,C12Q1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC Description of Artificial Sequence: Plasmid
FH Key Location/Qualifiers
FT source 1..7607
FEATURES Location/Qualifiers
source 1..7607
/organism="Synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 2594; DB 6; Length 7607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCGATCTTACTGCGCAGAGCGCTTTCACCCAGTACGACGAGAGTGAAGAGGT 60
DB 1334 ATCGATCTTACTGCGCAGAGCGCTTTCACCCAGTACGACGAGAGTGAAGAGGT 1393
QY 61 GAGGAGTTTGTGTGATTAATGATGAGACACCCGGGCAAGTTGACAGGCTTGTCAAT 120
DB 1394 GAGGAGTTTGTGTGATTAATGATGAGACACCCGGGCAAGTTGACAGGCTTGTCAAT 1453
QY 121 CACCGAGAGTAATCCGGGAGCCAGATATTAATGATGATGATGATGATGATGATGAT 180
DB 1454 CACCGAGAGTAATCCGGGAGCCAGATATTAATGATGATGATGATGATGATGATGAT 1513
QY 181 GCGATGTTTGTCTACAGTAAGTAAATTAATGCGGAGTGGGATGAGTGGGTTTG 240
DB 1514 GCGATGTTTGTCTACAGTAAGTAAATTAATGCGGAGTGGGATGAGTGGGTTTG 1573
QY 241 GCGGATATTTTATTTTAAATTTTAAAGTTTAAAGATTTTAAAGATTTTAAAGAT 300
DB 1574 GCGGATATTTTATTTTAAATTTTAAAGTTTAAAGATTTTAAAGATTTTAAAGAT 1633
QY 301 TTTTAAAGATCTGTGTCTGAACTGAGCTGAGCCCGAGCCGAGACCGAGCCGCTG 360
DB 1634 TTTTAAAGATCTGTGTCTGAACTGAGCTGAGCCCGAGCCGAGACCGAGCCGCTG 1693
QY 361 CAAAGCTTACCCGCGCTCTAAATGCGGCTGCTATCTGAGAGCCCGAGATCACTG 420
DB 1694 CAAAGCTTACCCGCGCTCTAAATGCGGCTGCTATCTGAGAGCCCGAGATCACTG 1753
QY 421 TGTCTAGAGATGAGTATAGTACGAGTACGCTGAGTCCGCGCTCTCTAACAACCTC 480
DB 1754 TGTCTAGAGATGAGTATAGTACGAGTACGCTGAGTCCGCGCTCTCTAACAACCTC 1813
QY 481 CTGAGATACACCCGCGTGTCCGCTGTGCCCATTAAACCAATTGCGGTGAGAGTTG 540

DB 1814 CTGAGATACACCCGCGTGTCCGCTGTGCCCATTAAACCAAGTTGCCGTGAGAGTTG 1873
QY 541 GCGCTGCCAGCGCTGTGGAATGATTCAGAGACTTGTAAACGAGCTGGGCAACCTTGG 600
DB 1874 GCGCTGCCAGCGCTGTGGAATGATTCAGAGACTTGTAAACGAGCTGGGCAACCTTGG 1933
QY 601 ACTGAGCTGTAAACGCCAGCCAGCATTAAGTGAACCTGTGATTCGTGTGTTAA 660
DB 1934 ACTGAGCTGTAAACGCCAGCCAGCATTAAGTGAACCTGTGATTCGTGTGTTAA 1993
QY 661 CGCCTTTGTTGCTGAATGAGTGTATGTTAATTAAGGCTGAGATTAATGTTAACT 720
DB 1994 CGCCTTTGTTGCTGAATGAGTGTATGTTAATTAAGGCTGAGATTAATGTTAACT 2053
QY 721 TGCATGCGCTGTTAAATGAGGCGGGCTTAAAGGTTAATATGCGCGGTGGCTAATCT 780
DB 2054 TGCATGCGCTGTTAAATGAGGCGGGCTTAAAGGTTAATATGCGCGGTGGCTAATCT 2113
QY 781 TGTTCATCTGACCTCATGAGAGCTTGGAGTGTGGAAGATTTTCTGCTGTGCGTA 840
DB 2114 TGTTCATCTGACCTCATGAGAGCTTGGAGTGTGGAAGATTTTCTGCTGTGCGTA 2173
QY 841 ACTTGTGGAACAGAGCTCTAACAGTACTTCTGTTTGGAGTTTCTGTGGGCTCAT 900
DB 2174 ACTTGTGGAACAGAGCTCTAACAGTACTTCTGTTTGGAGTTTCTGTGGGCTCAT 2233
QY 901 CCCAGCAAGTTAGTGTGCAAGTAAAGAGATTCAAGTGGGAATTTGAAGAGCTTT 960
DB 2234 CCCAGCAAGTTAGTGTGCAAGTAAAGAGATTCAAGTGGGAATTTGAAGAGCTTT 2293
QY 961 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGTGTGACAGAGCGCTTTTCCAG 1020
DB 2294 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGTGTGACAGAGCGCTTTTCCAG 2353
QY 1021 AGAAGTCAATCAAGCTTTGATTTTCCACACCGGGCGCGCTGCGCTGCTTGTGCTT 1080
DB 2354 AGAAGTCAATCAAGCTTTGATTTTCCACACCGGGCGCGCTGCGCTGCTTGTGCTT 2413
QY 1081 TTTTGAAGTTTAAAGATTAATGAGAGCGAAGAACCCATCTGAGCGGGGGTAACTGCG 1140
DB 2414 TTTTGAAGTTTAAAGATTAATGAGAGCGAAGAACCCATCTGAGCGGGGGTAACTGCG 2473
QY 1141 TGAATTTTCTGCGCATCATCTGTGAGAGCGGTTGTGACACACAAGATGCGCTGTAC 1200
DB 2474 TGAATTTTCTGCGCATCATCTGTGAGAGCGGTTGTGACACACAAGATGCGCTGTAC 2533
QY 1201 TGTGTCTTCCGTCGCCCGGCGATTAATCCGACGAGAGACAGACAGACAGAGAG 1260
DB 2534 TGTGTCTTCCGTCGCCCGGCGATTAATCCGACGAGAGACAGACAGACAGAGAG 2593
QY 1261 AAGCAGCGCGCGCGGAGAGAGCCCATGGAACCCGAGAGCGGCGCTGAGCCCTC 1320
DB 2594 AAGCAGCGCGCGGAGAGAGCCCATGGAACCCGAGAGCGGCGCTGAGCCCTC 2653
QY 1321 GGGATGATGTTGTGACAGTGTGCTGAACCTGTATCCAGAACTGAGACGATTTTGA 1380
DB 2654 GGGATGATGTTGTGACAGTGTGCTGAACCTGTATCCAGAACTGAGACGATTTTGA 2713
QY 1381 TACAGAGATGCGGAGCGGCTAAAGGGGCTAAAGGGAGCGGGGGCTTGTGAGGCTAC 1440
DB 2714 TACAGAGATGCGGAGCGGCTAAAGGGGCTAAAGGGAGCGGGGGCTTGTGAGGCTAC 2773
QY 1441 AGAGAGGCTAGGAATCTAGCTTTAGCTTAATGACCAACCGCTCTGAGTGTATAC 1500
DB 2774 AGAGAGGCTAGGAATCTAGCTTTAGCTTAATGACCAACCGCTCTGAGTGTATAC 2833
QY 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTGTGCGGCAAGATATTC 1560
DB 2834 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTGTGCGGCAAGATATTC 2893
QY 1561 CATAGAGAGCTGACCACTTACTGTGCTGACCGAGGGAGTAAATTTTGAAGGCTATTA 1620
DB 2894 CATAGAGAGCTGACCACTTACTGTGCTGACCGAGGGAGTAAATTTTGAAGGCTATTA 2953

1611 GGTATATGCAAGTGGCACTTAGGCCAGATTGCAAGTACAAAGATCAGCAACTTGTAA 1680
2954 GGTATATGCAAGTGGCACTTAGGCCAGATTGCAAGTACAAAGATCAGCAACTTGTAA 3013
1681 TATCAGAAATTGTTCTCATTTCTGGGAAAGGGCCGAGGGAGATGATAGGAGGA 1740
3014 TATCAGAAATTGTTCTCATTTCTGGGAAAGGGCCGAGGGAGATGATAGGAGGA 3073
1741 TAGGGTGGCTTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
3074 TAGGGTGGCTTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3133
1801 GGTGTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
3134 GGTGTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3193
1861 CAATACCAACCTTATCTACACGAGTGAAGCTTATGAGGTTTAACTGATGATGATGATGAT 1920
3194 CAATACCAACCTTATCTACACGAGTGAAGCTTATGAGGTTTAACTGATGATGATGATGAT 3253
1921 AGCCTGGAACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
3254 AGCCTGGAACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3313
1981 GTGTGCCCCCAAAAGCAGAGGCTTCAATTAGAAATGCTCTTTGAAAGGTGATCTTGGG 2040
3314 GTGTGCCCCCAAAAGCAGAGGCTTCAATTAGAAATGCTCTTTGAAAGGTGATCTTGGG 3373
2041 TATCTGTCTGAGGGTAACTCCAGGGTGGCCAGCAATGAGCTCCGACTGAGTGTGCTT 2100
3374 TATCTGTCTGAGGGTAACTCCAGGGTGGCCAGCAATGAGCTCCGACTGAGTGTGCTT 3433
2101 CATGCTAGTAAAGAGCGTGTGATTTAGCATTAACATGATGATGATGATGATGATGATGAT 2160
3434 CATGCTAGTAAAGAGCGTGTGATTTAGCATTAACATGATGATGATGATGATGATGATGAT 3493
2161 CAGGCGCTCTCAGATGCTGATCTGCGAGCGCACTGTCACTGCTGAGAAAGCACTTCA 2220
3494 CAGGCGCTCTCAGATGCTGATCTGCGAGCGCACTGTCACTGCTGAGAAAGCACTTCA 3553
2221 CGTAGCCAGCACTCTGCGAAGGCTGGCCAGTGTGTTAGCATTAACATGATGATGATGATGAT 2280
3554 CGTAGCCAGCACTCTGCGAAGGCTGGCCAGTGTGTTAGCATTAACATGATGATGATGATGAT 3613
2281 TTCTTGTGATTTGGGTAAACAGAGGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCA 2340
3614 TTCTTGTGATTTGGGTAAACAGAGGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCA 3673
2341 CACTTAAGATTTGCTTGAAGCCGAGAGCATGTCAGAGTGAACCTGAAAGGGGTGTTGA 2400
3674 CACTTAAGATTTGCTTGAAGCCGAGAGCATGTCAGAGTGAACCTGAAAGGGGTGTTGA 3733
2401 CATGACCATGAAGATCTGGAAGGTGCTGAGTGAATGAGACCCGACAGGTGAGACC 2460
3734 CATGACCATGAAGATCTGGAAGGTGCTGAGTGAATGAGACCCGACAGGTGAGACC 3793
2461 CTGGAAGTGTGGCGGTAAACATATTAGAACAGAGCTGTGATGCTGATGATGATGATGATGAT 2520
3794 CTGGAAGTGTGGCGGTAAACATATTAGAACAGAGCTGTGATGCTGATGATGATGATGATGAT 3853
2521 GCTGAGAGCCGATCATCTGT 2580
3854 GCTGAGAGCCGATCATCTGT 3913
2581 AGATACAGATTGAG 2594
3914 AGATACAGATTGAG 3927

RESULT 5
BD268208 11152 bp DNA linear PAR 17-JUL-2003
LOCUS BD268208

DEFINITION Adenovirus vector, packaging cell line, composition and method for production and use.
ACCESSION BD268208
VERSION BD268208.1 GI:33077976
KEYWORDS JP 2002534130-A/12.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 11152)
AUTHORS Nemerow,G.R., Seggern,D.J.V., Hallenbeck,P.L., Stevenson,S.C. and Skripchenko,Y.
TITLE Adenovirus vector, packaging cell line, composition and method for production and use
JOURNAL Patent: JP 2002534130-A 12 15-OCT-2002;
NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
COMMENT Artificial Sequence
PN JP 2002534130-A/12
PD 15-OCT-2002
PF 14-JAN-2000 JP 2000593765
PR 14-JAN-1999 US 60/115920
PI GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCHENKO
PC C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00,A61P43/00, PC C12N7/00,C12Q1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC Description of Artificial Sequence: Plasmid
FT Key Location/Qualifiers
FT source 1..11152
FEATURES
source /organism='Artificial Sequence'.
location/Qualifiers
1..11152
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 2594; DB 6; Length 11152;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCGATCTTACCTGCAAGAGGCTGGCTTCCACCCAGTGAAGAGATGAAAGAGGT 60
DB 1825 ATCGATCTTACCTGCAAGAGGCTGGCTTCCACCCAGTGAAGAGATGAAAGAGGT 1884
QY 61 GAGGAGTTTGTGTTAGATTATGTTAGAGACCCCGGAGCAGGTTGCAAGTCTTGTCAATTAT 120
DB 1885 GAGGAGTTTGTGTTAGATTATGTTAGAGACCCCGGAGCAGGTTGCAAGTCTTGTCAATTAT 1944
QY 121 CACCGAGGAATACGGGGGAGCCGATTTATGTTGCTTGCCTTATAGAGACTGT 180
DB 1945 CACCGAGGAATACGGGGGAGCCGATTTATGTTGCTTGCCTTATAGAGACTGT 2004
QY 181 GGCATGTTTGTCTACAGTAAGTGAATTAATGAGGAGGAGGAGTGAATGAGTGGGTTTG 240
DB 2005 GGCATGTTTGTCTACAGTAAGTGAATTAATGAGGAGGAGGAGTGAATGAGTGGGTTTG 2064
QY 241 GTGTGTAATTTTATTTTATTTTACAGTTTGTGTTTAAAGAAATTTGTAATTGGA 300
DB 2065 GTGTGTAATTTTATTTTATTTTACAGTTTGTGTTTAAAGAAATTTGTAATTGGA 2124
QY 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCCGAGCCGAGACCGAGACTG 360
DB 2125 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCCGAGCCGAGACCGAGACTG 2184
QY 361 CAAGACCTACCCGCGCTCTTAAATGAGGCTGTCTATCTGAGAGCCCGACATCACTG 420
DB 2185 CAAGACCTACCCGCGCTCTTAAATGAGGCTGTCTATCTGAGAGCCCGACATCACTG 2244
QY 421 TGTCTAAGAAATGCAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 2245 TGTCTAAGAAATGCAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2304
QY 481 CTGAGATACACCCGAGTGTGCTCCGCTGTGCCCATTTAAACAGTTGCCGTGAGACTTGGTG 540

Db 2305 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACAGTTCCTGTGAGAGTGGTG 2364
Qy 541 GCGCTGCCAGGCTGTGGAATGTATCGAGAGACTTGCTTAAAGAGCTTGCGAACCTTTGG 600
Db 2365 GCGCTGCCAGGCTGTGGAATGTATCGAGAGACTTGCTTAAAGAGCTTGCGAACCTTTGG 2424
Qy 601 ACTTGAGCTGTAAAGCCCCAGGCCATAAGGTGAACCTGTGATTTGGGTGTGTAA 660
Db 2425 ACTTGAGCTGTAAAGCCCCAGGCCATAAGGTGAACCTGTGATTTGGGTGTGTAA 2484
Qy 661 CGCCTTTGTTGCTGAATGAGTTGATGTAAATTAAGGTGAGATAATGTTTAACT 720
Db 2485 CGCCTTTGTTGCTGAATGAGTTGATGTAAATTAAGGTGAGATAATGTTTAACT 2544
Qy 721 TGCATGCGGTGTAAATGGCGCGGCTTAAAGGATATTAATGCGCGGTGAGTAACT 780
Db 2545 TGCATGCGGTGTAAATGGCGCGGCTTAAAGGATATTAATGCGCGGTGAGTAACT 2604
Qy 781 TGGTTACATCTGACCTCAATGAGAGCTTGGGAGTGTGGGAAGATTTCCTGTGCGGTA 840
Db 2605 TGGTTACATCTGACCTCAATGAGAGCTTGGGAGTGTGGGAAGATTTCCTGTGCGGTA 2664
Qy 841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGTTTTGAGAGTTTCTGTGGGCTCAT 900
Db 2665 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGTTTTGAGAGTTTCTGTGGGCTCAT 2724
Qy 901 CCCAGGCAAAAGTTAATGTCTGCAAGATTAAGAGAGATTAACAATGGGAAATTTGAAGCTTT 960
Db 2725 CCCAGGCAAAAGTTAATGTCTGCAAGATTAAGAGAGATTAACAATGGGAAATTTGAAGCTTT 2784
Qy 961 TGAATTCCTGTGAGCTGTGTTGATCTTTGAATCTGGGTCAACGAGGCGCTTTCCAAG 1020
Db 2785 TGAATTCCTGTGAGCTGTGTTGATCTTTGAATCTGGGTCAACGAGGCGCTTTCCAAG 2844
Qy 1021 AGAAGTCATCAAGAATTGGAATTTTCCACACCGGGGCGCGCTGCTGTGTGCTT 1080
Db 2845 AGAAGTCATCAAGAATTGGAATTTTCCACACCGGGGCGCGCTGCTGTGTGCTT 2904
Qy 1081 TTTTGAAGTTTATTAAGATTAATGAGCGGAAGAAACCATTTGAGCGGGGGGTACTGTC 1140
Db 2905 TTTTGAAGTTTATTAAGATTAATGAGCGGAAGAAACCATTTGAGCGGGGGGTACTGTC 2964
Qy 1141 TGGATTTTCTGGCCATGCACTGTGAGAGCGGTTGTGAGACACAAGAATCGCTGTAC 1200
Db 2965 TGGATTTTCTGGCCATGCACTGTGAGAGCGGTTGTGAGACACAAGAATCGCTGTAC 3024
Qy 1201 TGTGTCTTCCGTCCGCCCGGCGATTAACCGACGGAAGAGCAGACAGCAGAGAGG 1260
Db 3025 TGTGTCTTCCGTCCGCCCGGCGATTAACCGACGGAAGAGCAGACAGCAGAGAGG 3084
Qy 1261 AAGCCAGCGCGCGGGGCGAGAGCAGAGCCCATGGAACCCGAGACCGGCTTGACCTTC 1320
Db 3085 AAGCCAGCGCGCGGGGCGAGAGCAGAGCCCATGGAACCCGAGACCGGCTTGACCTTC 3144
Qy 1321 GGGAAATGAATGTTGTACAGGTGCTGAATCTGTATCGAATCGAGACGATTTTGACAT 1380
Db 3145 GGGAAATGAATGTTGTACAGGTGCTGAATCTGTATCGAATCGAGACGATTTTGACAT 3204
Qy 1381 TAACAGAGATGGGCGAGGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 1440
Db 3205 TAACAGAGATGGGCGAGGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 3264
Qy 1441 AGAGAGGCTTAGGAATCTAGACTTTTAAGCTTAATGACAGACACGCTCTGAGTGTATTAC 1500
Db 3265 AGAGAGGCTTAGGAATCTAGACTTTTAAGCTTAATGACAGACACGCTCTGAGTGTATTAC 3324
Qy 1501 TTTTCAACGATCAAGATTAATTGCGCTAATGAGCTTGATCTGTGCGCAGAGATATTTC 1560
Db 3325 TTTTCAACGATCAAGATTAATTGCGCTAATGAGCTTGATCTGTGCGCAGAGATATTTC 3384
Qy 1561 CATAGAGCAGCTGACCACTTACTGTGCTGACGCGAGGGATGATTTTGAAGAGCTATTAG 1620

Db 3385 CATAGAGCAGCTGACCACTTACTGTGCTGACGCCAGGGATGATTTTGAAGAGCTATTAG 3444
Qy 1621 GGTATATGCAAAAGGTGGCACTTAGGCCAGATTGCAATGCAAGATTCAGCAAACTTTGAAA 1680
Db 3445 GGTATATGCAAAAGGTGGCACTTAGGCCAGATTGCAATGCAAGATTCAGCAAACTTTGAAA 3504
Qy 1681 TATCAGAAATTTGTCTACATTTTCTGGAAAAGGGGCGGAGGTGAGATAGATAAGAGGA 1740
Db 3505 TATCAGAAATTTGTCTACATTTTCTGGAAAAGGGGCGGAGGTGAGATAGATAAGAGGA 3564
Qy 1741 TAGGTGCGCTTTAGATGATGATGATTAATATGTGCGCGGGGGTCTTGCCATGAGACG 1800
Db 3565 TAGGTGCGCTTTAGATGATGATGATTAATATGTGCGCGGGGGTCTTGCCATGAGACG 3624
Qy 1801 GGTGTTATTAATGAATGATTAAGGTTTACTGGCCCCAATTTTAAAGGGTACGGTTTCTGGC 1860
Db 3625 GGTGTTATTAATGAATGATTAAGGTTTACTGGCCCCAATTTTAAAGGGTACGGTTTCTGGC 3684
Qy 1861 CAATACCAACCTTATCTTACACGAGTGAAGCTTCTATGGGTTTAAACAATACCTGTGTGA 1920
Db 3685 CAATACCAACCTTATCTTACACGAGTGAAGCTTCTATGGGTTTAAACAATACCTGTGTGA 3744
Qy 1921 AGCTTGAAACGATGTAAAGGTTGCGGGCTGTGCTTTTACTGTGCTGGAAGGGGGTGT 1980
Db 3745 AGCTTGAAACGATGTAAAGGTTGCGGGCTGTGCTTTTACTGTGCTGGAAGGGGGTGT 3804
Qy 1981 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGTGCTTTGAAAGGTACTGTTGG 2040
Db 3805 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGTGCTTTGAAAGGTACTGTTGG 3864
Qy 2041 TATCTGTCTGAGGGTAACTCCAGGCTGCGCACATGTGGCTCCGACTGTGTGCTT 2100
Db 3865 TATCTGTCTGAGGGTAACTCCAGGCTGCGCACATGTGGCTCCGACTGTGTGCTT 3924
Qy 2101 CATCTAGTGAAGAGCGTGTGATTAAGCATTAACATGTATGTGCAACTCGAGAGA 2160
Db 3925 CATCTAGTGAAGAGCGTGTGATTAAGCATTAACATGTATGTGCAACTCGAGAGA 3984
Qy 2161 CAGGGCCCTCAGATGTGCTGACCTGTGAGAGCGCACTGTCACTGCTGAGAGACATTTCA 2220
Db 3985 CAGGGCCCTCAGATGTGCTGACCTGTGAGAGCGCACTGTCACTGCTGAGAGACATTTCA 4044
Qy 2221 CGTAGCCAGCCACTCTGCAAGGCTTGCCAGTGTGAGCATTAACATGACCCGCTG 2280
Db 4045 CGTAGCCAGCCACTCTGCAAGGCTTGCCAGTGTGAGCATTAACATGACCCGCTG 4104
Qy 2281 TTCCTTGATTTGGGTAAACAGAGAGGGGGTGTCTCTACCTTACCAATGCAATTTGAGTCA 2340
Db 4105 TTCCTTGATTTGGGTAAACAGAGAGGGGGTGTCTCTACCTTACCAATGCAATTTGAGTCA 4164
Qy 2341 CACTAAGATATTGTGCTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACCGGGGTGTTGA 2400
Db 4165 CACTAAGATATTGTGCTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACCGGGGTGTTGA 4224
Qy 2401 CATGACCATGAAGATCTGGAAGGTGTCTGAGGTACGATGAGACCCGCAACAGGTGCAACC 2460
Db 4225 CATGACCATGAAGATCTGGAAGGTGTCTGAGGTACGATGAGACCCGCAACAGGTGCAACC 4284
Qy 2461 CTGGAAGTGTGGCGGTAAACATATTAAGAACCAACCTGTGATGCTGATGTGACCGAGGA 2520
Db 4285 CTGGAAGTGTGGCGGTAAACATATTAAGAACCAACCTGTGATGCTGATGTGACCGAGGA 4344
Qy 2521 GCTGAGGCGCGATCACTTGGTGTGCTGACCGCGGCTGAGTTTGGCTCTAGCGATGA 2580
Db 4345 GCTGAGGCGCGATCACTTGGTGTGCTGACCGCGGCTGAGTTTGGCTCTAGCGATGA 4404
Qy 2581 AGATACAGATTGAG 2594
Db 4405 AGATACAGATTGAG 4418
RESULT 6
AX356041

LOCUS AX356041 11152 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 12 from Patent WO0183729.
ACCESSION AX356041
VERSION AX356041.1 GI:18620603
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences, artificial sequences.
REFERENCE
1 Nemerow, G.R., von Seggern, D.J. and Friedlander, M.
Vectors for ocular transduction and use thereof for genetic therapy
Patent: WO 0183729-A 12-08-NOV-2001;
Novartis AG (CH); The Scripps Research Institute (US); Nemerow,
Glen R. (US); Von Seggern, Daniel J. (US); Friedlander, Marcy
(US)
FEATURES
source Location/Qualifiers
1..11152
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Plasmid"
ORIGIN
Query Match 100.0%; Score 2594; DB 6; Length 11152;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGCATCTTACCTGCGCAGCAGGCTGGCTTTCACCCAGTGAAGAGAGAGAGGCT 60
1825 ATGCATCTTACCTGCGCAGCAGGCTGGCTTTCACCCAGTGAAGAGAGAGGCT 1884
61 GAGAGTTTGTGTGATTAATGATGAGACACCCCGGCGACGGTTCAGAGTCTTGTCAAT 120
1885 GAGAGTTTGTGTGATTAATGATGAGACACCCCGGCGACGGTTCAGAGTCTTGTCAAT 1944
121 CACCGAGAGAAATACCGGGGACCCAGATTAATGATGATGCTTGTATATGAGACCTGT 180
1945 CACCGAGAGAAATACCGGGGACCCAGATTAATGATGATGCTTGTATATGAGACCTGT 2004
181 GGCATGTTTGTCTCAGTAAAGTAAATTAATGAGAGTGGGATGATGATGAGTGGGTTTG 240
2005 GGCATGTTTGTCTCAGTAAAGTAAATTAATGAGAGTGGGATGATGATGAGTGGGTTTG 2064
241 GTGTGTAATTTTATTTTAAATTTTAAAGTTTGTGTTTAAAGATTTTGTATTTGA 300
2065 GTGTGTAATTTTATTTTAAATTTTAAAGTTTGTGTTTAAAGATTTTGTATTTGA 2124
301 TTTTAAAGTCTGTGTCTGAACCTGAGCCTGAGCCGAGCAGAACCGGAGCCTG 360
2125 TTTTAAAGTCTGTGTCTGAACCTGAGCCTGAGCCGAGCAGAACCGGAGCCTG 2184
361 CAAAGCCTACCGCGCTCTAAATGAGCGCTCTATCTTGAGAGCGCCGACATCACTTG 420
2185 CAAAGCCTACCGCGCTCTAAATGAGCGCTCTATCTTGAGAGCGCCGACATCACTTG 2244
421 TGTCTAAGAAATGCAATGTAAGTACGATAGCTGTGACTCGGCTCTTCTAACAACCTTC 480
2245 TGTCTAAGAAATGCAATGTAAGTACGATAGCTGTGACTCGGCTCTTCTAACAACCTTC 2304
481 CTGAGATACACCGGCTGTGCTGCGCTGCGCCATTAACCAAGTTGCGGTGAGAGTTGTTG 540
2305 CTGAGATACACCGGCTGTGCTGCGCTGCGCCATTAACCAAGTTGCGGTGAGAGTTGTTG 2364
541 GGCCTGCGCAGGCTGTGATATGAGAGCTTGCTTAACGAGCTGGGCAACTTTGG 600
2365 GGCCTGCGCAGGCTGTGATATGAGAGCTTGCTTAACGAGCTGGGCAACTTTGG 2424
601 ACTTGAAGTGTAAAGCCCGCAGGCAATAAGTGTAACTGTGATGCTGTGTGTTAA 660
2425 ACTTGAAGTGTAAAGCCCGCAGGCAATAAGTGTAACTGTGATGCTGTGTGTTAA 2484
661 CGCCTTTTGTGTAATGATGATGATTAATTAAGGATGAGATTAATGTTAACT 720
|||||

Db 2485 CGCCTTTTGTGTAATGATGATGATTAATTAAGGATGAGATTAATGTTAACT 2544
Qy 721 TGCATGCGGTGTAAATGAGCGCGGCTTAAAGGATATATATGCGCGGTCTAATCT 780
Db 2545 TGCATGCGGTGTAAATGAGCGCGGCTTAAAGGATATATATGCGCGGTCTAATCT 2604
Qy 781 TGTCTAAGTGTGATGATGAGAGCTTGGAGTGTGTTGAAAGATTTTCTGTGTGCTA 840
Db 2605 TGTCTAAGTGTGATGATGAGAGCTTGGAGTGTGTTGAAAGATTTTCTGTGTGCTA 2664
Qy 841 ACTGCTGAAACAGAGCTCTAAGACTACCTGTGTTTGGAGTTTCTGTGCGGTCTAT 900
Db 2665 ACTGCTGAAACAGAGCTCTAAGACTACCTGTGTTTGGAGTTTCTGTGCGGTCTAT 2724
Qy 901 CCCAGCAGAAATGATGCTGAGAAATTAAGAGATTAACAGTGGAAATTTGAAAGCTTT 960
Db 2725 CCCAGCAGAAATGATGCTGAGAAATTAAGAGATTAACAGTGGAAATTTGAAAGCTTT 2784
Qy 961 TGAATCTCTGTGTGAGCTGTTTGAATTTTGAATCTGTGTCAACGCGCTTTTCAAG 1020
Db 2785 TGAATCTCTGTGTGAGCTGTTTGAATTTTGAATCTGTGTCAACGCGCTTTTCAAG 2844
Qy 1021 AGAAGTCAATCAAGCTTTGATTTTCCACACCGGGGCGGCTGCGGTCTGTGCTT 1080
Db 2845 AGAAGTCAATCAAGCTTTGATTTTCCACACCGGGGCGGCTGCGGTCTGTGCTT 2904
Qy 1081 TTTTGAATTTTAAAGATTAATGAGCGGAAGAAACCATCTGAGCGGGGGTACTGTC 1140
Db 2905 TTTTGAATTTTAAAGATTAATGAGCGGAAGAAACCATCTGAGCGGGGGTACTGTC 2964
Qy 1141 TGAATTTTCTGCGCATGATCTGTGAGAGCGGTTTGTGAGACACAGAAATGCTGTAC 1200
Db 2965 TGAATTTTCTGCGCATGATCTGTGAGAGCGGTTTGTGAGACACAGAAATGCTGTAC 3024
Qy 1201 TGTGTCTTCCGTCGCGCGCGCGGATTAATACGAGAGAGACAGAGAGAGAGAGG 1260
Db 3025 TGTGTCTTCCGTCGCGCGCGCGGATTAATACGAGAGAGAGAGAGAGAGAGAGG 3084
Qy 1261 AAGCAGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 1320
Db 3085 AAGCAGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 3144
Qy 1321 GCGAATGAATTTGTACAGTGTGCTGAATCTGTATTCAGAACTGAGAGCATTTGACAT 1380
Db 3145 GCGAATGAATTTGTACAGTGTGCTGAATCTGTATTCAGAACTGAGAGCATTTGACAT 3204
Qy 1381 TACAGAGATGAGG 1440
Db 3205 TACAGAGATGAGG 3264
Qy 1441 AGAGAGCTAGAGATCTAGCTTTAGCTTAATGACAGACACCGTCTGTAGTATTTAC 1500
Db 3265 AGAGAGCTAGAGATCTAGCTTTAGCTTAATGACAGACACCGTCTGTAGTATTTAC 3324
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGACCTTGATGCTGTGGCGAGAAATTC 1560
Db 3325 TTTTCAACAGATCAAGATTAATGCGCTAATGACCTTGATGCTGTGGCGAGAAATTC 3384
Qy 1561 CATAGAGAGCTGACCACTTAATGCTGTGAGCGAGGAGATTTTGAAGAGGCTATTAG 1620
Db 3385 CATAGAGAGCTGACCACTTAATGCTGTGAGCGAGGAGATTTTGAAGAGGCTATTAG 3444
Qy 1621 GGTATATGCAAGGTGCACTTAGCGCAGATTTGCAAGTACCAAGTCAAACTTTGTA 1680
Db 3445 GGTATATGCAAGGTGCACTTAGCGCAGATTTGCAAGTACCAAGTCAAACTTTGTA 3504
Qy 1681 TATCAGAAATTTGTCTACATTTTCTGGAACGCGGCGAGGTGAGATATGATACGAGGA 1740
Db 3505 TATCAGAAATTTGTCTACATTTTCTGGAACGCGGCGAGGTGAGATATGATACGAGGA 3564
Qy 1741 TAGGATGAGCTTTGATGATGATGATTAATATGAGCGGAGGTGCTGTGATGAGCGG 1800
Db 3565 TAGGATGAGCTTTGATGATGATGATTAATATGAGCGGAGGTGCTGTGATGAGCGG 3624
|||||

QY 1801 GGTGGTATTATGAAATGTAAGTTACTGGCCCCAATTTTACCGGTAGCGTTTCCTGGC 1860
DB 3625 GGTGGTATTATGAAATGTAAGTTACTGGCCCCAATTTTACCGGTAGCGTTTCCTGGC 3684
QY 1861 CAATACCAACCTTATCTCAACAGGTGTAAGCTTCTATGGGTTTAACAATTAACCTGTGTGA 1920
DB 3685 CAATACCAACCTTATCTCAACAGGTGTAAGCTTCTATGGGTTTAACAATTAACCTGTGTGA 3744
QY 1921 AGCTTGAACCGATGTAAGGTTGCGGGCTGTGCTCTTTTACTGTCTGTGAAAGGGGGTGT 1980
DB 3745 AGCTTGAACCGATGTAAGGTTGCGGGCTGTGCTCTTTTACTGTCTGTGAAAGGGGGTGT 3804
QY 1981 GTGTGGCCCCAAGACAGGGCTTCAATTAAAGAAAGCCCTTTTGAAGAAGTGAACCTTGG 2040
DB 3805 GTGTGGCCCCAAGACAGGGCTTCAATTAAAGAAAGCCCTTTTGAAGAAGTGAACCTTGG 3864
QY 2041 TATCTGTCTGAGGTTAACTCCAGGGTGGCCACAATGTGGCTCCGACTGTGTGCTT 2100
DB 3865 TATCTGTCTGAGGTTAACTCCAGGGTGGCCACAATGTGGCTCCGACTGTGTGCTT 3924
QY 2101 CATGCTAGTGAAGACGTGTGTGTATTAAGCATTAACATGTATGTGCAATGCGAGGA 2160
DB 3925 CATGCTAGTGAAGACGTGTGTGTATTAAGCATTAACATGTATGTGCAATGCGAGGA 3984
QY 2161 CAGGGGCTCTGAGATGTCGACCTGTGCGAAGGCACTGTCACTGTGGAAGACATTTCA 2220
DB 3985 CAGGGGCTCTGAGATGTCGACCTGTGCGAAGGCACTGTCACTGTGGAAGACATTTCA 4044
QY 2221 CGTAGCCAGCACTCTCGAAGGCTGTGCGACATGTTTGAAGCATTAACATGACCCGCTG 2280
DB 4045 CGTAGCCAGCACTCTCGAAGGCTGTGCGACATGTTTGAAGCATTAACATGACCCGCTG 4104
QY 2281 TTCCTTGCATTTGGGTAAACAGAGAGGGGGTGTTCCTACCTTAACATGCAATTTGATCA 2340
DB 4105 TTCCTTGCATTTGGGTAAACAGAGAGGGGGTGTTCCTACCTTAACATGCAATTTGATCA 4164
QY 2341 CACTAAGATATTGCTTGAAGCCGAGAGAGCATGTCMAAGGTGAACCTGAACCGGGGTGTTGA 2400
DB 4165 CACTAAGATATTGCTTGAAGCCGAGAGAGCATGTCMAAGGTGAACCTGAACCGGGGTGTTGA 4224
QY 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGTACATGAGAACCCGACACAGGTGAGAAC 2460
DB 4225 CATGACCATGAAGATCTGGAAGGTGCTGAGTACATGAGAACCCGACACAGGTGAGAAC 4284
QY 2461 CTGCGAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGTGATGTGAACGAGGA 2520
DB 4285 CTGCGAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGTGATGTGAACGAGGA 4344
QY 2521 GCTGAAGGCCCGATCACTTGTGTCTGGCCCTGACCCGCGCTGAGTTTGGCTTACGAGATGA 2580
DB 4345 GCTGAAGGCCCGATCACTTGTGTCTGGCCCTGACCCGCGCTGAGTTTGGCTTACGAGATGA 4404
QY 2581 AGATACAGATTGAG 2594
DB 4405 AGATACAGATTGAG 4418
RESULT 7
LOCUS BD021940 11152 bp DNA linear PAT 27-AUG-2002
DEFINITION Packaging cell systems for use in promotion of the development of
ACCESSION BD021940
VERSION BD021940.1 GI:22563163
KEYWORDS JP 2001505047-A/12.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 11152)
AUTHORS Memerow,G.R. and Seggern,D.J.V.
TITLE Packaging cell systems for use in promotion of the development of
high-capacity adenoviral vectors

JOURNAL Patent: JP 2001505047-A 12 17-APR-2001;
COMMENT NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
PN JP 2001505047-A/12
PD 17-APR-2001
PF 24-SEP-1997 JP 1998515273
PR 25-SEP-1996 US 08/719806
PI GLEN R MEMEROW, DANIEL J VON SEGGERN
PC C12N5/10, C07K14/075, C12N15/09//A61K31/711, A61K35/76, A61K48/00,
PC A61B35/00
PC C12N5/00, C12N15/00
CC Strandedness: Double;
CC Topology: Circular;
FH Key Location/Qualifiers.
FEATURES
source location/Qualifiers
1..11152
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 2594; DB 6; Length 11152;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCGATCTTACCTGCAAGAGGCTGCTTCCACCAAGTGAAGAGATGAAGAGGT 60
DB 1825 ATCGATCTTACCTGCAAGAGGCTGCTTCCACCAAGTGAAGAGATGAAGAGGT 1884
QY 61 GAGAGATTGTGTTAGATTATGTGAGACACCCGGGCAAGTTGCAAGTCTTTCATTAT 120
DB 1885 GAGAGATTGTGTTAGATTATGTGAGACACCCGGGCAAGTTGCAAGTCTTTCATTAT 1944
QY 121 CACCGAGGAATTAAGGGGAGCCAGATATTATGTGTCCTTCTATAGAGACCTGT 180
DB 1945 CACCGAGGAATTAAGGGGAGCCAGATATTATGTGTCCTTCTATAGAGACCTGT 2004
QY 181 GGCATGTTTGTCTACAGTAAAGTAAATTAATGAGCAGTGTGATAGATGTGGGTTTG 240
DB 2005 GGCATGTTTGTCTACAGTAAAGTAAATTAATGAGCAGTGTGATAGATGTGGGTTTG 2064
QY 241 GTGTGTAATTTTATTTTAAATTTTAAACAGTTTGTGTTTAAAGATTTGTATTTGA 300
DB 2065 GTGTGTAATTTTATTTTAAATTTTAAACAGTTTGTGTTTAAAGATTTGTATTTGA 2124
QY 301 TTTTAAAGATGCTGTGTCTGAACCTGAGCCGAGCCGAGACCGAGACCTG 360
DB 2125 TTTTAAAGATGCTGTGTCTGAACCTGAGCCGAGCCGAGACCGAGACCTG 2184
QY 361 CAAGACCTACCCGCGTCTTAAATGAGCGCTGTATCTTGAAGCGCCGACATCACCTG 420
DB 2185 CAAGACCTACCCGCGTCTTAAATGAGCGCTGTATCTTGAAGCGCCGACATCACCTG 2244
QY 421 TGTCTAGGAATGCAATGTAGTACGATACGTGACTCCGGTCTTCTTACACACTTC 480
DB 2245 TGTCTAGGAATGCAATGTAGTACGATACGTGACTCCGGTCTTCTTACACACTTC 2304
QY 481 CTGAGATACACCGGTGTCCGCGTGTGCCCCATTTAAACAGTTGCGTGAAGATTGGTG 540
DB 2305 CTGAGATACACCGGTGTCCGCGTGTGCCCCATTTAAACAGTTGCGTGAAGATTGGTG 2364
QY 541 GCGGTGCGCAGCTGTGGAATGTATCGAGACTTGTCTTAAAGAGCTGGGACCTTTGG 600
DB 2365 GCGGTGCGCAGCTGTGGAATGTATCGAGACTTGTCTTAAAGAGCTGGGACCTTTGG 2424
QY 601 ACTTGAAGTGTAAAGCCCGCCAGCCATTAAGTGTAAACCTGTGATGTGTGTGTTAA 660
DB 2425 ACTTGAAGTGTAAAGCCCGCCAGCCATTAAGTGTAAACCTGTGATGTGTGTGTTAA 2484
QY 661 GCGCTTGTGTTGGAATGATGTATGTAATTAATTAAGAGGTGAAGTAATGTTAACT 720
DB 2485 GCGCTTGTGTTGGAATGATGTATGTAATTAATTAAGAGGTGAAGTAATGTTAACT 2544
QY 721 TGCATGGCGTGTAAATGGGCGGGCTTAAAGGATATATATGCGCGCTAATCT 780

D	2545	TCGATGCGCTGTAATGAGGCGGCGCTTAAAGGTAATATATGCGCGTGAATCT	2604
Q	781	TGCTTACATCTGACCTCATGAGCGCTTGGAGTGTGGAGATTTTCTGCTGCGTA	840
D	2605	TGGTATCATCTGACCTCATGAGCGCTTGGAGTGTGGAGATTTTCTGCTGCGTA	2664
Q	841	ACTTGTCTGGAACAGAGCTCTAACAGTACTCTTGGTTTGGAGGTTTCTGCGGCTCAT	900
D	2665	ACTTGTCTGGAACAGAGCTCTAACAGTACTCTTGGTTTGGAGGTTTCTGCGGCTCAT	2724
Q	901	CCGAGCGCAAGTTAGTCTGAGAAATTAAGAGGATTAACAAGTGGGATTTTGAAGCTTT	960
D	2725	CCGAGCGCAAGTTAGTCTGAGAAATTAAGAGGATTAACAAGTGGGATTTTGAAGCTTT	2784
Q	961	TGAATCTGTGTGAGCTGTGTTTATCTTGGATCTGAGTCAACGAGCGCTTTTCCAG	1020
D	2785	TGAATCTGTGTGAGCTGTGTTTATCTTGGATCTGAGTCAACGAGCGCTTTTCCAG	2844
Q	1021	AGAGGTCATGAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT	1080
D	2845	AGAGGTCATGAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT	2904
Q	1081	TTTGGAGTTTATAAAGGATAAATGAGCGAAGAAACCATCTGAGCGGGGGTACCTGC	1140
D	2905	TTTGGAGTTTATAAAGGATAAATGAGCGAAGAAACCATCTGAGCGGGGGTACCTGC	2964
Q	1141	TGATTTTCTGCGCATCTGTGTGAGAGCGGTTGTGAGACAGAGATGCGCTGTAC	1200
D	2965	TGATTTTCTGCGCATCTGTGTGAGAGCGGTTGTGAGACAGAGATGCGCTGTAC	3024
Q	1201	TGTTGTCTTCCGTCGCGCGCGGATTAATCCGACGAGAGAGACAGACAGACAGAGG	1260
D	3025	TGTTGTCTTCCGTCGCGCGCGGATTAATCCGACGAGAGAGACAGACAGACAGAGG	3084
Q	1261	AAGCAGAGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG	1320
D	3085	AAGCAGAGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG	3144
Q	1321	GGAATGATGTTGTATACAGTGTGCTGAACTGTATCCAGACCTGAGACATTTTGACAT	1380
D	3145	GGAATGATGTTGTATACAGTGTGCTGAACTGTATCCAGACCTGAGACATTTTGACAT	3204
Q	1381	TACGAGAGATGAGGCGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC	1440
D	3205	TACGAGAGATGAGGCGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC	3264
Q	1441	AGAGAGAGCTGAGATCTAGCTTTAGCTTAATGACAGACACCGTCTGAGTATTTAC	1500
D	3265	AGAGAGAGCTGAGATCTAGCTTTAGCTTAATGACAGACACCGTCTGAGTATTTAC	3324
Q	1501	TTTTCAACAGATCAAGATTAATGCGCTTAATGAGCTTGATCTGTGCGGAGAAATTC	1560
D	3325	TTTTCAACAGATCAAGATTAATGCGCTTAATGAGCTTGATCTGTGCGGAGAAATTC	3384
Q	1561	CATGAGACAGCTGACCACTTACTGCTGACCGCAGGGGATATTTTGAAGGCTATTAG	1620
D	3385	CATGAGACAGCTGACCACTTACTGCTGACCGCAGGGGATATTTTGAAGGCTATTAG	3444
Q	1621	GATATATGCAAAAGGTGCACTTAAAGCCAGATTGACAGTACAGATCAAGCAACTGTAA	1680
D	3445	GATATATGCAAAAGGTGCACTTAAAGCCAGATTGACAGTACAGATCAAGCAACTGTAA	3504
Q	1681	TATAGGAATTTTGTCTACATTTCTGGGAAAGCGGGCGAGGTGAGATAGATCGAGGA	1740
D	3505	TATAGGAATTTTGTCTACATTTCTGGGAAAGCGGGCGAGGTGAGATAGATCGAGGA	3564
Q	1741	TAGGCTGCGCTTTAGATGTAGCATGATTAATATGTGCGCGGGGCTGCTTGACATGACGG	1800
D	3565	TAGGCTGCGCTTTAGATGTAGCATGATTAATATGTGCGCGGGGCTGCTTGACATGACGG	3624
Q	1801	GGTGGTATTATGAATGTAAAGTTTACGCGCCCAATTTTACGGGTACGGTTTCTGCGC	1860

D	3625	GATGTTATTAATGAATGATTAAGTCTGAGCGCCCAATTTTACGGGTACGGTTTCTGCGC	3684
Q	1861	CAATACCAACCTTATCTTACACAGGTGATAGCTTCTATGGTTTAAACAATACCTGTGGA	1920
D	3685	CAATACCAACCTTATCTTACACAGGTGATAGCTTCTATGGTTTAAACAATACCTGTGGA	3744
Q	1921	AGCTTGACCGCATGTAGGGTTTGGGGCTGTGCTTTTACTGTCTGGAAGGGGGTGT	1980
D	3745	AGCTTGACCGCATGTAGGGTTTGGGGCTGTGCTTTTACTGTCTGGAAGGGGGTGT	3804
Q	1981	GTTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTGAAGGTATACCTTGG	2040
D	3805	GTTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTGAAGGTATACCTTGG	3864
Q	2041	TATCTGTCTGAGGGTAACTCAGAGGTGCGCACAATGTGACCTCCGACTGTGTTGCTT	2100
D	3865	TATCTGTCTGAGGGTAACTCAGAGGTGCGCACAATGTGACCTCCGACTGTGTTGCTT	3924
Q	2101	CATGCTAGTGAAGAAAGCTGTGCTGTGATTAAGCATTAACATGTATGTGCAACTGCA	2160
D	3925	CATGCTAGTGAAGAAAGCTGTGCTGTGATTAAGCATTAACATGTATGTGCAACTGCA	3984
Q	2161	CAGGAGCTCTGAGATGCTGACCTGTGAGAGAGCAATGTACCTGCTGAGAGACCATTC	2220
D	3985	CAGGAGCTCTGAGATGCTGACCTGTGAGAGAGCAATGTACCTGCTGAGAGACCATTC	4044
Q	2221	CGTAGCCAGCCACTCTGCAAGGCTGTGCAAGTGTGAGCATTAACATGACCCGCTG	2280
D	4045	CGTAGCCAGCCACTCTGCAAGGCTGTGCAAGTGTGAGCATTAACATGACCCGCTG	4104
Q	2281	TTCCTTGATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTAACTGAATTTGATCA	2340
D	4105	TTCCTTGATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTAACTGAATTTGATCA	4164
Q	2341	CACTAAGATATTGCTTGAAGCCGAGAGATGTCCAAGGTGAACCTGAACGGGGTGTGA	2400
D	4165	CACTAAGATATTGCTTGAAGCCGAGAGATGTCCAAGGTGAACCTGAACGGGGTGTGA	4224
Q	2401	CATGACCATGAAAGTCTGAAAGGTGTGAGATGATGAGACCCGACACAGGTGCAAGC	2460
D	4225	CATGACCATGAAAGTCTGAAAGGTGTGAGATGATGAGACCCGACACAGGTGCAAGC	4284
Q	2461	CTGCGAGTGTGGCGGTAAACATATTAGAACACAGCTGTGATGCTGATGTGACCGAGA	2520
D	4285	CTGCGAGTGTGGCGGTAAACATATTAGAACACAGCTGTGATGCTGATGTGACCGAGA	4344
Q	2521	GCTGAGGCGGATACCTTGGTGTGCGCTGCACCGGGCTGAGTTGGCTTACCGATGA	2580
D	4345	GCTGAGGCGGATACCTTGGTGTGCGCTGCACCGGGCTGAGTTGGCTTACCGATGA	4404
Q	2581	AGATACAGATTGAG 2594	
D	4405	AGATACAGATTGAG 4418	

RESULT 8

AD5001 11570 bp DNA linear VRL 09-SEP-2004

LOCUS Adenovirus type 5 left 32% of the genome (coordinates 0% to 32.39%)

DEFINITION as measured by <adv>)

ACCESSION X02996 J01967 J01968 J01970 J01971 J01972 J01974 J01976 J01977

VERSION X02996.1 GI:58484

KEYWORDS alternate splicing; DNA polymerase; overlapping genes; polymerase; RNA polymerase III; terminal protein; terminal repeat; transfer RNA.

SOURCE Human adenovirus type 5

ORGANISM Human adenovirus type 5

REFERENCE 1 (bases 1 to 194)

AUTHORS Steenbergh, P.H., Maat, J., van Ormondt, H., and Susenbach, J.S.

TITLE The nucleotide sequence at the termini of adenovirus type 5 DNA

JOURNAL Nucleic Acids Res. 4 (12), 4371-4389 (1977)

MEDLINE	78093872	
PUBMED	600739	
REFERENCE	2 (bases 1 to 1574)	
AUTHORS	Van Ormondt,H., Maat,J., De Waard,A. and Van der Eb,A.J.	
TITLE	The nucleotide sequence of the transforming HpaI-E fragment of adenovirus type 5 DNA	
JOURNAL	Gene 4 (4), 309-328 (1978)	
MEDLINE	79128735	
PUBMED	744889	
REFERENCE	3 (bases 1575 to 2809)	
AUTHORS	Maat,J. and Van Ormondt,H.	
TITLE	The nucleotide sequence of the transforming HindIII-G fragment of adenovirus type 5 DNA. The region between map positions 4.5 (HpaI site) and 8.0 (HindIII site)	
JOURNAL	Gene 6 (1), 75-90 (1979)	
MEDLINE	80004833	
PUBMED	478299	
REFERENCE	4	
AUTHORS	Perricaudet,M., Akusjarvi,G., Virtanen,A. and Pettersson,U.	
TITLE	Structure of two spliced mRNAs from the transforming region of human subgroup C adenoviruses	
JOURNAL	Nature 281 (5733), 694-696 (1979)	
MEDLINE	81012104	
PUBMED	551290	
REFERENCE	5 (bases 10524 to 10696)	
AUTHORS	Thimmappaya,B., Jones,N. and Shank,T.	
TITLE	A mutation which alters initiation of transcription by RNA polymerase III on the Ad5 chromosome	
JOURNAL	Cell 18 (4), 947-954 (1979)	
MEDLINE	80090080	
PUBMED	519773	
REFERENCE	6 (bases 1 to 6246)	
AUTHORS	Broker,T.R.	
TITLE	Appendix d: nucleotide sequences, transcription and translation analyses, and restriction endonuclease cleavage maps of group-c human adenoviruses	
JOURNAL	(in) Toozze,J. (Ed.):	
MEDLINE	DNA TUMOR VIRUSES: 937-1002;	
PUBMED	Cold Spring Harbor Laboratory (1980)	
REFERENCE	7 (bases 2804 to 4125)	
AUTHORS	Maat,J., van Beveren,C.P. and van Ormondt,H.	
TITLE	The nucleotide sequence of adenovirus type 5 early region E1: the region between map positions 8.0 (HindIII site) and 11.8 (SmaI site)	
JOURNAL	Gene 10 (1), 27-38 (1980)	
MEDLINE	81005097	
PUBMED	6250944	
REFERENCE	8	
AUTHORS	Perricaudet,M., Le Moulllec,J.M. and Petersson,U.	
TITLE	Predicted structure of two adenovirus tumor antigens	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3778-3782 (1980)	
MEDLINE	81054654	
PUBMED	6253988	
REFERENCE	9 (bases 1 to 4125)	
AUTHORS	van Ormondt,H., Maat,J. and van Beveren,C.P.	
TITLE	The nucleotide sequence of the transforming early region E1 of adenovirus type 5 DNA	
JOURNAL	Gene 11 (3-4), 239-309 (1980)	
MEDLINE	81165537	
PUBMED	6260576	
REFERENCE	10 (bases 10555 to 10733)	
AUTHORS	Fowlkes,D.M. and Shank,T.	
TITLE	Transcriptional control regions of the adenovirus VAI RNA gene	
JOURNAL	Cell 22 (2 Pt 2), 405-413 (1980)	
MEDLINE	81088343	
PUBMED	7448868	
REFERENCE	11 (bases 1653 to 4043)	
AUTHORS	Boe,J.L., Polder,L.J., Bernards,R., Schrier,P.I., van den Elsen,P.J., van der Eb,A.J. and van Ormondt,H.	
TITLE	The 2.2 kb E1b mRNA of human Ad2 and Ad5 codes for two tumor antigens starting at different AUG triplets	
JOURNAL	Cell 27 (1 Pt 2), 121-131 (1981)	
MEDLINE	82115327	

```

JOURNAL PUBMED 7326748
REFERENCE 12 (bases 4001 to 6246)
AUTHORS van Beveren,C.P., Maat,J., Dekker,B.M. and van Ormondt,H.
TITLE The nucleotide sequence of the gene for protein Iva2 and of the 5' leader segment of the major late mRNAs of adenovirus type 5
JOURNAL JOURNAL 8221179
PUBMED 7343420
REFERENCE 13 (bases 325 to 604)
AUTHORS Hearing,P. and Shank,T.
TITLE Functional analysis of the nucleotide sequence surrounding the cap site for adenovirus type 5 region E1A messenger RNAs
JOURNAL JOURNAL 8326891
MEDLINE 6876165
REMARK deletion mutants
AUTHORS 14 (bases 1 to 66)
TITLE Nagata,K., Guggenheim,R.A. and Hurwitz,J.
Specific binding of a cellular DNA replication protein to the origin of replication of adenovirus DNA
PROC. Natl. Acad. Sci. U.S.A. 80 (20), 6177-6181 (1983)
JOURNAL 84016017
MEDLINE 6336326
PUBMED 15 (bases 6242 to 11570)
REFERENCE Dekker,B.M. and van Ormondt,H.
The nucleotide sequence of fragment HindIII-C of human adenovirus type 5 DNA (map positions 17,1-31.7)
JOURNAL Gene 27 (1), 115-120 (1984)
MEDLINE 84183604
PUBMED 6325298
AUTHORS 16
Downey,J.F., Evelyn,G.M., Branton,P.B. and Bayley,S.T.
Peptide maps and N-terminal sequences of polypeptides from early region 1A of human adenovirus 5
J. Virol. 50 (1), 30-37 (1984)
JOURNAL 84138826
MEDLINE 6699947
PUBMED sites; cds start for E1a proteins
REMARK sites; splice sites in E1a 13S mRNA
COMMENT sites; splice sites and termini for E1b mRNAs
sites; splice sites and termini for E1b mRNAs
Notes on the presentation of ADENO in the EMBL data library: The genetic map of Adeno is customarily presented from left to right, the 0% position being left and the 100% position being right. The two strands of Adeno are normally represented like this: r-strand: 3'-----5'
l-strand: 5'-----3'
This often causes confusion because the generally accepted way to represent DNA molecules is:
3'-----5'
5'-----3'
Here Adeno virus sequences are always given in 5' to 3' direction and the sequence of the l-strand is displayed irrespective of the direction the viral transcription takes.
This sequence corresponds to bases 1 to 11560 of <ad3>, which serves as some basis for the annotation of sites. The differences between <ad3> and <ad5> are too many to report herein, however a printout of those is available upon request from genbank. The map coordinates in the sites presume 360 bases per map unit. although there are approximately 115 sequence differences between the two strains over this region, no site difference exceeds 0.02% by this calculation.
the sequence represents the early mra transcripts e1a and e1b and the intermediate mra transcript ix, all of which are transcribed rightwardly off the r-strand, the iya2 and ezb mras which are transcribed leftwardly off the l-strand ((indicated by '(c)' and 'comp strand' below)); and the 5' end of the 28 kb major late mra the cap sites and possible promoter sequences for these are summarized in the following table:
mra      cap site      possible promoter region -----
tattcata at bases 468-475 [6] elb          1702          499

```

tataaa at bases 1672-1678[6] 1x 3582
tataaa at bases 3551-3557 [6] 1x2 5838 +/- 2 (c)
tataaa at bases 5979-5974 on the comp strand [10]
major 6049 tataaa at bases 6018-6024 [10] as
with ad2, not all the transcripts from this region have been
characterized at the sequence level. the nine proteins given in
features table below are not the only possible gene products (see
the main adenovirus 2 entry).
large amounts of small rnas are produced from the vat and vai
genes late in development for unknown reasons. [5] and [6]
demonstrate that vai gene activity influences vai expression; that
the 5' flank affects the start site of the rna but that an
intragenic promoter (bases 10626 to 10690 below) determines whether
the rna is actually produced, and that there is striking similarity
between this rna and trna.

FEATURES
source

1. 11570
/organism="Human adenovirus type 5"
/mol_type="genomic DNA"
/db_xref="taxon:28285"
499..1632
/note="Primary transcript of E1A region"
join(499..1112,1229..1632)
/note="mRNA 1 (part 1)"
join(499..974,1229..1632)
/note="mRNA 2 (part 1)"
join(560..1112,1229..1545)
/note="unamed protein product; E1a protein from 18s mrna
(32k, regulation and transformation)"
/codon_start=1
/protein_id="CAB40663.1"
/db_xref="GI:4584382"
/db_xref="GOA:P03255"
/db_xref="UniProt/Swiss-Prot:P03255"
/translation="MRH1ICHGVIITEEMASLIDQLIEVYADNLPPSPFEPPTLH
ELYLDVYAPEDPNEBAVSQIFPDVSMVAOEGIDLPFPAQSPSPHLSRDEOP
EORALGPMVNLVEVLDLTCHEGAPSPDEDEBEGFULDYVHEPHGHCRCYH
RRNMGDPDIMSCLMYRCMGFYVSPVSEPPPEPPEPRAPRRPMAAIIIRRP

Query Match 100.0%; Score 2594; DB 14; Length 11570;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGATCTTACTCCGACGAGCTGGCTTTCCACCCCAATGACGAGAGATGAAGAGGT 60
917 ATGATCTTACTCCGACGAGCTGGCTTTCCACCCCAATGACGAGAGATGAAGAGGT 976
61 GAGAGTTTGTAGATTATGTGAGACACCCGGGACGAGTTGAGAGTCTTGCATTAT 120
977 GAGAGTTTGTAGATTATGTGAGACACCCGGGACGAGTTGAGAGTCTTGCATTAT 1036
121 CACCGAGGAATACGGGGGACCCAGATATTATGTGCTTGTCTATATAGAGACCTGT 180
1037 CACCGAGGAATACGGGGGACCCAGATATTATGTGCTTGTCTATATAGAGACCTGT 1096
181 GCGATGTTGTCTACAGTAATGAATAATTATGGGCACTGGGTATATAGAGTGGGTTTG 240
1097 GCGATGTTGTCTACAGTAATGAATAATTATGGGCACTGGGTATATAGAGTGGGTTTG 1156
241 GTGGGTAATTTTATTTTATTTTACAGTTTGTGGTTTAAAGATTGTTATTTGA 300
1157 GTGGGTAATTTTATTTTATTTTACAGTTTGTGGTTTAAAGATTGTTATTTGA 1216
301 TTTTAAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCGAGACCGAGAGCTTG 360
1217 TTTTAAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCGAGACCGAGAGCTTG 1276
361 CAGAGACTACCCGGCGCTTAAATATGGGCTGCTATCTTGAAGCGCCGACATCACTTG 420
1277 CAGAGACTACCCGGCGCTTAAATATGGGCTGCTATCTTGAAGCGCCGACATCACTTG 1336
421 TGTCTAGAGATGCAATAGTAGAGATAGCTGACTCGGCTCTTCTAACAACACTC 480

1337 TGTCTAGAGATGCAATAGTAGAGATAGCTGACTCGGCTCTTCTAACAACACTC 1396
481 CTGAGATACACCCGGGTGTCCGCTGTGCCCCCATTTAAACAGTTGCGCTGAGAGTTGGTG 540
1397 CTGAGATACACCCGGGTGTCCGCTGTGCCCCCATTTAAACAGTTGCGCTGAGAGTTGGTG 1456
541 GCGCGGCAAGCTGTGAATATGATTCGAGACTTGTCTTAAAGAGCTTGGCACTTTGG 600
1457 GCGCGGCAAGCTGTGAATATGATTCGAGACTTGTCTTAAAGAGCTTGGCACTTTGG 1516
601 ACTGAGCTGTAAACGCCCGACGACCAATAGGTTAAACCTGTGATTTGGTGTGTTAA 660
1517 ACTGAGCTGTAAACGCCCGACGACCAATAGGTTAAACCTGTGATTTGGTGTGTTAA 1576
661 GCGCTTGTGTTGCTGAATAGATGATGATTAATTAAGGTGAGATTAATGTTTAACT 720
1577 GCGCTTGTGTTGCTGAATAGATGATGATTAATTAAGGTGAGATTAATGTTTAACT 1636
721 TGCATGGGCTGTAAATATGGGCGGGGCTTAAAGGTTATATATGCGCGCTAATCT 780
1637 TGCATGGGCTGTAAATATGGGCGGGGCTTAAAGGTTATATATGCGCGCTAATCT 1696
781 TGGTACATCTGACCTCATGAGAGCTTGGAGTGTGTTGGAAGATTTTCTGCTGCGCTA 840
1697 TGGTACATCTGACCTCATGAGAGCTTGGAGTGTGTTGGAAGATTTTCTGCTGCGCTA 1756
841 ACTGCTGGAACAGAGCTCTTAACAGTACCTCTGTGTTTGGAGGTTTCTGCGGCTCAT 900
1757 ACTGCTGGAACAGAGCTCTTAACAGTACCTCTGTGTTTGGAGGTTTCTGCGGCTCAT 1816
901 CCCAGGCAAAATGTGTCTGCAAGATTAAAGAGATTACAGTGGAAATTTGAAGACTTT 960
1817 CCCAGGCAAAATGTGTCTGCAAGATTAAAGAGATTACAGTGGAAATTTGAAGACTTT 1876
961 TGAATCCTGTGAGAGCTGTTATCTTGAATCTGGGTACACAGCGCTTTTCCAAG 1020
1877 TGAATCCTGTGAGAGCTGTTATCTTGAATCTGGGTACACAGCGCTTTTCCAAG 1936
1021 AGAAGTCATCAAGACTTTGATTTTCCACACCGGGGCGCGCTGCGGCTGTGCTT 1080
1937 AGAAGTCATCAAGACTTTGATTTTCCACACCGGGGCGCGCTGCGGCTGTGCTT 1996
1997 TTTGAGATTTTAAAGATTAATGAGAGCAAGAAACCAATCTGAGCGGGGTTAACCCTGC 2056
1141 TGGATTTTCTGGCCATCTGTGAGAGCGGTTGAGACCAAAATGCGCCTGTAC 1200
2057 TGGATTTTCTGGCCATCTGTGAGAGCGGTTGAGACCAAAATGCGCCTGTAC 2116
1201 TGTGTCTTCCGTCGCGCGCGCATTAATACCGACGAGAGCAGACAGCAGAGAGG 1260
2117 TGTGTCTTCCGTCGCGCGCGCATTAATACCGACGAGAGCAGACAGCAGAGAGG 2176
1261 AAGCCAGCGCGCGCGCAGAGAGCAGCCCATGGAACCCGAGAGCCGCGCTGACCTTC 1320
2177 AAGCCAGCGCGCGCGCAGAGAGCAGCCCATGGAACCCGAGAGCCGCGCTGACCTTC 2236
1321 GGGATGAATGTTGTACAGGTGCTGAACCTGTATCCGAATCTAGAGAGCAATTTGAACAT 1380
2237 GGGATGAATGTTGTACAGGTGCTGAACCTGTATCCGAATCTAGAGAGCAATTTGAACAT 2296
1381 TACAGAGATGAGGCGAGGCTTAAAGGGGTTAAAGAGGAGACGGGGGCTTGTAGGCTAC 1440
2297 TACAGAGATGAGGCGAGGCTTAAAGGGGTTAAAGAGGAGACGGGGGCTTGTAGGCTAC 2356
1441 AGAGAGGCTTGAATTTAGCTTTTAAATGACCAAGACCGCTCTAGTGTATTAAC 1500
2357 AGAGAGGCTTGAATTTAGCTTTTAAATGACCAAGACCGCTCTAGTGTATTAAC 2416
1501 TTTTCAACAGATCAAGGATTAATGGCGTAAATGAGCTTGAATCTGCGCGCAGAAATTC 1560
2417 TTTTCAACAGATCAAGGATTAATGGCGTAAATGAGCTTGAATCTGCGCGCAGAAATTC 2476

OY	1561	LATGAGACAGCTGACCACTTA	CTGGCTGCAGCCAGGGGAGATTTG	AAGAGGCTATTAG	1620
Db	2477	CATGAGACAGCTGACCACTTA	CTGGCTGCAGCCAGGGGAGATTTG	AAGAGGCTATTAG	2536
OY	1621	GGTATATGCAAAAGGTGGCACTT	AGGCGCAGATTTGCAGATACAAAGATTCAGCAAACTTGTAA		1680
Db	2537	GGTATATGCAAAAGGTGGCACTT	AGGCGCAGATTTGCAGATACAAAGATTCAGCAAACTTGTAA		2596
OY	1661	TATCAGCAATTTGTTGCTACATTT	CTGGGAACGGGGCCGAGGTGGAGATTAATACGAGGA	1740	
Db	2597	TATCAGCAATTTGTTGCTACATTT	CTGGGAACGGGGCCGAGGTGGAGATTAATACGAGGA	2656	
OY	1741	TAGGGTGGCCCTTTAGATGTAGCAGAT	TAATAATATGAGCCGGGGGTGCTGGCATGACG	1800	
Db	2657	TAGGGTGGCCCTTTAGATGTAGCAGAT	TAATAATATGAGCCGGGGGTGCTGGCATGACG	2716	
OY	1801	GGTGGTTATTAATGATGTAAAGT	TTACTGGCCCAATTTTAAGCGTACGGTTTCTTGC	1860	
Db	2717	GGTGGTTATTAATGATGTAAAGT	TTACTGGCCCAATTTTAAGCGTACGGTTTCTTGC	2776	
OY	1861	CAATACCAACTTATCTTACACACG	GTATAGCTTCTATAGGGTTTAAACAATACCTGTGTGA	1920	
Db	2777	CAATACCAACTTATCTTACACACG	GTATAGCTTCTATAGGGTTTAAACAATACCTGTGTGA	2836	
OY	1921	AGCCGGAACCGATGTAAAGGTT	CCGGGGCTGTGCCCTTTATCTGCTGCAGAAAGGGGGTGT	1980	
Db	2837	AGCCGGAACCGATGTAAAGGTT	CCGGGGCTGTGCCCTTTATCTGCTGCAGAAAGGGGGTGT	2896	
OY	1981	GTGTGCCCCCAAAAGCAGGGCTT	CAATTTAAGAAATGCTCTTTGAAAAGTGTACTTTGG	2040	
Db	2897	GTGTGCCCCCAAAAGCAGGGCTT	CAATTTAAGAAATGCTCTTTGAAAAGTGTACTTTGG	2956	
OY	2041	TATCTGTCTGAAGGTTAACTCA	AGGATGCGCCACAATGTGGCCCTCCACTGTGGTTGCTT	2100	
Db	2957	TATCTGTCTGAAGGTTAACTCA	AGGATGCGCCACAATGTGGCCCTCCACTGTGGTTGCTT	3016	
OY	2101	CATGCTAGTAAAAACGATGGCTGT	ATTAAGCATTAACATGTGTATGTGGCACTCGAGGA	2160	
Db	3017	CATGCTAGTAAAAACGATGGCTGT	ATTAAGCATTAACATGTGTATGTGGCACTCGAGGA	3076	
OY	2161	CAGGGCTCTCAGATGTCTGACCT	GTGCGAAGCAACTGTCACTGTGAAGACATTTCA	2220	
Db	3077	CAGGGCTCTCAGATGTCTGACCT	GTGCGAAGCAACTGTCACTGTGAAGACATTTCA	3136	
OY	2221	CGTACCCAGCCACTCTCGCAAG	CGCTGGCCAGTGTTTAGCATTAACATCGAACCCGCTG	2280	
Db	3137	CGTACCCAGCCACTCTCGCAAG	CGCTGGCCAGTGTTTAGCATTAACATCGAACCCGCTG	3196	
OY	2281	TTCCCTTGCAATTTGGGATACAG	GAAGGGGGGTGTCTTACCTTAACCAATGCATTTGAATCA	2340	
Db	3197	TTCCCTTGCAATTTGGGATACAG	GAAGGGGGGTGTCTTACCTTAACCAATGCATTTGAATCA	3256	
OY	2341	CACATAAGATATTTGCTTAGACC	CCGAGACATGTCCAAAGTGAACCTGAACGGGGTGTTTGA	2400	
Db	3257	CACATAAGATATTTGCTTAGACC	CCGAGACATGTGTCCAAAGTGAACCTGAACGGGGTGTTTGA	3316	
OY	2401	CATGACCAATGAAGATCTGGAAG	ATGATCTAGATACATAGAACCCGCAACAAGTGTAGACC	2460	
Db	3317	CATGACCAATGAAGATCTGGAAG	ATGATCTAGATACATAGAACCCGCAACAAGTGTAGACC	3376	
OY	2461	CTGCGAGTGTGGCCGGTAAACAT	ATTATAGAACCAAGCCTGTGATGTGTGATGTAACGAGGA	2520	
Db	3377	CTGCGAGTGTGGCCGGTAAACAT	ATTATAGAACCAAGCCTGTGATGTGTGATGTAACGAGGA	3436	
OY	2521	GCTGAGGCCCGATCACTTGTGT	CTGCGCTGCACCCGCGCTGAAGTTGGCTCTACGATGA	2580	
Db	3437	GCTGAGGCCCGATCACTTGTGT	CTGCGCTGCACCCGCGCTGAAGTTGGCTCTACGATGA	3496	
OY	2581	AGATACAGATTAG	2594		
Db	3497	AGATACAGATTAG	3510		

LOCUS	BD268211	14455 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Adenovirus vector, packaging cell line, composition and method for production and use.				
ACCESSION	BD268211				
VERSION	BD268211.1	GI:33077979			
KEYWORDS	JP 2002534130-A/15.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	other sequences; artificial sequences.				
AUTHORS	1 (bases 1 to 14455) Nemerow,G.R., Seggern,D.J.V., Hallenbeck,P.L., Stevenson,S.C. and Skripchenko,Y.				
TITLE	Adenovirus vector, packaging cell line, composition and method for production and use				
JOURNAL	Patent: JP 2002534130-A 15 15-OCT-2002.				
COMMENT	NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE OS Artificial Sequence PN JP 2002534130-A/15 PD 15-OCT-2002 PP 14-JAN-2000 JP 2000593765 PR 14-JAN-1999 US 60/115920 PI GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCENKO PC C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00,A61P43/00, PC C12N7/00,C12O1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC C12N5/10, Description of Artificial Sequence: plasmid Key Location/Qualifiers FT source 1..14455 FT Location/Qualifiers FT 1..14455 /organism='Artificial Sequence'.				
FEATURES	source 1..14455 /location='Qualifiers' /organism='synthetic construct' /mol_type='genomic DNA' /db_xref='taxon:32630'				
ORIGIN					
Query Match	100.0%	Score 2594;	DB 6;	Length 14455;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 2594;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	ATCGATCTTACCTCCACGAGGCTGCGCTTTCACCCAGTGCAGCAGATGAAGAGG	60		
DB	1825	ATCATCTTACCTCCACGAGGCTGCGCTTTCACCCAGTGCAGCAGATGAAGAGG	18844		
QY	61	GAGAGATTGTGTAGATTATGTGAGACACCCGGGCACGGTTGCAGGCTCTTGCATTAT	120		
DB	1885	GAGAGATTGTGTAGATTATGTGAGACACCCGGGCACGGTTGCAGGCTCTTGCATTAT	19444		
QY	121	CACCGAGGATTAGGGGGACCCAGATTATATGTGTTGCGTTTGTCTATATGAGACCTGT	180		
DB	1945	CACCGAGGATTAGGGGGACCCAGATTATATGTGTTGCGTTTGTCTATATGAGACCTGT	20044		
QY	181	GGCATGTTTGTCTACAGTAACTGAAATTAATGAGCAGTGGGTGATAGTGTGGGTTTG	240		
DB	2005	GGCATGTTTGTCTACAGTAACTGAAATTAATGAGCAGTGGGTGATAGTGTGGGTTTG	20644		
QY	241	GTTGTGTATTTTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGAAATTTGTATTTGGA	300		
DB	2065	GTTGTGTATTTTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGAAATTTGTATTTGGA	21244		
QY	301	TTTTTTTAAAGGTCGTGTCTGAACCTGAGCCTGAGCCCGAGCAGAAACCGAGACTG	360		
DB	2125	TTTTTTTAAAGGTCGTGTCTGAACCTGAGCCTGAGCCCGAGCAGAAACCGAGACTG	21844		
QY	361	CAAGACTTACCCGCGCTCTTAAATTTGGCGCTGCTATCTTGAGACGCCGACATCACTG	420		
DB	2185	CAAGACTTACCCGCGCTCTTAAATTTGGCGCTGCTATCTTGAGACGCCGACATCACTG	22444		
QY	421	TGTCTAGAAATGCATATGTATGTAACGATAGCTGACTCCGGTCTCTTCTAACAACACTC	480		


```
Db 2245 TGTCTAGAGAAATGCAAAATGTAATGTAAGTACGTGACCTCGGCTCTTCTAAACACCTC 2304
Qy 481 CTGAGATACACCCCGGTGTCCCGCTGTGCCTCCATTAAACAGTTGCCGTGAGAGTGTG 540
Db 2305 CTGAGATACACCCCGGTGTCCCGCTGTGCCTCCATTAAACAGTTGCCGTGAGAGTGTG 2364
Qy 541 GGCCTCCGCAAGCTGTGAAATGTATCGAGACTTGTCTTAACGAGCTGTGGCAACCTTTGG 600
Db 2365 GGCCTCCGCAAGCTGTGAAATGTATCGAGACTTGTCTTAACGAGCTGTGGCAACCTTTGG 2424
Qy 601 ACTGAGCTGTAAACGCCCAAGGCCATTAAGGCTGTAACCTGTGATGCGTGTGTGTTAA 660
Db 2425 ACTGAGCTGTAAACGCCCAAGGCCATTAAGGCTGTAACCTGTGATGCGTGTGTGTTAA 2484
Qy 661 CGCTTTGTTTGTCTGAATGAGTGTATGTAACTTTAAATTAAGGCTGAGTAATGTTTAACT 720
Db 2485 CGCTTTGTTTGTCTGAATGAGTGTATGTAACTTTAAATTAAGGCTGAGTAATGTTTAACT 2544
Qy 721 TGCATGCGGTGTAAATGGGCGGGGCTTAAAGGCTATATATGCGCGTGGCTAATCT 780
Db 2545 TGCATGCGGTGTAAATGGGCGGGGCTTAAAGGCTATATATGCGCGTGGCTAATCT 2604
Qy 781 TGGTTACATCTGACCTCATGAGGCTTGAGAGTGTGGAGATTTTTCGTGTCGTGCGTA 840
Db 2605 TGGTTACATCTGACCTCATGAGGCTTGAGAGTGTGGAGATTTTTCGTGTCGTGCGTA 2664
Qy 841 ACTTGTGGAACAGAGCTCTTAACAGTACTCTTGTTTGTGAGGTTTCTGTGGGCTCAT 900
Db 2665 ACTTGTGGAACAGAGCTCTTAACAGTACTCTTGTTTGTGAGGTTTCTGTGGGCTCAT 2724
Qy 901 CCCGAGCAAAAGTTAGTCTGCAAGATTAAAGAGATTACAAAGTGGAAATTGAAAGCTTT 960
Db 2725 CCCGAGCAAAAGTTAGTCTGCAAGATTAAAGAGATTACAAAGTGGAAATTGAAAGCTTT 2784
Qy 961 TGAATTCCTGTGTGAGCTGTTGATCTTTGAATCTGGCTCACACAGGCGCTTTTCCAG 1020
Db 2785 TGAATTCCTGTGTGAGCTGTTGATCTTTGAATCTGGCTCACACAGGCGCTTTTCCAG 2844
Qy 1021 AGAAGGTCATCAAGACTTTGGATTTTTCACACCGGGCGCGCTGCGCTGTGCTT 1080
Db 2845 AGAAGGTCATCAAGACTTTGGATTTTTCACACCGGGCGCGCTGCGCTGTGCTT 2904
Qy 1081 TTTTGAATTTTAAAGATTAATGAGCCGAAAGAACCCATCTGAGCGGGGCTGACCTGC 2964
Db 2905 TTTTGAATTTTAAAGATTAATGAGCCGAAAGAACCCATCTGAGCGGGGCTGACCTGC 3024
Qy 1141 TGGATTTTCTGGCCATGCTGTGAGAGGCGTTGTGAGACAAAGATGCGCTGTAC 1200
Db 2965 TGGATTTTCTGGCCATGCTGTGAGAGGCGTTGTGAGACAAAGATGCGCTGTAC 3024
Qy 1201 TGTGTCTTCGCTCCGCGCGCGATTAATCCGACGAGAGCAGCAGCAGCAGAGAG 1260
Db 3025 TGTGTCTTCGCTCCGCGCGCGATTAATCCGACGAGAGCAGCAGCAGCAGAGAG 3084
Qy 1261 AAGCCAGCGCGCGCGCGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGTGACCTC 1320
Db 3085 AAGCCAGCGCGCGCGCGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGTGACCTC 3144
Qy 1321 GGGAAATGTTTGTATACAGGTGCTGAATCTGTATCCAACTGAGACGCAATTTTGACAT 1380
Db 3145 GGGAAATGTTTGTATACAGGTGCTGAATCTGTATCCAACTGAGACGCAATTTTGACAT 3204
Qy 1381 TACAGAGATGAGCGAGGCTTAAAGGGGCTTAAAGAGGAGCGGCGGCTGTGAGGCTAC 1440
Db 3205 TACAGAGATGAGCGAGGCTTAAAGGGGCTTAAAGAGGAGCGGCGGCTGTGAGGCTAC 3264
Qy 1441 AGAGAGGCTTAAAGATTAAGTTTACTTAAATACAGACAGACCTGTCTGAGTATTAAC 1500
Db 3265 AGAGAGGCTTAAAGATTAAGTTTACTTAAATACAGACAGACCTGTCTGAGTATTAAC 3324
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTTAATGAGCTTGTCTGTGCGCAGAGTATTC 1560
Db 3325 TTTTCAACAGATCAAGATTAATGCGCTTAATGAGCTTGTCTGTGCGCAGAGTATTC 3384
Qy 1561 CATAGAGAGCTGACCACTTACTGCTGCACAGCGGAGATTTTGTAGAGAGCTATTAG 1620
Db 3385 CATAGAGAGCTGACCACTTACTGCTGCACAGCGGAGATTTTGTAGAGAGCTATTAG 3444
Qy 1621 GGTATATGCAAAAGGTGGCACTTAGGCCAATTCAGATTAAGATCAAGATCAAGATCAAG 1680
Db 3445 GGTATATGCAAAAGGTGGCACTTAGGCCAATTCAGATTAAGATCAAGATCAAGATCAAG 3504
Qy 1681 TATCAGGAATTTGTTGCTACATTTCTGGGGAACGGGGCGAGGTGAGATAGATACGAGAGA 1740
Db 3505 TATCAGGAATTTGTTGCTACATTTCTGGGGAACGGGGCGAGGTGAGATAGATACGAGAGA 3564
Qy 1741 TAGGGTGGCTTTAGATGATGATGATTAATATATGTGCGCGGGGTGCTTGTGACAGCG 1800
Db 3565 TAGGGTGGCTTTAGATGATGATGATTAATATATGTGCGCGGGGTGCTTGTGACAGCG 3624
Qy 1801 GGTGTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Db 3625 GGTGTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3684
Qy 1861 CAATACCAACCTTATCTTACACAGGCTTAAGCTTATGAGGTTTAAACAATACCTGTGGA 1920
Db 3685 CAATACCAACCTTATCTTACACAGGCTTATGAGGTTTAAACAATACCTGTGTGGA 3744
Qy 1921 AGCTTGACCGATGTAAAGGTTGCGGGCTGTCTTTTACTGTCTGTGAGAGGGGCTGT 1980
Db 3745 AGCTTGACCGATGTAAAGGTTGCGGGCTGTCTTTTACTGTCTGTGAGAGGGGCTGT 3804
Qy 1981 GTGTGCGCCCAAAAGCGAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATCTTGG 2040
Db 3805 GTGTGCGCCCAAAAGCGAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATCTTGG 3864
Qy 2041 TATCTGTCTGAGGGTAACTCCAGAGTGGCCCAATATGAGGCTCCGACGTGTGCTT 2100
Db 3865 TATCTGTCTGAGGGTAACTCCAGAGTGGCCCAATATGAGGCTCCGACGTGTGCTT 3924
Qy 2101 CATGCTAGTAAAGCGTGTGATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAG 2160
Db 3925 CATGCTAGTAAAGCGTGTGATTAAGCATTAAGCATTAAGCATTAAGCATTAAGCATTAAG 3984
Qy 2161 CAGGCGCTCTCAATGCTGTGACCTGTGACGAGCACTGTCACTGTGAAAGCATTTCA 2220
Db 3985 CAGGCGCTCTCAATGCTGTGACCTGTGACGAGCACTGTCACTGTGAAAGCATTTCA 4044
Qy 2221 CGTAGCCAGCACTCTGCAAGGCTGTGCAAGTGTGAGCATTAACATACGACCCGCTG 2280
Db 4045 CGTAGCCAGCACTCTGCAAGGCTGTGCAAGTGTGAGCATTAACATACGACCCGCTG 4104
Qy 2281 TTCCTTGCATTTTGGTAAACAGAGGGGCTGTCTTCACTTAAACCAATGCAATTTGAGTCA 2340
Db 4105 TTCCTTGCATTTTGGTAAACAGAGGGGCTGTCTTCACTTAAACCAATGCAATTTGAGTCA 4164
Qy 2341 CACTTAATATTTGTTTGAAGCCCGAGACATGTCCAAAGTGAACCTGAAACGGGGTGTGGA 2400
Db 4165 CACTTAATATTTGTTTGAAGCCCGAGACATGTCCAAAGTGAACCTGAAACGGGGTGTGGA 4224
Qy 2401 CATGACCATGAAGATCTGAAGGTGTGAGAGTACGAGAGCCGCAACAGGTGACAGCC 2460
Db 4225 CATGACCATGAAGATCTGAAGGTGTGAGAGTACGAGAGCCGCAACAGGTGACAGCC 4284
Qy 2461 CTGCAATGTGCGGTAAACATATTAGAAACAGCCTGTGATGCTGATGTGACCGAGGA 2520
Db 4285 CTGCAATGTGCGGTAAACATATTAGAAACAGCCTGTGATGCTGATGTGACCGAGGA 4344
Qy 2521 GCTGAGGCCGAGATCACTTGTGTGCTGTGCTGACACCGGCGTGAAGTTTGGCTTACGAGTGA 2580
Db 4345 GCTGAGGCCGAGATCACTTGTGTGCTGTGCTGACACCGGCGTGAAGTTTGGCTTACGAGTGA 4404
Qy 2581 AGATACAGATTGAG 2594
Db 4405 AGATACAGATTGAG 4418
```


RESULT 10
AX356044
LOCUS AX356044 14455 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 15 from Patent WO0183729.
ACCESSION AX356044
VERSION AX356044.1 GI:18620606
KEYWORDS
ORGANISM
SOURCE
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Nemerow, G.R., von Seggern, D.J. and Friedlander, M.
Vectors for ocular transduction and use thereof for genetic therapy
Patent: WO 0183729-A, 15 08-NOV-2001;
Novartis AG (CH) ; The Scripps Research Institute (US) ; Nemerow,
Glen R. (US) ; Von Seggern, Daniel J. (US) ; Friedlander, Marcy
(US)
FEATURES
source
1. .14455
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Plasmid"
ORIGIN
Query Match 100.0%; Score 2594; DB 6; Length 14455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCATCTTACCTGCGCACGAGGCTGGCTTTCACCCAGTACGACGAGATGAAGAGGT 60
DB 1825 ATGCATCTTACCTGCGCACGAGGCTGGCTTTCACCCAGTACGACGAGATGAAGAGGT 1884
QY 61 GAGAGTTTGTTAGATTAGTGTGGAGACCCCGGGGCGGTTGAGGCTTGTCAATTAT 120
DB 1885 GAGAGTTTGTTAGATTAGTGTGGAGACCCCGGGGCGGTTGAGGCTTGTCAATTAT 1944
QY 121 CACCGAGGAATACGGGGGACCCAGATATTATGTGCTTGTCTATATGAGACCTGT 180
DB 1945 CACCGAGGAATACGGGGGACCCAGATATTATGTGCTTGTCTATATGAGACCTGT 2004
QY 181 GGCATGTTTGTCTACAGTAAGTGAATTTATGGGCGATGGGGTATAGATGTGGGTTTG 240
DB 2005 GGCATGTTTGTCTACAGTAAGTGAATTTATGGGCGATGGGGTATAGATGTGGGTTTG 2064
QY 241 GTGTGCTAATTTTTTTTAAATTTTACAGTTTGTGGTTTAAAGATTTTGTATTGTA 300
DB 2065 GTGTGCTAATTTTTTTTAAATTTTACAGTTTGTGGTTTAAAGATTTTGTATTGTA 2124
QY 301 TTTTAAAAAGTCTGTGTCTGAACTGAGCTGAGCCCGAGCCAGAACCGAGCCTG 360
DB 2125 TTTTAAAAAGTCTGTGTCTGAACTGAGCTGAGCCCGAGCCAGAACCGAGCCTG 2184
QY 361 CAAGACTTACCCGCGCTCTTAAATGAGGCGCTGTCTATCTTGAGAGCCCGAGATCACTG 420
DB 2185 CAAGACTTACCCGCGCTCTTAAATGAGGCGCTGTCTATCTTGAGAGCCCGAGATCACTG 2244
QY 421 TGTCTAAGAAATGCAATAGTACTAGGATAGCTGTGACTCGGCTCTTCAACACACCTC 480
DB 2245 TGTCTAAGAAATGCAATAGTACTAGGATAGCTGTGACTCGGCTCTTCAACACACCTC 2304
QY 481 CTGAGATACACCCGGGTGTCCTGCTGTGCCCATTTAAACCAAGTTGCGGTGAGAGTTGGT 540
DB 2305 CTGAGATACACCCGGGTGTCCTGCTGTGCCCATTTAAACCAAGTTGCGGTGAGAGTTGGT 2364
QY 541 GGCCTGCGCAGGCTGTGAAATGATGAGAGACTTGTCTTACGAGGCTGGGCAACTTTGG 600
DB 2365 GGCCTGCGCAGGCTGTGAAATGATGAGAGACTTGTCTTACGAGGCTGGGCAACTTTGG 2424
QY 601 ACTTAGCTGTAAAGGCCCGAGGCCATAGGTGTAACTGTGATTGCTGTGGTTAA 660

DB 2425 ACTTAGCTGTAAAGGCCCGAGGCCATAGGTGTAACTGTGATTGCTGTGGTTAA 2484
QY 661 GGCCTTGTGTTGCTGAATGAGCTGATGTAAATTTAAAGGCTGATATGTTTAACT 720
DB 2485 GGCCTTGTGTTGCTGAATGAGCTGATGTAAATTTAAAGGCTGATATGTTTAACT 2544
QY 721 TGCATGCGGCTGTTAAATGAGGCGGCGCTTAAAGGCTATATATGCGCGGCTAACT 780
DB 2545 TGCATGCGGCTGTTAAATGAGGCGGCGCTTAAAGGCTATATATGCGCGGCTAACT 2604
QY 781 TGGTTACATCTGACCTTCATGAGAGGCTTGGAGTGTGTTGAAATTTTCTGCTGTGTA 840
DB 2605 TGGTTACATCTGACCTTCATGAGAGGCTTGGAGTGTGTTGAAATTTTCTGCTGTGTA 2664
QY 841 ACTTGTGGAACAGAGCTCTTAACATACCTCTTGTGTTTGGAGGTTCTGTGGGCTCAT 900
DB 2665 ACTTGTGGAACAGAGCTCTTAACATACCTCTTGTGTTTGGAGGTTCTGTGGGCTCAT 2744
QY 901 CCCAGGCAAGTTAGTGTGCAATTAAAGAGATTCAAGTGGGAATTTGAAAGGCTTT 960
DB 2725 CCCAGGCAAGTTAGTGTGCAAGTTAAAGAGATTCAAGTGGGAATTTGAAAGGCTTT 2784
QY 961 TGAATCTGTGTGAGCTGTTGATTCTTTGAACTGTGGTCAACAGGCGCTTTCCAG 1020
DB 2785 TGAATCTGTGTGAGCTGTTGATTCTTTGAACTGTGGTCAACAGGCGCTTTCCAG 2844
QY 1021 AGAAGTCTATCAAGACTTTTGGATTTTCCACACCGGGGCGGCTGCGGCTGTGCTT 1080
DB 2845 AGAAGTCTATCAAGACTTTTGGATTTTCCACACCGGGGCGGCTGCGGCTGTGCTT 2904
QY 1081 TTTTGAATTTTAAAGATTAATGAGACGAAACCACTGTGAGGCGGGGTTACCTGC 1140
DB 2905 TTTTGAATTTTAAAGATTAATGAGACGAAACCACTGTGAGGCGGGGTTACCTGC 2964
QY 1141 TGAATTTTGTGGCCATCTGTGTGAGAGCGGTTGTGACACAAAGATGCTGCTTAC 1200
DB 2965 TGAATTTTGTGGCCATCTGTGTGAGAGCGGTTGTGACACAAAGATGCTGCTTAC 3024
QY 1201 TGTGTCTTCCGTCCGCGCGCGGCTAAATCCGAGGAGACACAGACGAGCAGAGG 1260
DB 3025 TGTGTCTTCCGTCCGCGCGCGGCTAAATCCGAGGAGACACAGACGAGCAGAGG 3084
QY 1261 AAGCAGGCGGCGGCGGAGGAGCAGAGCCCATGAAACCCGAGAGCCGCGCTGACCTC 1320
DB 3085 AAGCAGGCGGCGGCGGAGGAGCAGAGCCCATGAAACCCGAGAGCCGCGCTGACCTC 3144
QY 1321 GGGAAATGAATGTTTACAGTGTGCTGAACTGTATTCAGAACTGAGACCATTTTGAAT 1380
DB 3145 GGGAAATGAATGTTTACAGTGTGCTGAACTGTATTCAGAACTGAGACCATTTTGAAT 3204
QY 1381 TACAGAGATGGGCAAGGGGCTTAAAGGGGTTAAAGGGAGGGGGGCTGTGAGGCTAC 1440
DB 3205 TACAGAGATGGGCAAGGGGCTTAAAGGGGTTAAAGGGAGGGGGGCTGTGAGGCTAC 3264
QY 1441 AGAGAGGCTAGGAATCTAGCTTTTACCTTATATGACAGACACCGTCTCTGATGATTAAC 1500
DB 3265 AGAGAGGCTAGGAATCTAGCTTTTACCTTATATGACAGACACCGTCTCTGATGATTAAC 3324
QY 1501 TTTTCAACAGATCAAGATTAATGGCTTAATGATGATGCTGTGCGCAGAAATATTC 1560
DB 3325 TTTTCAACAGATCAAGATTAATGGCTTAATGATGATGCTGTGCGCAGAAATATTC 3384
QY 1561 CATAGAGACGTGACCACTTACTGCTTCAGCCAGGGGATATTTTGAAGAGGCTATTAG 1620
DB 3385 CATAGAGACGTGACCACTTACTGCTTCAGCCAGGGGATATTTTGAAGAGGCTATTAG 3444
QY 1621 GGTATATGCAAAAGGTGCACTTAGGCTAGATTGCAAGTACAGATCAGCAAACTGTAA 1680
DB 3445 GGTATATGCAAAAGGTGCACTTAGGCTAGATTGCAAGTACAGATCAGCAAACTGTAA 3504
QY 1681 TATCAGGAATGTTGCTACATTTCTGGGAAAGGGGCGGAGGTGAGATGATACGAGGA 1740
DB 3505 TATCAGGAATGTTGCTACATTTCTGGGAAAGGGGCGGAGGTGAGATGATACGAGGA 3564

QY	1741	TAGGGTGGCCTTTAGATGATGATGATTAATATATGAGGCCGGGGGGCTTTGGCATGAGACGG	1800
Db	3555	TAGGGTGGCCTTTAGATGATGATGATTAATATATGAGGCCGGGGGGCTTTGGCATGAGACGG	3624
QY	1801	GATGGTTATTTATGATGTATAGGTTTACTGAGCCCAATTTTATAGCGGTACGTTTTCTGGC	1868
Db	3625	GATGGTTATTTATGATGTATAGGTTTACTGAGCCCAATTTTATAGCGGTACGTTTTCTGGC	3684
QY	1861	CAATACCAACTTATATCTTACACAGGTGTAACTTCTATGGGTTTAACAATACCTGTGTGA	1920
Db	3685	CAATACCAACTTATATCTTACACAGGTGTAACTTCTATGGGTTTAACAATACCTGTGTGA	3744
QY	1921	AGCGTGAAGCCGATGTATGAGGGTTCCGGGGCTGGCCCTTTTAACTGCTGTGGAAGGGGGTGGT	1980
Db	3745	AGCGTGAAGCCGATGTATGAGGGTTCCGGGGCTGGCCCTTTTAACTGCTGTGGAAGGGGGTGGT	3804
QY	1981	GTGTGCGCCCAAAAGCAGGGCTTCAATTAAAGAAATGCTCTTTTGAAGAGTGTACCTTGGG	2040
Db	3805	GTGTGCGCCCAAAAGCAGGGCTTCAATTAAAGAAATGCTCTTTTGAAGAGTGTACCTTGGG	3864
QY	2041	TATCTCTGTGTAGGGTAACTCCAGGGTGGCCCAATGTGCTTCCGACTGTGTGTTGCTT	2100
Db	3865	TATCTCTGTGTAGGGTAACTCCAGGGTGGCCCAATGTGCTTCCGACTGTGTGTTGCTT	3924
QY	2101	CATGCTAGTGAAGAAAGCGTGGCTGTGATTAAGCATTAACATGTGATGTGGCAACTCCGAGA	2160
Db	3925	CATGCTAGTGAAGAAAGCGTGGCTGTGATTAAGCATTAACATGTGATGTGGCAACTCCGAGA	3984
QY	2161	CAGGGCCTCTCAGATGTCTGACCTGTGCTCGGACGGCAACTGTCACTGTGAAAGACATTTCA	2220
Db	3985	CAGGGCCTCTCAGATGTCTGACCTGTGCTCGGACGGCAACTGTCACTGTGAAAGACATTTCA	4044
QY	2221	CGTAGCCACGCACTCTCGCAAGGCTTGCCCACTGTGTAAGCATTAACATGTGATGTGGCACTG	2280
Db	4045	CGTAGCCACGCACTCTCGCAAGGCTTGCCCACTGTGTAAGCATTAACATGTGATGTGGCACTG	4104
QY	2281	TTCCCTTGCAATTTGGGGTAAACAGAGGGGGGGTGTCTCTTACCTTACCAATGCAATTTGAGTCA	2340
Db	4105	TTCCCTTGCAATTTGGGGTAAACAGAGGGGGGGTGTCTCTTACCTTACCAATGCAATTTGAGTCA	4164
QY	2341	CACTAAGATATTTGCTTGAGCCCGAAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTTTGA	2400
Db	4165	CACTAAGATATTTGCTTGAGCCCGAAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTTTGA	4224
QY	2401	CATACCAATGAAGATCTGGAAGGTGTGAGGTAAAGATGATGATGATACCCGACACAGGTGCAAGCC	2460
Db	4225	CATACCAATGAAGATCTGGAAGGTGTGAGGTAAAGATGATGATGATACCCGACACAGGTGCAAGCC	4284
QY	2461	CTGCGAGTGTGGCGGTAAACATATTTAAGGAACAGACCTGTGATGTGTGATGTGAACCGAGA	2520
Db	4285	CTGCGAGTGTGGCGGTAAACATATTTAAGGAACAGACCTGTGATGTGTGATGTGAACCGAGA	4344
QY	2521	GCTGAGGCCGATCACTTGTTGTGCTGTGACCCGCGCTGAGTGTGGCTTACGATGATGA	2580
Db	4345	GCTGAGGCCGATCACTTGTTGTGCTGTGACCCGCGCTGAGTGTGGCTTACGATGATGA	4404
QY	2581	AGATACAGATTGAG 2594	
Db	4405	AGATACAGATTGAG 4418	
RESULT 11			
BD021943			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
unclassified.			
unclassified.			

REFERENCE	1 (bases 1 to 1445)	Memorov,G.R. and Seggern,D.J.V.
AUTHORS		
TITLE	Packaging cell systems for use in promotion of the development of high-capacity adenoviral vectors	
JOURNAL	Patent: JP 2001505047-A 15 17-Apr-2001; NOVARTIS AG,THE SCRIPPS RESEARCH INSTITUTE	
COMMENT	PN JP 2001505047-A/15 PD 17-APR-2001 PF 24-SEP-1997 JP 1998515273 PR 25-SEP-1996 US 08/719806 PI GLEN R MEMEROV, DANIEL J VON SEGGERN PC C12N5/10,C07K14/075,C12N15/09//A61K31/711,A61K35/76,A61K48/00, PC A61P35/00, PC C12N5/00,C12N15/00 CC Strandedness: Double; CC Topology: Circular; FH Location/Qualifiers.	
FEATURES	source Location/Qualifiers. 1..1445 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"	
ORIGIN	Query Match 100.0%; Score 2594; DB 6; Length 1445; Best Local Similarity 100.0%; Pred. No. 0; Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGCATCTTACTCTCCACGAGCGCGCTTCCACCCAGTCAGCGAGATGAAGAGGT	60
DB	1825 ATGCATCTTACTCTCCACGAGCGCGCTTCCACCCAGTCAGCGAGATGAAGAGGT	1884
QY	61 GAGAGTTTGTGTAGATTATGTGTGAGACACCCGCGGACGGTTGCAGTCTTGCATTAT	120
DB	1885 GAGAGTTTGTGTAGATTATGTGTGAGAGACCCGCGGACGGTTGCAGTCTTGCATTAT	1944
QY	121 CACCGGAGGAATACGGGGGACCCGAGATTATATGTGTTGCTTTCCTATATGAGACCTGT	180
DB	1945 CACCGGAGGAATACGGGGGACCCGAGATTATATGTGTTGCTTTCCTATATGAGACCTGT	2004
QY	181 GGCATGTTTGCTCAGTAAGTGAATAATTATGGCAGTGGGTGATAGAGTGGTGGTTTG	240
DB	2005 GGCATGTTTGCTCAGTAAGTGAATAATTATGGCAGTGGGTGATAGAGTGGTGGTTTG	2064
QY	241 GTGTGTAAATTTTTTTTTTAATTTTACAGTTTGTGTGTTAAAGAAATTTTGAATTTGTA	300
DB	2065 GTGTGTAAATTTTTTTTTTAATTTTACAGTTTGTGTGTTTAAAGAAATTTTGAATTTGTA	2124
QY	301 TTTTTTAAAGGCTCGTGTCTGAACCTGACCTGAGCCCGACCGAACCAGACCTG	360
DB	2125 TTTTTTAAAGGCTCGTGTCTGAACCTGACCTGAGCCCGACCGAACCAGACCTG	2184
QY	361 CAAAGACCTACCCGCGCTCTAAATATGCGCGCTGATCTTGAGAGCGCCGACATCATCTG	420
DB	2185 CAAAGACCTACCCGCGCTCTAAATATGCGCGCTGATCTTGAGAGCGCCGACATCATCTG	2244
QY	421 TGTCTAAGAAATGCAATATGATAGCGATATGCTGTGACTCCGCTCTTTCTTACACACTC	480
DB	2245 TGTCTAAGAAATGCAATATGATAGCGATATGCTGTGACTCCGCTCTTTCTTACACACTC	2304
QY	481 CTGAGATACACCCGGTGTCCCGCTGTGCCCCATTAAACAAGTTGGCGGTAGAGTTGGTG	540
DB	2305 CTGAGATACACCCGGTGTCCCGCTGTGCCCCATTAAACAAGTTGGCGGTAGAGTTGGTG	2364
QY	541 GCGGTGCGCAGGCTGTGGAATGTATCGAGACCTTGCTTAAAGAGCTGTGGCAACTTTGG	600
DB	2365 GCGGTGCGCAGGCTGTGGAATGTATCGAGACCTTGCTTAAAGAGCTGTGGCAACTTTGG	2424
QY	601 ACTTGAACCTTAAACGCCGACGCAATAAGTGTAAACCTGTATTTGCGGTGTGGTTAA	660
DB	2425 ACTTGAACCTTAAACGCCGACGCAATAAGTGTAAACCTGTATTTGCGGTGTGGTTAA	2484
QY	661 CGCCTTTGTTGTGTAATGAATTGATGTAAATTTAAATAAAGGCTGAGATATGTTTAATCT	720

Db 2485 CGCCTTGTGTGCTGATGATGATGATTAAGTTAAAGGGGATGATATGTTAACT 2544
QY 721 TGAATGGCGGTTAAATGGGGCGGGGCTTAAGGGTATATATATGCGCGTGGCTAATCT 780
Db 2545 TGCATGGCGGTTAAATGGGGCGGGGCTTAAGGGTATATATATGCGCGTGGCTAATCT 2604
QY 781 TGGTTACATCTGACCTCATGAGAGGCTTGGAGTGTGTTGGAAGATTTTTCGTGTGCGTA 840
Db 2605 TGGTTACATCTGACCTCATGAGAGGCTTGGAGTGTGTTGGAAGATTTTTCGTGTGCGTA 2664
QY 841 ACTTGCTGGAACAGAGCTCTTAACAGTACCTTGTGTTTGGAGGTTTCTGTGGGCGCTCAT 900
Db 2665 ACTTGCTGGAACAGAGCTCTTAACAGTACCTTGTGTTTGGAGGTTTCTGTGGGCGCTCAT 2724
QY 901 CCCAGGCAAGTTAGTGTGCGAGATTAAGAGATTAACAATGGGAATTTGGAAGAGCTTT 960
Db 2725 CCCAGGCAAGTTAGTGTGCGAGATTAAGAGATTAACAATGGGAATTTGGAAGAGCTTT 2784
QY 961 TGAATCTGTGTGAGCTGTTTGAATCTTGTGAATCTGGGTACACAGAGCGCTTTTCCAAG 1020
Db 2785 TGAATCTGTGTGAGCTGTTTGAATCTTGTGAATCTGGGTACACAGAGCGCTTTTCCAAG 2844
QY 1021 AGAAGTCAATGAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGTGCTT 1080
Db 2845 AGAAGTCAATGAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGTGCTT 2904
QY 1081 TTTTGAAGTTTATTAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTAACTGC 1140
Db 2905 TTTTGAAGTTTATTAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTAACTGC 2964
QY 1141 TGAATTTTCTGCGCATGTCATCTGTGAGAGCGGTTGTGAGACACAGATATGCTGTCTAC 1200
Db 2965 TGAATTTTCTGCGCATGTCATCTGTGAGAGCGGTTGTGAGACACAGATATGCTGTCTAC 3024
QY 1201 TGTGTCTTCCGTCGCGCGCGCGCATTAACCGACCGAGAGACAGAGAGAGAGAGAGAG 1260
Db 3025 TGTGTCTTCCGTCGCGCGCGCGCATTAACCGACCGAGAGAGAGAGAGAGAGAGAGAG 3084
QY 1261 AAGCAGCGCGCGCGCGAG 1320
Db 3085 AAGCAGCGCGCGCGCGAG 3144
QY 1321 GGGATGATGATGTTGTAAGGTGCTGAACCTGTATCAAGACTGAGACGCAATTTTGACAT 1380
Db 3145 GGGATGATGATGTTGTAAGGTGCTGAACCTGTATCAAGACTGAGACGCAATTTTGACAT 3204
QY 1381 TACAGAGATGGGCGAGGGGCTTAAGGGGTTAAAGAGGAGCGGGGGGCTGTGAGAGCTAC 1440
Db 3205 TACAGAGATGGGCGAGGGGCTTAAGGGGTTAAAGAGGAGCGGGGGGCTGTGAGAGCTAC 3264
QY 1441 AGAGAGGCTAGGAATCTAGCTTTAGCTTAATGACACAGACACGCTCTGATGTATTAAC 1500
Db 3265 AGAGAGGCTAGGAATCTAGCTTTAGCTTAATGACACAGACACGCTCTGATGTATTAAC 3324
QY 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTCTGTGGCGCAGAAATATTC 1560
Db 3325 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTCTGTGGCGCAGAAATATTC 3384
QY 1561 CATAGAGCGCTGACCACTTAATGCTGTGAGCAGGGGAGTATTTTGAAGAGGCTATTAG 1620
Db 3385 CATAGAGCGCTGACCACTTAATGCTGTGAGCAGGGGAGTATTTTGAAGAGGCTATTAG 3444
QY 1621 GGTATATGCAAGGTGGCACTTAGGCGCAAGTTGCAAGTACAGATCAGCAAACTTGTA 1680
Db 3445 GGTATATGCAAGGTGGCACTTAGGCGCAAGTTGCAAGTACAGATCAGCAAACTTGTA 3504
QY 1681 TATCAGGAATTTGTTACATTTCTGGGAACGGGGCGAGGGTGAAGATGATACGAGGA 1740
Db 3505 TATCAGGAATTTGTTACATTTCTGGGAACGGGGCGAGGGTGAAGATGATACGAGGA 3564
QY 1741 TAGGGTGGCTTAAATGATGATGATTAATATGTCGGGGGGGTCCTTGGCATGAGCGG 1800

Db 3565 TAGGGTGGCTTAAATGATGATGATTAATATGTCGGGGGGGTCCTTGGCATGAGCGG 3624
QY 1801 GGTGTTATTTATGATGTAAGGTTTACTGCGCCCAATTTTAAGGGTAAAGGTTTCTCGGC 1860
Db 3625 GGTGTTATTTATGATGTAAGGTTTACTGCGCCCAATTTTAAGGGTAAAGGTTTCTCGGC 3684
QY 1861 CAATTAACAACCTTATCTACACGGGTGAAGCTCTATAGGTTTAAACAAATCTGTGTGA 1920
Db 3685 CAATTAACAACCTTATCTACACGGGTGAAGCTCTATAGGTTTAAACAAATCTGTGTGA 3744
QY 1921 AGCTGGACCGATGTAAGGGTTGCGGGCTGTGCTTTTACTGTCTGTGAAGGGGGTGT 1980
Db 3745 AGCTGGACCGATGTAAGGGTTGCGGGCTGTGCTTTTACTGTCTGTGAAGGGGGTGT 3804
QY 1981 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATCTTGGG 2040
Db 3805 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATCTTGGG 3864
QY 2041 TATCTGTGAGGGTAACTCCAAGGTGCGCAACATGTGAGCTCCGACTGTGTTGCTT 2100
Db 3865 TATCTGTGAGGGTAACTCCAAGGTGCGCAACATGTGAGCTCCGACTGTGTTGCTT 3924
QY 2101 CATGCTAGTAAAGCGTGTGCTGTGATTAAAGATACATGATGTGGAACCTGCGAGGA 2160
Db 3925 CATGCTAGTAAAGCGTGTGCTGTGATTAAAGATACATGATGTGGAACCTGCGAGGA 3984
QY 2161 CAGGGCTCTCAAGTCTGATCTGTGAGAGCGCAACGTGCACCTGTGGAAGACATTTCA 2220
Db 3985 CAGGGCTCTCAAGTCTGATCTGTGAGAGCGCAACGTGCACCTGTGGAAGACATTTCA 4044
QY 2221 CGTAGCCAGCACTCTGCAAGGCTGGCAGATGTTTGTGAGCATTAACATGACCCGCTG 2280
Db 4045 CGTAGCCAGCACTCTGCAAGGCTGGCAGATGTTTGTGAGCATTAACATGACCCGCTG 4104
QY 2281 TTCCTTCATTTTGGGTAAACAGAGAGGGGGTCTTCTTACCTTAACAAATGCAATTTGAGTCA 2340
Db 4105 TTCCTTCATTTTGGGTAAACAGAGAGGGGGTCTTCTTACCTTAACAAATGCAATTTGAGTCA 4164
QY 2341 CACTTAAGTATTTGTTGAGCCCGAGACATGTCCAAGGTGAACCTGAAACGGGGTGTGGA 2400
Db 4165 CACTTAAGTATTTGTTGAGCCCGAGACATGTCCAAGGTGAACCTGAAACGGGGTGTGGA 4224
QY 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTGAGTGAAGAGAGAGAGAGAGAGAGAG 2460
Db 4225 CATGACCATGAAGATCTGGAAGGTGCTGAGGTGAGTGAAGAGAGAGAGAGAGAGAGAG 4284
QY 2461 CTGCGAGTGTGCGGTAAACATTAATTAAGAACCAAGCTGTGATGCTGATGTGAACCGAGA 2520
Db 4285 CTGCGAGTGTGCGGTAAACATTAATTAAGAACCAAGCTGTGATGCTGATGTGAACCGAGA 4344
QY 2521 GCTGAGGCCGATCACTTGTGTGCTGCGCTGCAACCGGCGCTGAGTTTGGCTAGCGATGA 2580
Db 4345 GCTGAGGCCGATCACTTGTGTGCTGCGCTGCAACCGGCGCTGAGTTTGGCTAGCGATGA 4404
QY 2581 AGATACAGATTGAG 2594
Db 4405 AGATACAGATTGAG 4418

RESULT 12
CO854906 32802 bp DNA linear PAT 23-AUG-2004
LOCUS
DEFINITION Sequence 3 from Patent WO2004066947.
ACCESSION CO854906
VERSION CO854906.1 GI:51510466
KEYWORDS
SOURCE unidentified adenovirus
ORGANISM unidentified adenovirus
VIRUSES; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE
1 Hu, F. and Wu, B.
AUTHORS
TITLE Therapy for primary and metastatic cancers
JOURNAL Patent: WO 2004066947-A 3 12-AUG-2004;

Db 2897 GTGTCCGCCAAAAGCAGGGCTTCAATTAGAAATGCTCTTTGAAAAGGTGACCTTGG 2956
QY 2041 TATCCGTGTGAGAGGTAACTCCAGGGGTGGCCCAATGTGGCTCCGACTGTGTGCTT 2100
Db 2957 TATCCGTGTGAGAGGTAACTCCAGGGGTGGCCCAATGTGGCTCCGACTGTGTGCTT 3016
QY 2101 CATGCTAGTGAAGAGCGTGTGTGATTAGCAATGATGATGTGGCACTGGCAGGA 2160
Db 3017 CATGCTAGTGAAGAGCGTGTGTGATTAGCAATGATGATGTGGCACTGGCAGGA 3076
QY 2161 CAGGGCTCTCAAGTGTGACTGTGTGGACGGCAATGTGACCTGTGTGAAGCACTTCA 2220
Db 3077 CAGGGCTCTCAAGTGTGACTGTGTGGACGGCAATGTGACCTGTGTGAAGCACTTCA 3136
QY 2221 CGTAGCCAGCAGCTCTGCAAGGCTGGCCAGTGTGTTGACATTAACCTACTGACCCGCTG 2280
Db 3137 CGTAGCCAGCAGCTCTGCAAGGCTGGCCAGTGTGTTGACATTAACCTACTGACCCGCTG 3196
QY 2281 TTCCTTGCAATTTGGGTAAAGAGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCA 2340
Db 3197 TTCCTTGCAATTTGGGTAAAGAGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCA 3256
QY 2341 CACTAAGATATTTGCTTGAAGCCGAGACATGTCCAAAGTGAACCTGAAACGGGGGTGTTGA 2400
Db 3257 CACTAAGATATTTGCTTGAAGCCGAGACATGTCCAAAGTGAACCTGAAACGGGGGTGTTGA 3316
QY 2401 CATGACCATGAAGATCTGAAAGGTGTGAGGTAGATGAGACCCGACCAAGTGCAGACC 2460
Db 3317 CATGACCATGAAGATCTGAAAGGTGTGAGGTAGATGAGACCCGACCAAGTGCAGACC 3376
QY 2461 CTGCGAGTGTGGCCGTAAACATATTAGAACACAGCCTGTGATGCTGATGTGACCCGAGGA 2520
Db 3377 CTGCGAGTGTGGCCGTAAACATATTAGAACACAGCCTGTGATGCTGATGTGACCCGAGGA 3436
QY 2521 GCTGAGGCCGATCACTTGTGTGTGCTGTGACCCGCGCTGAGTTGGCTGTAGGATGA 2580
Db 3437 GCTGAGGCCGATCACTTGTGTGTGCTGTGACCCGCGCTGAGTTGGCTGTAGGATGA 3496
QY 2581 AGATACAGATTGAG 2594
Db 3497 AGATACAGATTGAG 3510

RESULT 13
AX084506 33699 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 3 from Patent WO0104282.
ACCESSION AX084506
VERSION AX084506.1 GI:13185914
KEYWORDS
SOURCE Human adenovirus C
ORGANISM Human adenovirus C
VIRUSES; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE 1 Wold, W.S., Toch, K., Doronin, K. and Tollefson, A.B.
AUTHORS
TITLE Replication-competent anti-cancer vectors
JOURNALS Patent: WO 0104282-A 3 18-JAN-2001;
Saint Louis University (US)
FEATURES
source location/Qualifiers
1..33699 /organism="Human adenovirus C"
/mol_type="unassigned DNA"
/db_xref="taxon:129951"

ORIGIN
Query Match 100.0%; Score 2594; DB 6; Length 33699;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATCGATCTTACCGCAGCAGGCTGTGCTTCCACCCAGTACGACGAGATGAAAGGCT 60
Db 917 ATCGATCTTACCGCAGCAGGCTGTGCTTCCACCCAGTACGACGAGATGAAAGGCT 976

QY 61 GAGAGTTGTGTGATTAATGAGAGACCCCGGACAGGTGGCAGGTCTTGTCAATAT 120
Db 977 GAGAGTTGTGTGATTAATGAGAGACCCCGGACAGGTGGCAGGTCTTGTCAATAT 1036
QY 121 CACCGAGGAATACGGGGAGCCAGATATTAATGTGTGCTTTGCTATATAGAGACTGT 180
Db 1037 CACCGAGGAATACGGGGAGCCAGATATTAATGTGTGCTTTGCTATATAGAGACTGT 1096
QY 181 GGCATGTTGTCTACAGTAAAGTAAATTAATGGGCGAGTGGGATGAGAGGTGGGTTG 240
Db 1097 GGCATGTTGTCTACAGTAAAGTAAATTAATGGGCGAGTGGGATGAGAGGTGGGTTG 1156
QY 241 GTGTGTAATTTTATTTTAAATTTTACAGTTTGTGTGTTTAAAGATTTGTATGTGA 300
Db 1157 GTGTGTAATTTTATTTTAAATTTTACAGTTTGTGTGTTTAAAGATTTGTATGTGA 1216
QY 301 TTTTAAAAAGGTCTGTGTCTGAACTTGAGCTTGAGCCGAGCCAGAACCGGAGCTTG 360
Db 1217 TTTTAAAAAGGTCTGTGTCTGAACTTGAGCTTGAGCCGAGCCAGAACCGGAGCTTG 1276
QY 361 CAAGACCTACCCGCGCTCTTAAATAGCGGCTGTCTATCTTGAGACGCGCAATCACTTG 420
Db 1277 CAAGACCTACCCGCGCTCTTAAATAGCGGCTGTCTATCTTGAGACGCGCAATCACTTG 1336
QY 421 TGTCTAGAGAAAGCAATAGTAAAGTACGATAGCTGTGACTCGGTCCTTCAACACACTC 480
Db 1337 TGTCTAGAGAAAGCAATAGTAAAGTACGATAGCTGTGACTCGGTCCTTCAACACACTC 1396
QY 481 CTGAGATACACCCGCGTGTGCTGCTGCTGCTTAAACCAATTTGCCGTGAGTTGGTG 540
Db 1397 CTGAGATACACCCGCGTGTGCTGCTGCTGCTTAAACCAATTTGCCGTGAGTTGGTG 1456
QY 541 GCGCTGCCAGGCTGTGGAATGTATGAGAGACTTGCTTAAAGAGCTGGGCAACTTTGG 600
Db 1457 GCGCTGCCAGGCTGTGGAATGTATGAGAGACTTGCTTAAAGAGCTGGGCAACTTTGG 1516
QY 601 ACTTGAAGCTGTAACGCCCCAGGCCATTAAGGTGTAACCTGTGATGCTGTGTGTTAA 660
Db 1517 ACTTGAAGCTGTAACGCCCCAGGCCATTAAGGTGTAACCTGTGATGCTGTGTGTTAA 1576
QY 661 GCGCTTGTGTGCTGAATGAGTTGATGATTAATTAAGAGGTGAGATTAATGTTTAACT 720
Db 1577 GCGCTTGTGTGCTGAATGAGTTGATGATTAATTAAGAGGTGAGATTAATGTTTAACT 1636
QY 721 TGCATGCGGTGTTAAATGGGCGGGGCTTAAAGGGTATATATATGCGCGGTATCT 780
Db 1637 TGCATGCGGTGTTAAATGGGCGGGGCTTAAAGGGTATATATATGCGCGGTATCT 1696
QY 781 TGGTTACATCTGACCTCATGAGGCTTGAGAGTGTGTAAGATTTTCTGCTGTGCGTA 840
Db 1697 TGGTTACATCTGACCTCATGAGGCTTGAGAGTGTGTAAGATTTTCTGCTGTGCGTA 1756
QY 841 ACTTGTGGAACAGAGCTCTAACAGTACCTTGTGTTTGAAGTTTCTGTGGGCTCAT 900
Db 1757 ACTTGTGGAACAGAGCTCTAACAGTACCTTGTGTTTGAAGTTTCTGTGGGCTCAT 1816
QY 901 CCCAGGAAAGTGTACTGTGCAAGATTAAGAGATTAACAAGGGAATTTGAAGACTT 960
Db 1817 CCCAGGAAAGTGTACTGTGCAAGATTAAGAGATTAACAAGGGAATTTGAAGAGCTT 1876
QY 961 TGAATTCCTGTGTGAGGCTGTTGATTTCTTGAATCTGTGATCAGAGCGCTTTTCAG 1020
Db 1877 TGAATTCCTGTGTGAGGCTGTTGATTTCTTGAATCTGTGATCAGAGCGCTTTTCAG 1936
QY 1021 AGAAGTCAACAAGCTTTGATTTTTCACACCGGGGCGCTGCGCTGTGTTGCTT 1080
Db 1937 AGAAGTCAACAAGCTTTGATTTTTCACACCGGGGCGCTGCGCTGTGTTGCTT 1996
QY 1081 TTTTGAAGTTTAAAGATTAATGAGCGAAGAACCATCTGAGCGGGGGGTACTCTG 1140
Db 1997 TTTTGAAGTTTAAAGATTAATGAGCGAAGAACCATCTGAGCGGGGGGTACTCTG 2056
QY 1141 TCGATTTTCTGCGCATGATCTGTGAGAGCGGTTGTGAGACAAAGATTCGCTGTAC 1200

Db	2057	TGGAATTTTCTGCGCATGCATCTGTGGAAGCGGTGTGAGACAAAGAAATGCCCTGTAC	2116
Qy	1201	TGTTGTCTTCCGTCGCGCCCGCGCATAAATACCGACCGAGAGACGACGACGACGAGAGG	1266
Db	2117	TGTTGTCTTCCGTCGCGCCCGCGCATAAATACCGACCGAGAGACGACGACGACGAGAGG	2176
Qy	1261	AAGCAGGCGCGCGCGGCGAGAGACGACGACCCCATGGAATCCGAGAGCGCGCTGTGACCTTC	1322
Db	2177	AAGCAGGCGCGCGCGGCGAGAGACGACGACCCCATGGAATCCGAGAGCGCGCTGTGACCTTC	2238
Qy	1321	GCGAATGAATGTGTGACAGATGCGCTGAATCTGTATCCAGACTGAGACCGCATTTTGAACAT	1380
Db	2237	GCGAATGAATGTGTGACAGATGCGCTGAATCTGTATCCAGACTGAGACCGCATTTTGAACAT	2296
Qy	1381	TACAGAGGATGGCGAGGGGCTTAAAGGGGGTAAAGAGAGCGGGGGGCTTGTAGCTTAC	1440
Db	2297	TACAGAGGATGGCGAGGGGCTTAAAGGGGGTAAAGAGAGCGGGGGGCTTGTAGGCTTAC	2356
Qy	1441	AGAGAGGCTTAGGAATCTAGCTTTTAACTTAATGACCAAGACCGTCTTGAATGTATTAC	1500
Db	2357	AGAGAGGCTTAGGAATCTAGCTTTTAACTTAATGACCAAGACCGTCTTGAATGTATTAC	2418
Qy	1501	TTTTCAACAGATCAAGGTAATTTGGCTTAATGAGCTTGAATCGCTGGGCGGAGAAATTC	1566
Db	2417	TTTTCAACAGATCAAGGTAATTTGGCTTAATGAGCTTGAATCGCTGGGCGGAGAAATTC	2476
Qy	1561	CATGAGAGCTGACCACTTACTGCGCTGACAGCGAGGATGTTTGAAGAGGCTATTAG	1620
Db	2477	CATGAGAGCTGACCACTTACTGCGCTGACAGCGAGGATGTTTGAAGAGGCTATTAG	2538
Qy	1621	GGTATATGCAAAAGGTGGCATTTAGCGCAGATTGCAAGTACAGCAAACTTTGAAA	1680
Db	2537	GGTATATGCAAAAGGTGGCATTTAGCGCAGATTGCAAGTACAGCAAACTTTGAAA	2598
Qy	1681	TATACGGAATTTGTGTCTACATTTCTGGGGAACGGGGCCGAGGTGAGATATACGAGGA	1740
Db	2597	TATACGGAATTTGTGTCTACATTTCTGGGGAACGGGGCCGAGGTGAGATATACGAGGA	2656
Qy	1741	TAGGGTGGCCTTTAGATGTAGCATGATTAATATGTGCGCGGGGGGCTTGCATATGACGG	1800
Db	2657	TAGGGTGGCCTTTAGATGTAGCATGATTAATATGTGCGCGGGGGGCTTGCATATGACGG	2716
Qy	1801	GGTGGTTATTAATGAATGTAAAGGTTTACTGCGCCCAATTTTAAAGCGGTACGGTTTTCTGGC	1860
Db	2717	GGTGGTTATTAATGAATGTAAAGGTTTACTGCGCCCAATTTTAAAGCGGTACGGTTTTCTGGC	2776
Qy	1861	CAATACCAACCTTATCTTACACCGGTATGACTTCTATGCGTTTAAACAATACCTGTGTGGA	1920
Db	2777	CAATACCAACCTTATCTTACACCGGTATGACTTCTATGCGTTTAAACAATACCTGTGTGGA	2836
Qy	1921	AGCCTGACCGCATGTAAAGGGTTCGCGGGCTGTGCTTTTACGTGCTGCGAAGGGGGTGGT	1980
Db	2837	AGCCTGACCGCATGTAAAGGGTTCGCGGGCTGTGCTTTTACGTGCTGCGAAGGGGGTGGT	2896
Qy	1981	GTTGTCGCCCCCAAAAGCAGGGCTTCAATTAAGAAAATGCTCTTTGAAAAGGTATCCTTGGG	2040
Db	2897	GTTGTCGCCCCCAAAAGCAGGGCTTCAATTAAGAAAATGCTCTTTGAAAAGGTATCCTTGGG	2956
Qy	2041	TATCTCTGTCTGAGGGTAACTCCAGGGTGTGCGCACAATGTGGCTTCGACTGTGTGCTTT	2100
Db	2957	TATCTCTGTCTGAGGGTAACTCCAGGGTGTGCGCACAATGTGGCTTCGACTGTGTGCTTT	3016
Qy	2101	CATCTAGTGAAGAAAGCGTGGCTGTGATTAAACATTAACATGTATGTGGCACTGCGAGGA	2160
Db	3017	CATCTAGTGAAGAAAGCGTGGCTGTGATTAAACATTAACATGTATGTGGCACTGCGAGGA	3076
Qy	2161	CAGGGCCTTCTCAGATGCTGACCTGTGCGACGGCACTGTGCACTGTCTGTAAGACCATTTCA	2220
Db	3077	CAGGGCCTTCTCAGATGCTGACCTGTGCGACGGCACTGTGCACTGTCTGTAAGACCATTTCA	3136
Qy	2221	CGTAGCCAGCACTCTGCGCAAGGCTGTGCGCACTGTGTTGAGCATTAATATCTGACCCGCTG	2280

Db	3137	CGTAGCAGCACCCTCTGCGCAAGGCGCTGGCCAGTAGTCTTGAGACATAACATTA	CTGACCCGCTG	3136
Oy	2281	TTCCCTTGCAATTTGGGTAAACAGAGAGGGGGGTGTTCTCACTTACCAATGCAATTTG	AGTCA	2340
Db	3197	TTCCCTTGCAATTTGGGTAAACAGAGAGGGGGGTGTTCTCACTTACCAATGCAATTTG	AGTCA	3256
Oy	2341	CACATTAATATATTTGCTTGAAGCCCCAGAGACATGTCCAAAGTGAACCTGAAACGGGG	GTGTTGA	2400
Db	3257	CACATTAATATATTTGCTTGAAGCCCCAGAGACATGTCCAAAGTGAACCTGAAACGGGG	GTGTTGA	3316
Oy	2401	CATGACCATGAAGATCTGGAAGGGTGTGAGGTACATGATGAGAACCCGACACAGAGTGC	AGACACC	2460
Db	3317	CATGACCATGAAGATCTGGAAGGGTGTGAGGTACATGATGAGAACCCGACACAGAGTGC	AGACACC	3376
Oy	2461	CTGCGAGTGTGGCGGTAAACATATTTAGAAACAGACCTGTGATGCTGATGTGAACCGA	AGAA	2520
Db	3377	CTGCGAGTGTGGCGGTAAACATATTTAGAAACAGACCTGTGATGCTGATGTGAACCGA	AGAA	3436
Oy	2521	GCTTAGAGCCCGATCTACCTTGTTGGTGTGAGCTGTGACCCCGGTGTGATTTGGCTCTG	ACCATGA	2580
Db	3437	GCTTAGAGCCCGATCTACCTTGTTGGTGTGAGCTGTGACCCCGGTGTGATTTGGCTCTG	ACCATGA	3496
Oy	2581	AGATACAGATTGAG	2594	
Db	3497	AGATACAGATTGAG	3510	

LOCUS	AX084507	34448 bp	DNA	linear	PAT 28-FEB-2001
DEFINITION	Sequence 4 from Patent WO0104282.				
ACCESSION	AX084507				
VERSION	AX084507.1	GI:13185915			
KEYWORDS					
SOURCE	Human adenovirus C				
ORGANISM	Human adenovirus C				
REFERENCE	1	Wold, W.S., Toth, K., Doronin, K. and Tollefson, A.E.			
AUTHORS		Replication-competent anti-cancer vectors			
TITLE		Patent: WO 0104282-A 4 18-JAN-2001;			
JOURNAL		Saint Louis University (US)			
FEATURES		Location/Qualifiers			
source		1..34448			
		/organism="Human adenovirus C"			
		/mol_type="unassigned DNA"			
		/db_xref="taxon:129951"			
ORIGIN					
Query Match		100.0%; Score 2594; DB 6; Length 34448;			
Best Local Similarity		100.0%; Pred. No. 0;			
Matches 2594; Conservative		0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATCGATCTTACCTGCCACGAGSCTGCTTTCACCAACGATGACGACGAGATGAAGAGG	60		
DB	917	ATCGATCTTACCTGCCACGAGSCTGCTTTCACCAACGATGACGAGATGAAGAGG	976		
QY	61	GAGGAGTTTGTTAGATTATGTGAGACACCCCGGCGACGGTTGCAGGCTTGTCAATTAT	120		
DB	977	GAGGAGTTTGTTAGATTATGTGAGACACCCCGGCGACGGTTGCAGGCTTGTCAATTAT	1036		
QY	121	CACCGAGAGAAATCGGGGGACCCAGATATTAATGTGTGCTTGTCTATATGAGACCTGT	180		
DB	1037	CACCGAGAGAAATCGGGGGACCCAGATATTAATGTGTGCTTGTCTATATGAGACCTGT	1096		
QY	181	GGCATGTTTGTCTACAGTAAGTAAATTAATGCGGACATGGGTGATAGAGTGTGGGTTTG	240		
DB	1097	GGCATGTTTGTCTACAGTAAGTAAATTAATGCGGACATGGGTGATAGAGTGTGGGTTTG	1156		
QY	241	GTTGGGTAATTTTATTTTATTTTATTTTACAGTTTGTGTTTAAAGAAATTTGATATGTA	300		
DB	1157	GTTGGGTAATTTTATTTTATTTTATTTTACAGTTTGTGTTTAAAGAAATTTGATATGTA	1216		

QY	301	TTTTTTTAAAAAGGTCCTGTGTCTGTACCTGTAGCCTGTAGACCCTGAGCAACCGGAGCCTG	360
Db	1217	TTTTTTTTAAAAAGGTCCTGTGTCTGTAACTGTAGCCTGTAGACCCTGAGCAACCGGAGCCTG	1276
QY	361	CAAGACCTACCCCGCGCTCTTAAATVGGGCGCTGTCTATCTGTAGACGGCCGACATCACCTG	420
Db	1277	CMAGACCTACCCCGCGCTCTTAAATVGGGCGCTGTCTATCTGTAGACGGCCGACATCACCTG	1336
QY	421	TGTCGTAGAAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCTTCTTAACACACTC	480
Db	1337	TGTCGTAGAAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCTTCTTAACACACTC	1396
QY	481	CTGAGATPACACCCCGTGTGTCCCGCTGTGTCCCATTTAAACCAAGTTGCCGTGAGAGTGGTG	540
Db	1397	CTGAGATPACACCCCGTGTGTCCCGCTGTGTCCCATTTAAACCAAGTTGCCGTGAGAGTGGTG	1456
QY	541	GGCGTCGACAGGCGTGTGGAAATGTATCGAGAGACTTGCTTAAAGAGCTGTGGGCAACTTTGG	600
Db	1457	GGCGTCGACAGGCGTGTGGAAATGTATCGAGAGACTTGCTTAAAGAGCTGTGGGCAACTTTGG	1516
QY	601	ACTTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATGTGGTGTGTGTAA	660
Db	1517	ACTTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATGTGGTGTGTGTAA	1576
QY	661	CGCCTTTGTGTCTGCAATGAGTGTATGTAAATTTAAAGGGGTGAGATATATTTTAATCT	720
Db	1577	CGCCTTTGTGTGTCTGCAATGAGTGTATGTAAATTTAAAGGGGTGAGATATATTTTAATCT	1636
QY	721	TGCATGGCGGTATTAATVGGGCGGGGGCTTAAAGGGTATTAATCGCGCGTGGCTAAATCT	780
Db	1637	TGCATGGCGGTATTAATVGGGCGGGGGCTTAAAGGGTATTAATCGCGCGTGGCTAAATCT	1696
QY	781	TGCTTAACTCTGACCTCATVAGAGCCTTGGAGTGTTTGGAGATTTTCTGTGTGCGTA	840
Db	1697	TGCTTAACTCTGACCTCATVAGAGCCTTGGAGTGTTTGGAGATTTTCTGTGTGCGTA	1756
QY	841	ACTTGCTGTAAACAGAGCTCTTACAGTACTCTTGCTTTTGGAGGTTTCTGTGGGCTCAT	900
Db	1757	ACTTGCTGTAAACAGAGCTCTTACAGTACTCTTGCTTTTGGAGGTTTCTGTGGGCTCAT	1816
QY	901	CCGAGGCAAAATTAAGTGTGACGAATTTAAGAGGATTAACAATGGGAAATTTGAAGGCTTT	960
Db	1817	CCGAGGCAAAATTAAGTGTGACGAATTTAAGAGGATTAACAATGGGAAATTTGAAGGCTTT	1876
QY	961	TGAATCCCTGTGTAGCTGTTTGATCTTTGAAATCTGGGTCACACAGGCGCTTTTCCAAG	1020
Db	1877	TGAATCCCTGTGTGTAGCTGTTTGATCTTTGAAATCTGGGTCACACAGGCGCTTTTCCAAG	1936
QY	1021	AGAAAGTTCATCAAGACTTTGGATTTTTCACACCGGGGCGGCTGTGCGTCTGTTCCTT	1080
Db	1937	AGAAAGTTCATCAAGACTTTGGATTTTTCACACCGGGGCGGCTGTGCGTCTGTTCCTT	1996
QY	1081	TTTTGAGTTTATTAAGGATTAATVGGAGCGAAGAAACCATCTGACGGGGGGGTAACTCGC	1140
Db	1997	TTTTGAGTTTATTAAGGATTAATVGGAGCGAAGAAACCATCTGACGGGGGGGTAACTCGC	2056
QY	1141	TGGAATTTCTGGCATGTACTGTGAGAGCGGTTGTGAGACACAAGAAATGCGCTGTAC	1200
Db	2057	TGGAATTTCTGGCATGTACTGTGAGAGCGGTTGTGAGACACAAGAAATGCGCTGTAC	2116
QY	1201	TGTTGTCTTCCGTCCGCCCGCGATATAATCCGACGGAGAGCAGACGACGACGAGAGG	1260
Db	2117	TGTTGTCTTCCGTCCGCCCGCGATATAATCCGACGGAGAGCAGACGACGACGAGAGG	2176
QY	1261	AAGCAGCGCGCGCGGAGAGACAGACCCATGGAACCCGAGAGCCGGCTTGAACCTTC	1320
Db	2177	AAGCAGCGCGCGCGGAGAGACAGACCCATGGAACCCGAGAGCCGGCTTGAACCTTC	2236
QY	1321	GGGAATGAATTTGTACAGGTGTGCTGAACCTGTATCCAAACTGAGACGCAATTTTGAACAAT	1380
Db	2237	GGGAATGAATTTGTACAGGTGTGCTGAACCTGTATCCAAACTGAGACGCAATTTTGAACAAT	2296
QY	1381	TACAGAGATGGCAGGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC	1440

Db	2297	TAAGAGAGATGGGCGAGGGGCTTAAAGGGGGTTAAAGAGGAGCGGGGGCTTGTGAGGCTTAC	2356
Qy	1441	AGAGGAGCTAGAGATCTTACCTTTTAGCTTAAATGACGACAACCGTCTGAGTATTAAC	1500
Db	2357	AGAGGAGGCTTAGGATCTTACCTTTTAGCTTAAATGACGACAACCGTCTGAGTATTAAC	2416
Qy	1501	TTTTCAACAGATCAAGGATTAATTCGGCTAATGAGCTTGATCTGTGCGCGAAGATATTC	1560
Db	2417	TTTTCAACAGATCAAGGATTAATTCGGCTAATGAGCTTGATCTGTGCGCGAAGATATTC	2476
Qy	1561	CATAGAGCAGCTGACCACTTACTGGCTGCGACGAGGGGATGATTTTATAGGAGGCTATTAAG	1620
Db	2477	CATAGAGCAGCTGACCACTTACTGGCTGCGACGAGGGGATGATTTTATAGGAGGCTATTAAG	2536
Qy	1621	GGTATATGCAAAAGGTGGCACTTAGCGGCAGATTCAGAGTACAGATCAGCAACTTGTAAA	1680
Db	2537	GGTATATGCAAAAGGTGGCACTTAGCGGCAGATTCAGAGTACAGATCAGCAACTTGTAAA	2596
Qy	1681	TATCAGGAATTTGTTGCTACATTTTCTGGAACGGGGCCGAGGTGAGATAGATACGAGGA	1740
Db	2597	TATCAGGAATTTGTTGCTACATTTTCTGGAACGGGGCCGAGGTGAGATAGATACGAGGA	2656
Qy	1741	TAGGGTGGCCCTTAAAGATGATGACAGATTAATATGTGGCCGGGGGGTGCTTGCATATGACGG	1800
Db	2657	TAGGGTGGCCCTTAAAGATGATGACAGATTAATATGTGGCCGGGGGGTGCTTGCATATGACGG	2716
Qy	1801	GGTGGTATTTATGATGATGTAGAGTTTACTGGCCCCAATTTTATAGCGGTACGGTTTTCTGGC	1860
Db	2717	GGTGGTATTTATGATGATGTAGAGTTTACTGGCCCCAATTTTATAGCGGTACGGTTTTCTGGC	2776
Qy	1861	CAATACCAACCTTATCTCTACACGGGTGTAAGCTTCTATGGGTTTACATATCTGTGTGA	1920
Db	2777	CAATACCAACCTTATCTCTACACGGGTGTAAGCTTCTATGGGTTTACATATCTGTGTGA	2836
Qy	1921	AGCGTGAACCGATGTAAAGGGTTGGGGCTGTGGCTTTATCTGGCTGTGAAGGGGGGGT	1980
Db	2837	AGCGTGAACCGATGTAAAGGGTTGGGGCTGTGGCTTTATCTGGCTGTGAAGGGGGGGT	2896
Qy	1981	GTTGTCGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTACTTTGGG	2040
Db	2897	GTTGTCGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTACTTTGGG	2956
Qy	2041	TATCTGTCTGAGGGTAACTCCAGGGTGGCCCAATGTGGCTCCGACTGTGGTCTT	2100
Db	2957	TATCTGTCTGAGGGTAACTCCAGGGTGGCCCAATGTGGCTCCGACTGTGGTCTT	3016
Qy	2101	CATCTCTAGTAAAAAGCTGGCTGTGATTAAGCATTAATGATGTATGTGGCAATCGCGAGA	2160
Db	3017	CATCTCTAGTAAAAAGCTGGCTGTGATTAAGCATTAATGATGTATGTGGCAATCGCGAGA	3076
Qy	2161	CAGGGCCCTCAGATGTGACTGCTGCGACGGGCACTGTACACTGTGTGAAGCATTTCA	2220
Db	3077	CAGGGCCCTCAGATGTGACTGCTGCGACGGGCACTGTACACTGTGTGAAGCATTTCA	3136
Qy	2221	CGTAGCCAGCCACTCTTCGCAAGGCTTGCGCAGATGTTTGAACATTAACATCTGACCCGCTG	2280
Db	3137	CGTAGCCAGCCACTCTTCGCAAGGCTTGCGCAGATGTTTGAACATTAACATCTGACCCGCTG	3196
Qy	2281	TTCTTTCGATTTTGGGTAAACGAGAGGGGGGTTCCTTACCTTAACAAATGCAATTTGAATCA	2340
Db	3197	TTCTTTCGATTTTGGGTAAACGAGAGGGGGGTTCCTTACCTTAACAAATGCAATTTGAATCA	3256
Qy	2341	CACATTAAGATTTTGGTTAGCCCGAGACATGTCCAAAGTGAACCTGAAACGGGGGTTTGA	2400
Db	3257	CACATTAAGATTTTGGTTAGCCCGAGACATGTCCAAAGTGAACCTGAAACGGGGGTTTGA	3316
Qy	2401	CATGACCATGAAGAATCTGGAAGGTGCTGAAGTACGATGAGAACCCGCAACAGGTGCAGACC	2460
Db	3317	CATGACCATGAAGAATCTGGAAGGTGCTGAAGTACGATGAGAACCCGCAACAGGTGCAGACC	3376
Qy	2461	CTGCGAGTGTGGCGGTAAACATATTAGAAACAGGCTGTGATGTGGATGTGACCGAGGA	2520

Db 3377 CTGCGAGTGTGGCGGTAAACATATTAGAACACGCGCTGTGATGCTGATGATGACCGAGGA 3436

QY 2521 GCTAGAGCCCGCATCACTTGTGTCTGCGCTGACACCGCGCTGAGTTGGCTTAGCGATGA 2580

Db 3437 GCTAGAGCCCGCATCACTTGTGTCTGCGCTGACACCGCGCTGAGTTGGCTTAGCGATGA 3496

QY 2581 AGATACAGATTGAG 2594

Db 3497 AGATACAGATTGAG 3510

RESULT 15

LOCUS AY339865 35934 bp DNA linear VRL 13-AUG-2003

DEFINITION Human adenovirus C serotype 5, complete genome.

ACCESSION AY339865

VERSION AY339865.1 GI:33465830

KEYWORDS

SOURCE Human adenovirus C

ORGANISM Human adenovirus C

REFERENCE 1 (bases 1 to 35934)

AUTHORS McAllister,D.L., Lu,F., Thomas,B.K., Hutchins,B.M. and Sugerman,B.J.

TITLE Complete Nucleic Acid Sequence of the Adenovirus Type 5 Reference Material

JOURNAL BioProcessing (2003) In press

REFERENCE 2 (bases 1 to 35934)

AUTHORS Sugerman,B.J., McAllister,D.L. and Hutchins,B.M.

TITLE Direct Submission

JOURNAL Submitted (09-JUN-2003) Process Sciences, Can1 Inc., Schering-Plough Corporation, 3525 John Hopkins Court, San Diego, CA 92121, USA

FEATURES

source 1.35934

/organism="Human adenovirus C"

/viroion

/mol_type="genomic DNA"

/serotype="5"

/db_xref="taxon:129951"

1.103

/note="5' inverted terminal repeat"

/rpt_type="inverted"

468..1632

/gene="E1A"

468..475

/gene="E1A"

join(560..1112,1229..1545)

/note="E1A"

/note="derived from the E1A 13S mRNA"

/codon_start=1

/product="32 kDa protein"

/protein_id="AA019284.1"

/db_xref="GI:33465831"

/translation="MRHICGCVTEEMASLDLIIEVLADNLPPSPHPEPTLH
ELTLDVTPEDPNEBAVSQIFPDSVLAIVOGIDLTFFPAPGSPHPHLSRQEP
EQRLAGVSPNVLVEVIDLTCHGAFPSDDDEBGEFVLADVHGHGCRSCHY
RPRNGDPIIMCSLCYMRTCGMFVSPVSEPEPEPEPARPTRPKMAAIIARRP
SPVRECNSTSDSCSGSPSNTPEIHPVPLCPIFVAVRGRRAVECIEDLLNEP
GQPLDSCRRPR"

join(560..974,1229..1545)

/gene="E1A"

/note="derived from the E1A 12S mRNA"

/codon_start=1

/product="27 kDa protein"

/protein_id="AA019285.1"

/db_xref="GI:33465832"

/translation="MRHICGCVTEEMASLDLIIEVLADNLPPSPHPEPTLH
ELTLDVTPEDPNEBAVSQIFPDSVLAIVOGIDLTFFPAPGSPHPHLSRQEP
EQRLAGVSPNVLVEVIDLTCHGAFPSDDDEBGEFVLADVHGHGCRSCHY
RPRNGDPIIMCSLCYMRTCGMFVSPVSEPEPEPEPARPTRPKMAAIIARRP
SPVRECNSTSDSCSGSPSNTPEIHPVPLCPIFVAVRGRRAVECIEDLLNEP
GQPLDSCRRPR"

975..1228

CDS

intron

intron

polyA_signal

polyA_site

gene

TATA_signal

CDS

gene="E1A"

/note="E1A 12S"

1113..1228

/gene="E1A"

/note="E1A 13S"

1611..1616

/gene="E1A"

1632

/gene="E1A"

1672..3509

/gene="E1B"

1672..1678

/gene="E1B"

1714..2244

/gene="E1B"

/codon_start=1

/product="E1B 19K"

/protein_id="AA019286.1"

/db_xref="GI:33465833"

/translation="MEANECLDPSAVNLLIPOSNSTSWWRFLMGSSQAKLVCRIK
EDYKWEFELLKSCGELFDLSLNLGHQALFQEKVITLDFSTPGRAAAVAFLSFLKDK
WSEETHLSGYLIDPLAMHLMRAVVRHNRLLLSVPAIIPTEEOOQOEARRRR
QESPPNPRAGIDPRE"

2019..3509

/gene="E1B"

/codon_start=1

/product="E1B 55K"

/protein_id="AA019287.1"

/db_xref="GI:33465834"

/translation="MEBRNPSERGVPAFGSGHASYGCGECPATVFRPBGNTD
GGAHAAAGSQAAGAPMPESPSPGSGMAYOVALYELRIILITTEGQSLG
VREKGECEATBEARNLAFSLMTRRPECITFQOIKDCANEDLILAKYLSLEULTY
WLQRPDDDEBAIRYAKVALRPDCRYKSKLVNINCCYISGNGAVEIDIEDYAFR
CSMINMPGVGMDGVVIMNVRFTGPNFSGTVFLANTLILHGVSYFNNTCVAFR
DVRVGCAPFYCCMGVCPKPSRASIKKCLPERCTGLISGNSRHRNVASDCCFM
LVKSAVAVKHMVCGNEDRASOMLTGSDGCHLTKTTHVASHSKRAVPEHNTLTR
CSLHGRRGVPLPQCNLSHTKILIBESSKTNKNGVPMTHKIMKLYRDETRR
CRPECGGKHTRNOPVMDVTELRPHLVLACTRAGSSDEDDT"

3551..3556

/note="PIX TATA box"

3609..4031

/note="PIX TATA box"

/codon_start=1

/product="PIX 9"

/protein_id="AA019288.1"

/db_xref="GI:33465835"

/translation="MSTNSPDGSIYSSVLTTRMPWAGVRONVMGSSIDGRVPLRANS
TTLVYVSGPLTETASAAASAAATRGIVTPRAEPLASSAASSSARDCLTA
LLAQDLSLTRLELVNSQQLDLRQOVSLKASSPPNAV"

4038..4043

/note="E1B/protein IX"

4070

/note="E1B/protein IX"

complement(join(4091..5427,5706..5718))

/codon_start=1

/product="E2B 19a2"

/protein_id="AA019289.1"

/db_xref="GI:33465836"

/translation="METRGRRLPALOHQODPOAHPGQARAAPLHRDPVADSDPA
PVERHDPGSGRAPTAVORPQPARGMDLDRDAYOVELMDRLLELGLTQSLMP
TADGILKPLKRFASLOELSLGGERLADLVYENKVRMDLMBVAPILDDDSGSLNT
QLOPGLVIGTGTGCKSGLRLNLISQLISPTETVEFFLAPQVMTIPPSLEKAEWO
ICEGNVAPGPDGTIIPOSGLRPRFVNKAYDLDLEHNVDSDPNIIQAQAARPIA
IIMDCHEMLNGHKGVSKFFHAFPSKLHDKPKCTGYVLVLVHNMNRPRMAGNIA
LKIQSKHLISPRMPSOLNFRVNTYTGGLSLILKQDFRHHAQSSCDWILYNT
TPQHEALQWCYLHRDGLMPLYNLIGSLHYVLKIRHTLNDROBWSAAYARATPK"

4952

/note="compared to Ad2WT of NC_001405; his to gln change"

4952

/replac="c"

/note="compared to GenBank Accession Number M73260"

/replac="g"

complement(5197..8367)

CDS

variation

```

/codon_start=1
/product="HE2B 120K DNA polymerase"
/protein_id="AA019290.1"
/db_xref="GI:33465837"
/translation="MDSHLRDVYIKLRPPRADIWTLGSRGVNRSIVTLEPQGGQGAQAEVEFHGPNPGEGLKREPLCFILNRQGVNLVQDVPHVRCQCAFYSGHCSGRRIQFVEFHINSHSNMWRKEIOPFPIGHPPTERLFVYVDVETVYMAAFQGLVFPMLVMFPGDDEGVPVTHAPADLAALGMDRMWDMDLTPCIPREMAIGROGRTPRDLOMIMARLMSFPVANSNHLADMLSEHGLSPDEELTYLEKLKRSIKGIPRFLXYIGHNINSGDEILVLAQVINNRRESVGPPEFRTINPFRAGKILFNDVTFALNPSRKRDPLMLWEGCGDDTDFKYQYLKVMVRDTPALHTKSLRKAAQAYALPVEGSCAAYVQVYMLGSRSESDGPIIOEWMDREEFVNLREMLMKKGQDKDI1KETLDYCALVQVYAEVLYNKLRLSDYFVRSDVGLTDSFNVGSPPTSSNSHAIFGQVLFAPVASEMSEELYEDRGKABHDELVSFVRSATRGRCQPTVIGLIREPLVYDQIGASALATHMPMKNPLNPNVREBALAARMQALDIQCKITVFDKRLIPGFTVDADPDETDQDLPPEPCSRKGRICWTERNLRGEVATSDVLTVLNRMGRVHLVDEPRTVPEMCAVEYVQNLNTAKSERDRKQRTIRSI1AKLSNALYGSFATKLDNKKTVLSQMDMAKRTIAGOVNITKSSERLEFDNLGAEVWPAFOREYSPQQLADSDASEDEBARPTFPYSPGTPGHVATYKLPPIFLDSEEGDMCLHTLERVDPLVDNRNDSHSLASFTVAMTRAVSEMSSEELYEDRGKTPLEDRPLKSYVGDTDSLFTYTERGRLMERTRGKRIKKGHNLYPDEERPELTIVYGCETVACAGADAYSPESVFLAPKLYALSLHCPGSGASSKGLRKKGHAASBETDYDTCCKVLADQGDRORFSTSRISLKRITLASAOPGAPFTVQTLTRTLRPMKDMTLARLDERHLLPYSERPYPNREEICWIEMP"
/complement(5448..5705)
/notes="for E2B Iya2 mRNA"
6018..6024
/notes="major late mRNA TATA box"
/complement(8563..10544)
/notes="putative precursor"
/codon_start=1
/product="E2B pTP 75K"
/protein_id="AA019291.1"
/db_xref="GI:33465838"
/translation="MEHFLPLRNIIMNRVDPRASTTAAGITWMSRYIYGHRLMLEBILAPCAPLRLWPLRQPPPEPLVGYQYLVRCDNIVPDSYSLRATYELSQGHQVYVQGHQVNTMSMACVTYTGTAHFRVDMDDPOSTLOVOOALILAEVVDLALQMRFGFQVNLNMGSGRHILAPNSAAAATADADAGCGEEVEVEMLMDYDILRCONELAGMADRMGSGRHILAPNSAAAATIRLRKLTYENTIISSSTARNDPDRRPPRATVLSLPCDCBRLRLR1QAGPKDMDVLSLTLRLKTYENTIISSSTARNDPDRRPPRATVLSLPCDCBRLDLALERSDPDADSLSLGSGVPTQLKLCIVASVSLPGSGPPPTNRMGTGVFCVLRPRENGRAVATEMRRRRGEWIERPVDRLPRRRRRRVPPPPPEEESGALMBEELRLEEEEAFAVEFVETDVTVALIRLEEELTVSANSQGFNVAQVFEAMEERLEALGDIDNENSTRLRWVWFVFVAEHTATLTNLTALFORTLRVAPARHVEVLAQVVARADAGGVQYSRRTWNGSLNAFESQLMARISNDLAATYTERAGRDLOEEELQGMATAYQDNGDVCELRKQAAVNDTEIDSVSELSERFKLTGPVLFQRRQIDELNRVVAFASNLAAQHQLLEARGADVLPPLPAPBEPPLPGARPRHRF"
8783
/notes="compared to Ad2wt of NC_001405; Ieu to phe change"
/replace="a"
8783
/notes="compared to GenBank Accession Number M73260"
/replace="g"
11050..12297
/codon_start=1
/product="L1 52, 55K"
/protein_id="AA019292.1"
/db_xref="GI:33465839"
/translation="MHVPLRQMRPPPOQROBOQROTGRASPPTTASGATSAVDAAADGVEPPRRRAHYLDLDESEGRLARIGAPBEPHRYQLRDTREAVVPCONLFRDIDVAGBEPBEMRDRKFRAGRGRLRHGLNBERLREDEPDARTGTISPARAVAAADLTVTAAEQYTNQEIINPQKSPNNHYRITVAREEVALIGLMLMDPSALEQDPSKELAAQELITYAQHSQDNEAFRDALINIVYBEGRWLIDLINIIQSIYVGRSISLADKAAIINYSMLSLGKPYARKIYHTPYVPIDKEVKILEGYMRNALVYLTLSDLGYRNERIHKAVSVSRNARLSDLEMLMSLORALAGTSGDRBEASVYDAGADLRMAPSRALBMAAGPGLAVALAPARAGNAGVEVEYDEDDVEYBDEGEY"
11284
/notes="compared to GenBank Accession Number M73260"
/replace="c"

```

Db	917	ATGATCTTACCTGCGCACGAGGCTGGCTTCCACCAGTACGACGAGCATGAAGAGGCT	976
QY	61	GAGGAGTTTGTGTAGTTATATGTGGAGCACCCCGGGGACGGTTGACAGTCTGTGCATTAT	120
Db	977	GAGGAGTTTGTGTAGTTATATGTGGAGCACCCCGGGGACGGTTGACAGTCTGTGCATTAT	1036
QY	121	CACCGGAGGAATACGGGGGACCCGAGATATATGTGTCCGCTTGTCTATATAGAGACCTGT	180
Db	1037	CACCGGAGGAATACGGGGGACCCGAGATATATGTGTCCGCTTGTCTATATAGAGACCTGT	1096
QY	181	GGCATGTTTGTCTACAGTAAAGTAAATATATGCGCAGTGGGTGTATAGTGTGGTTTG	240
Db	1097	GGCATGTTTGTCTACAGTAAAGTAAATATATGCGCAGTGGGTGTATAGTGTGGTTTG	1156
QY	241	GTGTGTAAATTTTTTTTTTAATTTTTTACGTTTTGTGTGTAAAGATTTTTGTATGTGGA	300
Db	1157	GTGTGTAAATTTTTTTTTTAATTTTTTACGTTTTGTGTGTAAAGATTTTTGTATGTGGA	1216
QY	301	TTTTTTTAAAGGTCGTGTCTGACCTGAGCCTGAGCCGAGCCGAGAACCGGAGCCTG	360
Db	1217	TTTTTTTAAAGGTCGTGTGTCTGACCTGAGCCTGAGCCGAGCCGAGAACCGGAGCCTG	1276
QY	361	CAAGACCTACCCCGCTCTTAAATTGGCGCGCTGTACTGTAGAGCGCCGACATCACCTG	420
Db	1277	CAAGACCTACCCCGCTCTTAAATTGGCGCGCTGTACTGTAGAGCGCCGACATCACCTG	1336
QY	421	TGTCTAAGAAATGCATATGATATGATACGATAGCTGTACTCCGGTCTTCTTAACACCTC	480
Db	1337	TGTCTAAGAAATGCATATGATATGATACGATAGCTGTACTCCGGTCTTCTTAACACCTC	1396
QY	481	CTGAGATACACCGGCTGTGCGCGTGGCGCCCATTAACAGATGGCCGTGAGAGTTGGT	540
Db	1397	CTGAGATACACCGGCTGTGCGCGTGGCGCCCATTAACAGATGGCCGTGAGAGTTGGT	1456
QY	541	GGCCTGCGCAGGCTGTGGAAATGATATCGAGGACTTGCCTTAACGAGCCTTGGCAACTTTGG	600
Db	1457	GGCCTGCGCAGGCTGTGGAAATGATATCGAGGACTTGCCTTAACGAGCCTTGGCAACTTTGG	1516
QY	601	ACTTGAAGCTGTAACGCCCCAGGSCCATATAGGTGTAACCTGTGATTTGGCTGTGGTTAA	660
Db	1517	ACTTGAAGCTGTAACGCCCCAGGSCCATATAGGTGTAACCTGTGATTTGGCTGTGGTTAA	1576
QY	661	CGCCTTGTCTTGCATGATAGTTATATGATAGTTTAAATTAAGGGGAGATATATGTTTAAT	720
Db	1577	CGCCTTGTCTTGCATGATAGTTATATGATAGTTTAAATTAAGGGGAGATATATGTTTAAT	1636
QY	721	TGCATGAGGCTGTAAATATGGGCGGGGCTTAAAGGGATATATATCGCCGTGGGCTAATCT	780
Db	1637	TGCATGAGGCTGTAAATATGGGCGGGGCTTAAAGGGATATATATCGCCGTGGGCTAATCT	1696
QY	781	TGTTTACATCTGACCTCATATGAGGCTTGGAGGTGTGGAAATTTTTCTGCTGTGGCTA	840
Db	1697	TGTTTACATCTGACCTCATATGAGGCTTGGAGGTGTGGAAATTTTTCTGCTGTGGCTA	1756
QY	841	ACTTGTCTGGAACAGAGCTCTTAACAGTACTCTTGTGTTTGGAGGTTTCTGTGGGCTCAT	900
Db	1757	ACTTGTCTGGAACAGAGCTCTTAACAGTACTCTTGTGTTTGGAGGTTTCTGTGGGCTCAT	1816
QY	901	CCGAGGCAAGTATAGTTCGACAGATTTAAGAGATTAACAATGGGAATTTTGAAGACTTT	960
Db	1817	CCGAGGCAAGTATAGTTCGACAGATTTAAGAGATTAACAATGGGAATTTTGAAGACTTT	1876
QY	961	TGAATATCTGTGTGAGCTGTGTTGAATCTTTGAATCTTGGGTCAACGAGCGCTTTTCAAG	1020
Db	1877	TGAATATCTGTGTGAGCTGTGTTGAATCTTTGAATCTTGGGTCAACGAGCGCTTTTCAAG	1936
QY	1021	AGAGGTCTATCAAGCTTTTGAATTTTTCACAACCGGGGCGGCTGTGCTGTGCTT	1088
Db	1937	AGAGGTCTATCAAGCTTTTGAATTTTTCACAACCGGGGCGGCTGTGCTGTGCTT	1996
QY	1081	TTTGTAGTTTATTAAGGATTAATGGAGCGAAGAAACCATCTGAGCGGGGGGTCTGTGC	1140

Db 1997 TTTGATGTTTAAAGATTAATGAGAGGAAGAAACCATCTGAGCGGGGGTACCTGC 2056
Qy 1141 TGGATTTTCTGGCCATGATCTGTGAGAGCGGTTGTGAGACAAAGATGCGCTGTAC 1200
Db 2057 TGGATTTTCTGGCCATGATCTGTGAGAGCGGTTGTGAGACAAAGATGCGCTGTAC 2116
Qy 1201 TGTGTCTTCCGTCGCGCGGATNATCCGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db 2117 TGTGTCTTCCGTCGCGCGGATNATCCGAGGAGAGAGAGAGAGAGAGAGAGAGAG 2176
Qy 1261 AAGCAGCGCGCGCGAG 1320
Db 2177 AAGCAGCGCGCGCGAG 2236
Qy 1321 GGGATGAAATGTTGTACAGGTGCTGAACTGTATCAAGACTGAGAGAGAGAGAGAG 1380
Db 2237 GGGATGAAATGTTGTACAGGTGCTGAACTGTATCAAGACTGAGAGAGAGAGAGAG 2296
Qy 1381 TACAGAGATGGGCGGGGCTTAAAGGGGGTAAAGAGGAGAGAGAGAGAGAGAGAGAG 1440
Db 2297 TACAGAGATGGGCGGGGCTTAAAGGGGGTAAAGAGGAGAGAGAGAGAGAGAGAGAG 2356
Qy 1441 AGAGAGAGCTAGAAATCTAGCTTTAGCTTAATGACAGACACCGTCTGAGTATAC 1500
Db 2357 AGAGAGAGCTAGAAATCTAGCTTTAGCTTAATGACAGACACCGTCTGAGTATAC 2416
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTCTGCGCAGAGATATTC 1560
Db 2417 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTCTGCGCAGAGATATTC 2476
Qy 1561 CATGAGAGAGCTGACCACTTACTGCTGACAGCGGGAGATATTTGAGAGAGATATAG 1620
Db 2477 CATGAGAGAGCTGACCACTTACTGCTGACAGCGGGAGATATTTGAGAGAGATATAG 2536
Qy 1621 GGTATATGCAAAAGGTGCACTTAGCGCAGATTGCAAGTACAGAACTGTATAA 1680
Db 2537 GGTATATGCAAAAGGTGCACTTAGCGCAGATTGCAAGTACAGAACTGTATAA 2596
Qy 1681 TATCAGGAATGTTGCTACATTTCTGAGGACGGGGCGAGGTGAGATAGATACGAGGA 1740
Db 2597 TATCAGGAATGTTGCTACATTTCTGAGGACGGGGCGAGGTGAGATAGATACGAGGA 2656
Qy 1741 TAGGATGCGCTTGAAGTATGATGATTAATATGAGCGGGGCTTGGCATGAGAGG 1800
Db 2657 TAGGATGCGCTTGAAGTATGATGATTAATATGAGCGGGGCTTGGCATGAGAGG 2716
Qy 1801 GGTGTTATTTATGATGATGATTTACTGAGCCCAATTTAGCGGTATCGTCTGAGC 1860
Db 2717 GGTGTTATTTATGATGATGATTTACTGAGCCCAATTTAGCGGTATCGTCTGAGC 2776
Qy 1861 CAATACCAACCTTATCTTACAGGTGAGGCTTCTAGGGTTTAACAATACCTGTGTGA 1920
Db 2777 CAATACCAACCTTATCTTACAGGTGAGGCTTCTAGGGTTTAACAATACCTGTGTGA 2836
Qy 1921 AGCTTGACCGATGATGAGGTTTCGGGGCTGTGCTTTTACTGCTGCTGAGAGGGGCTGT 1980
Db 2837 AGCTTGACCGATGATGAGGTTTCGGGGCTGTGCTTTTACTGCTGCTGAGAGGGGCTGT 2896
Qy 1981 GTGTGCGCCCAAAAGAGAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGATCCTTGGG 2040
Db 2897 GTGTGCGCCCAAAAGAGAGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGATCCTTGGG 2956
Qy 2041 TATCTGTCTGAGGGTAACTCAGGGTGCAGCAATGTGAGCTTCCGACTGTGTGTGCTT 2100
Db 2957 TATCTGTCTGAGGGTAACTCAGGGTGCAGCAATGTGAGCTTCCGACTGTGTGTGCTT 3016
Qy 2101 CATGCTAGTGAAGAGCGGTGCTGTGATTAAGCATTAACATGATGATGAGCACTGAGAGA 2160
Db 3017 CATGCTAGTGAAGAGCGGTGCTGTGATTAAGCATTAACATGATGATGAGCACTGAGAGA 3076
Qy 2161 CAGGGGCTCTCAGATGCTGACTGCTGAGAGAGGCACTGTCACTGCTGAGAGACCATTTCA 2220
Db 3077 CAGGGGCTCTCAGATGCTGACTGCTGAGAGAGGCACTGTCACTGCTGAGAGACCATTTCA 3136

Qy 2221 CGTAGCCAGCCACTCTCCCAAGGCTTGCCAGTGTGTTTGAAGATTAAGTACTGAGCCGCTG 2280
Db 3137 CGTAGCCAGCCACTCTCCCAAGGCTTGCCAGTGTGTTTGAAGATTAAGTACTGAGCCGCTG 3196
Qy 2281 TTCCTTGATTTGGGTAAAGAGAGGGGGGTGTTCTTACTTACCAATGCAATTTGATCA 2340
Db 3197 TTCCTTGATTTGGGTAAAGAGAGGGGGGTGTTCTTACTTACCAATGCAATTTGATCA 3256
Qy 2341 CACTAAGATATTTGCTTGAAGCCGAGAGCATGTCCAAGGTGAACCTGAAAGGGGTGTTGA 2400
Db 3257 CACTAAGATATTTGCTTGAAGCCGAGAGCATGTCCAAGGTGAACCTGAAAGGGGTGTTGA 3316
Qy 2401 CATGACCATGAAGATCTGAAAGGTGCTGAGATGATGAGACCCGACACAGGTGAGACC 2460
Db 3317 CATGACCATGAAGATCTGAAAGGTGCTGAGATGATGAGACCCGACACAGGTGAGACC 3376
Qy 2461 CTGAGAGTGGCGGGTAAACATATTAGGAACGAGCTGTGATGCTGATGATGAGACAGGA 2520
Db 3377 CTGAGAGTGGCGGGTAAACATATTAGGAACGAGCTGTGATGCTGATGATGAGACAGGA 3436
Qy 2521 GCTGAGGCCGATCATTTGTGCTGCTGAGCCGAGCCGCTGAGATTGGCTTAGGAGATGA 2580
Db 3437 GCTGAGGCCGATCATTTGTGCTGCTGAGCCGAGCCGCTGAGATTGGCTTAGGAGATGA 3496
Qy 2581 AGATACAGATTGAG 2594
Db 3497 AGATACAGATTGAG 3510

Search completed: October 30, 2005, 22:52:22
Job time : 11083 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 17:47:52, Search time 1352 Seconds
(without alignments)
11357.847 Million cell updates/sec

Title: US-10-790-562-33_COPY_459_3052

Perfect score: 2594

Sequence: 1 atgcatcttaccctgcacga.....cgatgaagatcacagatcgag 2594

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 'N_Geneseq_16Dec04:':
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2594	100.0	3408	9	ACC70006 Nucleotid
2	2594	100.0	7090	5	AAH20746 Plasmid S
3	2594	100.0	7607	3	AAAS9076 Nucleotid
4	2594	100.0	7607	6	ABA94278 Nucleotid
5	2594	100.0	7607	9	AA156864 DNA sequ
6	2594	100.0	7607	10	ADB75124 Chromosom
7	2594	100.0	7607	10	ADP48758 Plasmid P
8	2594	100.0	11152	2	AAV32373 Complete
9	2594	100.0	11152	3	AAAS9047 Nucleotid
10	2594	100.0	11152	6	ABA94256 Nucleotid
11	2594	100.0	11152	10	ADB75153 Plasmid P
12	2594	100.0	14455	2	AAV32374 Complete
13	2594	100.0	14455	2	AAAS9050 Nucleotid
14	2594	100.0	14455	6	ABA94259 Nucleotid
15	2594	100.0	14455	10	ADB75156 Plasmid P
16	2594	100.0	14455	10	ADB75156 Plasmid P
17	2594	100.0	32802	13	ADR41671 S98-100 (
18	2594	100.0	33699	4	AAAC85020 Adenoviru
19	2594	100.0	34448	4	AAAC85021 Adenoviru
20	2594	100.0	34448	4	AAAC85021 Adenoviru

21	2594	100.0	35934	8	ABZ82331 Human ade
22	2594	100.0	35935	2	AAV07258 Adenoviru
23	2594	100.0	35935	6	AAAC85026 Complete
24	2594	100.0	35935	6	ABZ82331 Human ade
25	2594	100.0	35935	6	ABZ82331 Human ade
26	2594	100.0	35935	8	ACA61116 Adenoviru
27	2594	100.0	35935	8	ACA61117 Adenoviru
28	2594	100.0	35935	10	ACA60761 Human ade
29	2594	100.0	35935	13	ADR41672 Wild type
30	2594	100.0	35939	5	AAV32374 Complete
31	2594	100.0	37339	5	AAV32374 Complete
32	2582	99.5	33592	4	AAAC85018 Adenoviru
33	2582	99.5	33592	4	AAAC85023 Adenoviru
34	2582	99.5	33592	4	AAAC85019 Adenoviru
35	2582	99.5	33592	4	AAAC85024 Adenoviru
36	2582	99.5	33592	4	AAAC85022 Adenoviru
37	2582	99.5	33592	6	AAAD27972 Recombina
38	2582	99.5	33592	6	AAAC85025 Adenoviru
39	2498	96.3	35937	6	ABZ82331 Human ade
40	2498	96.3	35937	9	AACT70007 Nucleotid
41	2497.4	96.3	35759	10	ADP60698 Adenoviru
42	2497.4	96.3	35759	13	ADP60698 Adenoviru
43	2497	96.3	4853	10	ADK5745 Human ade
44	2161	83.3	34303	2	AAV07261 Adenoviru
45	1830	70.5	2500	9	AAAC85140 Human ade

ALIGNMENTS

RESULT 1	ACCT70006	standard; cDNA; 3408 BP.
ID	ACCT70006	standard; cDNA; 3408 BP.
XX	ACCT70006	
AC	ACCT70006	
XX	ACCT70006	
DT	29-JUL-2003	(first entry)
XX	29-JUL-2003	(first entry)
DE	Nucleotide sequence of the E1a protein of human adenovirus type 5.	
XX	Nucleotide sequence of the E1a protein of human adenovirus type 5.	
KW	Cancer; hyperproliferative disorder; viral vector; H19 promoter; H19 carcinoma; sarcoma; adenoma; ganglioblastoma; bladder carcinoma; E1a; gene; 89.	
KM	Human adenovirus type 5.	
OS	Human adenovirus type 5.	
XX	Human adenovirus type 5.	
XX	Human adenovirus type 5.	
FT	Key	Location/Qualifiers
FT	CDS	44..1029
FT	exon	/*tag= a
FT	exon	/product= "E1a protein"
FT	exon	/note= "contains an intron"
FT	exon	44..598
FT	exon	/*tag= b
FT	exon	/number= 1
FT	exon	599..714
FT	exon	/*tag= c
FT	exon	/number= 1
FT	exon	715..1026
FT	exon	/*tag= d
FT	exon	/number= 2
XX	W02003035883-A2.	
PN	W02003035883-A2.	
XX	W02003035883-A2.	
XX	01-MAY-2003.	
PD	01-MAY-2003.	
XX	01-MAY-2003.	
XX	22-OCT-2002; 2002WC-IL000843.	
PF	22-OCT-2002; 2002WC-IL000843.	
XX	22-OCT-2001; 2001US-00012131.	
XX	22-OCT-2001; 2001US-00012131.	
XX	(YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.	
PA	(YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.	
XX	(YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.	
XX	(YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.	
PI	Hochberg A, Ayesh S;	
XX	Hochberg A, Ayesh S;	

QY 481 CTGAGATACACCCGGTSGTCCCGCTGTGCCCATTTAAACGATGGCCGTGAGATGGTG 540
Db 3645 CTGAGATACACCCGGTSGTCCCGCTGTGCCCATTTAAACGATGGCCGTGAGATGGTG 3704
QY 541 GGGCTGCGCAGGCTGTGGAATGTATCGAGGACTTTCCTTAAACGAGCCTGGGCAACTTTGG 600
Db 3705 GGGCTGCGCAGGCTGTGGAATGTATCGAGGACTTTCCTTAAACGAGCCTGGGCAACTTTGG 3764
QY 601 ACTTGACACTGTAAACGCCGCCAGCATAGGTGTAAACCTGTGATGCGTGTGTGTTAA 660
Db 3765 ACTTGACACTGTAAACGCCGCCAGCATAGGTGTAAACCTGTGATGCGTGTGTGTTAA 3824
QY 661 CGCCTTGTGTGCTGAATGAGTTGATGTAACTTTAAATTAAGGGTGAGATTAATGTTTAACT 720
Db 3825 CGCCTTGTGTGCTGAATGAGTTGATGTAACTTTAAATTAAGGGTGAGATTAATGTTTAACT 3884
QY 721 TGCATGCGGTGTAAATGGGCGGGGCTTAAAGGGTATATATGCGCGGTGGCTAATCT 780
Db 3885 TGCATGCGGTGTAAATGGGCGGGGCTTAAAGGGTATATATGCGCGGTGGCTAATCT 3944
QY 781 TGGTTACATCTGACCTCAATGAGGCTTGGGAGTGTGGAGATTTTCTGCTGCGCTA 840
Db 3945 TGGTTACATCTGACCTCAATGAGGCTTGGGAGTGTGGAGATTTTCTGCTGCGCTA 4004
QY 841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTGTGTTTGGAGGTTTCTGTGGGCTCAT 900
Db 4005 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTGTGTTTGGAGGTTTCTGTGGGCTCAT 4064
QY 901 CCCAGGCAAGTTAGTCTGCAGATTTAAGAGGATTAACAAGTGGGAATTTGAAGACTTT 960
Db 4065 CCCAGGCAAGTTAGTCTGCAGATTTAAGAGGATTAACAAGTGGGAATTTGAAGACTTT 4124
QY 961 TGAATCCTGTGTGAGGCTGTTTGAATCTTGAATCTGGGTCAACGAGGCGCTTTCAG 1020
Db 4125 TGAATCCTGTGTGAGGCTGTTTGAATCTTGAATCTGGGTCAACGAGGCGCTTTCAG 4184
QY 1021 AGAAGTCATCAAGACTTTGGAATTTTCCACACCGGGCGCGCTGCGCTGTGGCTT 1080
Db 4185 AGAAGTCATCAAGACTTTGGAATTTTCCACACCGGGCGCGCTGCGCTGTGGCTT 4244
QY 1081 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGGTACCTGC 1140
Db 4245 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGGTACCTGC 4304
QY 1141 TGGATTTCTGGCCATGATCTGTGAGAGCGGTTGTGAGACACAAGAACTGCTGTAC 1200
Db 4305 TGGATTTCTGGCCATGATCTGTGAGAGCGGTTGTGAGACACAAGAACTGCTGTAC 4364
QY 1201 TGTGTCTTCCGTCCGCCCGCGCATATATACGACGAGAGGAGCAGCAGCAGAGG 1260
Db 4365 TGTGTCTTCCGTCCGCCCGCGCATATATACGACGAGAGGAGCAGCAGCAGAGG 4424
QY 1261 AAGCAGCGCGCGGGGCGAGAGCAGAGCCCATGMAACCCGAGAGCCGGCTGAGCCCTC 1320
Db 4425 AAGCAGCGCGCGGGGCGAGAGCAGAGCCCATGMAACCCGAGAGCCGGCTGAGCCCTC 4484
QY 1321 GGGAAATGAAATGTTGTAAGAGTGGCTGAATCTGTATCCAGAACTGAGACGATTTTGA 1380
Db 4485 GGGAAATGAAATGTTGTAAGAGTGGCTGAATCTGTATCCAGAACTGAGACGATTTTGA 4544
QY 1381 TACAGAGATGGGCAAGGGCTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 1440
Db 4545 TACAGAGATGGGCAAGGGCTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 4604
QY 1441 AAGAGAGCTAAGAACTTACCTTTTACCTTAATGACCAAGACCGTCTGAGGTATTAC 1500
Db 4605 AAGAGAGCTAAGAACTTACCTTTTACCTTAATGACCAAGACCGTCTGAGGTATTAC 4664
QY 1501 TTTTCAACAGATCAAGGATTAATGCGCTAATGAGCTTGAATCTGCTGCGCAGAAATTC 1560
Db 4665 TTTTCAACAGATCAAGGATTAATGCGCTAATGAGCTTGAATCTGCTGCGCAGAAATTC 4724

QY 1561 CATAGACAGCTGACCACTTACTGCTGAGCCAGGGGATGATTTTGAAGGCTATTAG 1620
Db 4725 CATAGACAGCTGACCACTTACTGCTGAGCCAGGGGATGATTTTGAAGGCTATTAG 4784
QY 1621 GGTATATGCAAGAGTGGACTTAAAGCCAGATTGCAAGTACAAATCAGCAACTTGTAAA 1680
Db 4785 GGTATATGCAAGAGTGGACTTAAAGCCAGATTGCAAGTACAAATCAGCAACTTGTAAA 4844
QY 1681 TATCAGAAATTTGCTCACTTTCTGGGAAACGGGGCCGAGGTGAGATATATACCGAGGA 1740
Db 4845 TATCAGAAATTTGCTCACTTTCTGGGAAACGGGGCCGAGGTGAGATATATACCGAGGA 4904
QY 1741 TAAAGTGGCCTTATAGATGTAGCATGATTAATATGTGGCCGGGGGTCTTGAGATGAG 1800
Db 4905 TAAAGTGGCCTTATAGATGTAGCATGATTAATATGTGGCCGGGGGTCTTGAGATGAG 4964
QY 1801 GGTGTATTTATGATGATTAAGTTTACTGGCCCCCAATTTTACGGGTTCCTGGC 1860
Db 4965 GGTGTATTTATGATGATTAAGTTTACTGGCCCCCAATTTTACGGGTTCCTGGC 5024
QY 1861 CAATACCAACCTTATCTTACACGGGTACCTTCTATGGGTTTAACAATACCTGTGGA 1920
Db 5025 CAATACCAACCTTATCTTACACGGGTACCTTCTATGGGTTTAACAATACCTGTGGA 5084
QY 1921 AGCCTGGAACGATGTAGGGGTGGGGCTGACCTTTTACTGTGCTGGAAGGGGTGCT 1980
Db 5085 AGCCTGGAACGATGTAGGGGTGGGGCTGACCTTTTACTGTGCTGGAAGGGGTGCT 5144
QY 1981 GTGTGCCCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGGG 2040
Db 5145 GTGTGCCCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGGG 5204
QY 2041 TATCTGTCTGAGGGTAACTTCAAGGGTCCGCAAAATGGCCCTGAGTGGTGT 2100
Db 5205 TATCTGTCTGAGGGTAACTTCAAGGGTCCGCAAAATGGCCCTGAGTGGTGT 5264
QY 2101 CATCTGTGTAAAGCGGTGCTGTGATTAAGCATPAACATGATATGTGGCAACTGGAGGA 2160
Db 5265 CATCTGTGTAAAGCGGTGCTGTGATTAAGCATPAACATGATATGTGGCAACTGGAGGA 5324
QY 2161 CAGGAGCTCTCAGATGTGACCTGTGGAAGGGAACGTGACCTGTGGAAGACCATTTCA 2220
Db 5325 CAGGAGCTCTCAGATGTGACCTGTGGAAGGGAACGTGACCTGTGGAAGACCATTTCA 5384
QY 2221 CGTAGCCAGCACTCTGCAAGGCTGTGGCCAGTGTGAGAGATTAACAATGACCGGCTG 2280
Db 5385 CGTAGCCAGCACTCTGCAAGGCTGTGGCCAGTGTGAGAGATTAACAATGACCGGCTG 5444
QY 2281 TTTCTTGATTTGGGTAAACAGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGATCA 2340
Db 5445 TTTCTTGATTTGGGTAAACAGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGATCA 5504
QY 2341 CACTAAGATATTGCTTGAACCCGAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGGA 2400
Db 5505 CACTAAGATATTGCTTGAACCCGAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGGA 5564
QY 2401 CATGACATGAAGATCTGGAAGGTCTGAGGTACATGAGACCCGACACAGGTGAGACC 2460
Db 5565 CATGACATGAAGATCTGGAAGGTCTGAGGTACATGAGACCCGACACAGGTGAGACC 5624
QY 2461 CTGAGAGTGGCGGTAAACATATTAGGAACAGAGCTGTGATGTGATGTCGAGGA 2520
Db 5625 CTGAGAGTGGCGGTAAACATATTAGGAACAGAGCTGTGATGTGATGTCGAGGA 5684
QY 2521 GCTGAGGCCCATTCATTTGTGCTGCGCTGCAACCCGCGTGAATTTGAGTTCAGCATGA 2580
Db 5685 GCTGAGGCCCATTCATTTGTGCTGCGCTGCAACCCGCGTGAATTTGAGTTCAGCATGA 5744
QY 2581 AGATACAGATTGAG 2594
Db 5745 AGATACAGATTGAG 5758

ID	Accession	Standard	DNA	Length	BP
XX	AAAS9076	AAA59076	standard	7607	BP
XX	AC	AAA59076			
XX	DT	07-NOV-2000	(first entry)		
XX	DE	Nucleotide sequence of plasmid GRES-El-SV40-Hygro.			
XX	KW	Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;			
XX	OS	ss.			
XX	XX	Synthetic.			
XX	FN	WO20042208-A1.			
XX	PD	20-JUL-2000.			
XX	PP	14-JAN-2000; 2000MO-EP000265.			
XX	PR	14-JAN-1999; 99US-0115920P.			
XX	PA	(NOVS) NOVARTIS AG.			
XX	PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.			
XX	PA	(SCRI) SCRIPPS RES INST.			
XX	PI	Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC;			
XX	DR	Skripchenko Y,			
XX	XX	WPI, 2000-476068/41.			
XX	XX	New nucleic acid comprising an adenovirus tripartite leader nucleotide			
XX	XX	for producing high-capacity and targeted vectors for adenovirus-based			
XX	XX	gene therapy.			
XX	XX	Example 6; Page 190-192; 212pp; English.			
XX	XX	The specification describes a nucleic acid molecule comprising an			
XX	XX	adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence			
XX	XX	comprising two different TPL exons or three same or different TPL exons.			
XX	XX	The nucleic acid is used to produce an adenovirus vector particle,			
XX	XX	deliver an exogenous gene to a target cell, pseudotype recombinant viral			
XX	XX	vectors, target an adenovirus vector to a cell, produce a modified			
XX	XX	adenovirus, deliver a heterologous gene to an animal and produce a			
XX	XX	gutless adenoviral vector particle. The present sequence represents			
XX	XX	plasmid GRES-El-SV40-Hygro, which is used in the course of the invention			
XX	XX				
XX	XX	Sequence 7607 BP, 1838 A; 1733 C; 2001 G; 2035 T; 0 U; 0 Other;			
XX	XX				
XX	XX	Query Match 100.0%; Score 2594; DB 3; Length 7607;			
XX	XX	Best Local Similarity 100.0%; Pred. No. 0;			
XX	XX	Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
XX	XX				
XX	XX	1 ATGCATCTTACCTGCGACGAGGCTGCTTTCCACCAGTGACGACGAGATGAAGAGGT 60			
XX	XX	1334 ATTCATCTTACCTGCGACGAGGCTGCTTTCCACCAGTGACGACGAGATGAAGAGGT 1393			
XX	XX				
XX	XX	61 GAGAGTTTGGTTAGATTATGTGAGAGACCCCGGGGACGGTGGAGGCTTTGTCATTAT 120			
XX	XX	1394 GAGAGTTTGGTTAGATTATGTGAGAGACCCCGGGGACGGTGGAGGCTTTGTCATTAT 1453			
XX	XX				
XX	XX	121 CACCGAGGAATTAAGGGGAGACCCAGATATTATGTGTTGGCTTTCATATGAGACCTGT 180			
XX	XX	1454 CACCGAGGAATTAAGGGGAGACCCAGATATTATGTGTTGGCTTTCATATGAGACCTGT 1513			
XX	XX				
XX	XX	181 GGCATGTTTGTCTACAGTAAGTGAATAATTAAGGAGGAGTGGATGATAGAGTGGGTTTG 240			
XX	XX	1514 GGCATGTTTGTCTACAGTAAGTGAATAATTAAGGAGGAGTGGATGATAGAGTGGGTTTG 1573			
XX	XX				
XX	XX	241 GTGAGGTAATTTTTTTTTTAAATTTTAAAGTGGTTTAAAGATTTTGTATGTGA 300			
XX	XX	1574 GTGAGGTAATTTTTTTTTTAAATTTTAAAGTGGTTTAAAGATTTTGTATGTGA 1633			

QY	301	TTTTTTAAAAAGGTCCTGTGCTGTGAACCTGAGCCGAGCCGAGCCAGAACCCGAGGACCTG	360
Db	1634	TTTTTTAAAAAGGTCCTGTGCTGTGAACCTGAGCCGAGCCGAGCCAGAACCCGAGGACCTG	1693
QY	361	CAGAAGCTACCCGCGCTCTAAATAGCGCGCTGCTATCTGAGAGCCGCGACATCACTG	420
Db	1694	CAGAAGCTACCCGCGCTCTAAATAGCGCGCTGCTATCTGAGAGCCGCGACATCACTG	1755
QY	421	TGTCAGAGAAATGCATATGTAGTACCGATACCTGGATCTCCGTCCTCTAACACACTC	480
Db	1754	TGTCAGAGAAATGCATATGTAGTACCGATACCTGGATCTCCGTCCTCTAACACACTC	1813
QY	481	CTGAGATACACCCGATGCTCCGCTGTGCCCCCATTTAAACCAATGGCCGTGAGATTTGGTG	540
Db	1814	CTGAGATACACCCGATGCTCCGCTGTGCCCCCATTTAAACCAATGGCCGTGAGATTTGGTG	1877
QY	541	GCGCTCCGACAGCTGTGGAATGTATCGAGACCTGCTTAAAGAGCTTGGCAACTTTGG	600
Db	1874	GCGCTCCGACAGCTGTGGAATGTATCGAGACCTGCTTAAAGAGCTTGGCAACTTTGG	1933
QY	601	ACTTGAAGCTGTAAACGCCCCAGGCGCATPAAAGGTGTAACCTGTGATTTGGTGTGTAA	660
Db	1934	ACTTGAAGCTGTAAACGCCCCAGGCGCATPAAAGGTGTAACCTGTGATTTGGTGTGTAA	1993
QY	661	GCGCTTGTGTTGCTGAATGAGTTGATGTAACTTAAATPAAAGGTCAGATAATGTTTAACT	720
Db	1994	GCGCTTGTGTTGCTGAATGAGTTGATGTAACTTAAATPAAAGGTCAGATAATGTTTAACT	2053
QY	721	TGCATGGCGGTGTAAATGGGGCGGGGCTTAAAGGGTATATATACCGCGGTGGCTAACT	780
Db	2054	TGCATGGCGGTGTAAATGGGGCGGGGCTTAAAGGGTATATATACCGCGGTGGCTAACT	2113
QY	781	TGCTTACACTGACCTCATGAGGCTTGGAGTGTGTGGAAGATTTTCTGCTGACCTA	840
Db	2114	TGCTTACACTGACCTCATGAGGCTTGGAGTGTGTGGAAGATTTTCTGCTGACCTA	2173
QY	841	ACTTGCTGGAACAGAGCTCTAACAGTACTCTTGATTTTGGAGGTTTCTGTGGGCTCAT	900
Db	2174	ACTTGCTGGAACAGAGCTCTAACAGTACTCTTGATTTTGGAGGTTTCTGTGGGCTCAT	2233
QY	901	CCGAGGCAAAATGTAGTGTGACGAATTTAAGAGATTTCAATGGGAAATTTAAGAGCTT	960
Db	2234	CCGAGGCAAAATGTAGTGTGACGAATTTAAGAGATTTCAATGGGAAATTTAAGAGCTT	2293
QY	961	TGAATCTCTGTGTGAGCTGTTTGATTTCTTTGAATCTGGGTCACAGCGCTTTTCCAA	1020
Db	2294	TGAATCTCTGTGTGAGCTGTTTGATTTCTTTGAATCTGGGTCACAGCGCTTTTCCAA	2353
QY	1021	AGAAGGTCATCAACACTTTGGATTTTTCACACCGGGGGCGGCTGCGCTGTGTGCTT	1080
Db	2354	AGAAGGTCATCAACACTTTGGATTTTTCACACCGGGGGCGGCTGCGCTGTGTGCTT	2413
QY	1081	TTTTGAGTTTTATPAAAGATPAAATGAGACGAGAAACCCATCTGAGCGGGGGGTACTGCG	1140
Db	2414	TTTTGAGTTTTATPAAAGATPAAATGAGACGAGAAACCCATCTGAGCGGGGGGTACTGCG	2473
QY	1141	TGGAATTTTCTGCGCATGCACTGTGTGAGAGCGGTTGTGAGACACAGAATCGCTGCTAC	1200
Db	2474	TGGAATTTTCTGCGCATGCACTGTGTGAGAGCGGTTGTGAGACACAGAATCGCTGCTAC	2533
QY	1201	TGTTGTCTTCCGTCGCGCGCGCGCATATPACCGACGGAGGACAGCACAAGAGAGAGG	1260
Db	2534	TGTTGTCTTCCGTCGCGCGCGCGCATATPACCGACGGAGGACAGCACAAGAGAGG	2593
QY	1261	AAGCCAGGCGGCGGCGCAGAGACGAGCCCATGGAACCCGAGAGCGGACCTGAGCCCTC	1320
Db	2594	AAGCCAGGCGGCGGCGCAGAGACGAGCCCATGGAACCCGAGAGCGGACCTGAGCCCTC	2653
QY	1321	GGGAATGAATGTGTGAAGGTGGCTGAACGTGTATCCGAATGAGACGCAATTTTGAAT	1380
Db	2654	GGGAATGAATGTGTGAAGGTGGCTGAACGTGTATCCGAATGAGACGCAATTTTGAAT	2713

1381 TACAGAGATGGGCGGGGCTAAAGGGGGTAAAGAGGAGCGGGGCTTGTGAGCTAC 1440
2714 TACAGAGGATGGGCGGGGCTAAAGGGGGTAAAGAGGAGCGGGGCTTGTGAGCTAC 2773
1441 AGAGAGGCTAGGAATTTAGCTTTAGCTTAAATACACAGACCCGCTAGATATAC 1500
2774 AGAGAGGCTAGGAATTTAGCTTTAGCTTAAATACACAGACCCGCTAGATATAC 2833
1501 TTTTCAACAGATCAAGATTAATTCGGCTAATGAGCTTATCTGCGGAGAGATATTC 1560
2834 TTTTCAACAGATCAAGATTAATTCGGCTAATGAGCTTATCTGCGGAGAGATATTC 2893
1561 CATAGACAGCTGACCACTTACTGCTGACCGACGAGGATGATTTTGAAGAGCTATTAG 1620
2894 CATAGACAGCTGACCACTTACTGCTGACCGACGAGGATGATTTTGAAGAGCTATTAG 2953
1621 GGTATATGCAAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAAGTCAAACTTGTA 1680
2954 GGTATATGCAAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAAGTCAAACTTGTA 3013
1681 TATCAGGAATTTGTTGCTACATTTCTGGGAAGGGGCGAGGTGAGATGATACGAGGA 1740
3014 TATCAGGAATTTGTTGCTACATTTCTGGGAAGGGGCGAGGTGAGATGATACGAGGA 3073
1741 TAGGATGGCTTTAGATGTAGCATGATTAATATATGAGCGGCGGCTGCTGATGACGG 1800
3074 TAGGATGGCTTTAGATGTAGCATGATTAATATATGAGCGGCGGCTGCTGATGACGG 3133
1801 GGTGTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
3134 GGTGTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3193
1861 CAATACCAACCTTATCTCACAAGGTGTAAGCTTCTATGAGTTTAACAATACCTGTGGA 1920
3194 CAATACCAACCTTATCTCACAAGGTGTAAGCTTCTATGAGTTTAACAATACCTGTGGA 3253
1921 AGCTGAGCCGATGATGAGGCTTGGGCTGTGCTTTTACTGTGCTGAGAGGGGCTGCT 1980
3254 AGCTGAGCCGATGATGAGGCTTGGGCTGTGCTTTTACTGTGCTGAGAGGGGCTGCT 3313
1981 GTGTGCCCCCAAAAGCAAGGCTTCAATTAAGAAAGCCCTTTGAAAGGTGATCTTGGG 2040
3314 GTGTGCCCCCAAAAGCAAGGCTTCAATTAAGAAAGCCCTTTGAAAGGTGATCTTGGG 3373
2041 TATCTGTCTGAGGTAATCTCCAGGGTGGCCACATGTGCTCCGACTGTGTGCTT 2100
3374 TATCTGTCTGAGGTAATCTCCAGGGTGGCCACATGTGCTCCGACTGTGTGCTT 3433
2101 CATGCTAGTGAAGACGCTGCTGTGATTAAGCATTAATGATGTGCAATCGGAGGA 2160
3434 CATGCTAGTGAAGACGCTGCTGTGATTAAGCATTAATGATGTGCAATCGGAGGA 3493
2161 CAGGGCCCTCTGAGATGCTGACTGCTCGGACGGCAACGTGCACTGCTGAAACCATTC 2220
3494 CAGGGCCCTCTGAGATGCTGACTGCTCGGACGGCAACGTGCACTGCTGAAACCATTC 3553
2221 CGTAGCCAGCACTCTCGCAAGGCTGCGCAGTGTGTTGAGCATTAATCTGACCCGCTG 2280
3554 CGTAGCCAGCACTCTCGCAAGGCTGCGCAGTGTGTTGAGCATTAATCTGACCCGCTG 3613
2281 TTCTTTGCAATTTGGGTAACAGAGGGGGGTTTCTTACTTACCAATGCAATTTGAGTGA 2340
3614 TTCTTTGCAATTTGGGTAACAGAGGGGGGTTTCTTACTTACCAATGCAATTTGAGTGA 3673
2341 CACTAAGATTAATGCTTGAAGCCGAGAGCATGTCAGGAACTGAAACGAGGCTGTTTGA 2400
3674 CACTAAGATTAATGCTTGAAGCCGAGAGCATGTCAGGAACTGAAACGAGGCTGTTTGA 3733
2401 CATGACCATGAAGATCTGGAAGGTGCTGAGTACATGATGAGACCCGACCAAGGTGACACC 2460
3734 CATGACCATGAAGATCTGGAAGGTGCTGAGTACATGATGAGACCCGACCAAGGTGACACC 3793
2461 CTGCGAGTGTGGCGGTAACATATTAGAAACAGCCTGTGATGCTGATGTGACCGAGGA 2520

DB 3794 CTGCGAGTGTGGCGGTAACATATTAGAAACAGCCTGTGATCTGGATGTGACCGAGGA 3853
QY 2521 GCTGAGCCCGATCACTTGTGTGCTGCTGACACCCGCGCTGAGTTTGGCTTACCATGA 2580
DB 3854 GCTGAGCCCGATCACTTGTGTGCTGCTGACACCCGCGCTGAGTTTGGCTTACCATGA 3913
QY 2581 AGATTACGATTTGAG 2594
DB 3914 AGATTACGATTTGAG 3927
RESULT 4
ABA94278
ID ABA94278 standard; DNA; 7607 BP.
XX
AC ABA94278;
XX
DT 13-MAR-2002 (first entry)
DE
XX Nucleotide sequence of plasmid GRES-E1-SV40-Hygro.
XX
XX Adenovirus; Inverted terminal repeat sequence; ITRS; ocular disease;
KM fiber protein; photoreceptor; rhodopsin; starardt disease gene; STDgi;
KM ophthalmological; antiinflammatory; antidiabetic; cyostatic;
KM gene therapy; tripartite leader; TPL; ss.
OS Synthetic.
XX WO200183729-A2.
PN 08-NOV-2001.
XX
PD 30-APR-2001; 2001WO-EP004863.
XX
PF 01-MAY-2000; 2000US-00562934.
PR
XX
XX (NOVS) NOVARTIS AG
PA (SRI) SCRIPPS RES INST.
PA (NEME/) NEMEROW G R.
PA (VSEG/) VON SEGGERN D J.
PA (FRIE/) FRIEDLANDER M.
PI Nemerow GR, Von Seggern DJ, Friedlander M;
XX
XX WPI; 2002-082846/11.
DR
XX
XX Polynucleotide for making vectors, useful for treating ocular diseases,
PT e.g., retinitis pigmentosa, comprises adenovirus inverted terminal repeat
PT sequences, packaging signal and photoreceptor-specific promoter.
XX
XX Example 5; Page 139-141; 149pp; English.
XX
XX The invention provides an isolated polynucleotide comprising adenovirus
XX (AV) inverted terminal repeat sequences (ITRS), AV packaging signal
XX (AV) operatively linked to ITRS and a photoreceptor-specific promoter. A
XX recombinant AV vector (AVV) comprising the polynucleotide is useful for
XX targeted delivery of a gene product to the eye (especially to the
XX vitreous cavity), for treating an ocular disease, e.g., retinal
XX degenerative disease, retinitis pigmentosa, Stargardt's disease, a mamal
XX retinopathies, retinal vascularizations, and retinoblastoma, of a mamal
XX preferably human. The AVV comprises a fiber protein that specifically or
XX selectively binds to receptors that are expressed on cells (preferably
XX photoreceptors in the eye). Preferably, the recombinant virus comprise a
XX fiber protein from an adenovirus type D subgroup or is a chimeric protein
XX containing a portion of the N-terminus of an adenovirus type 2 or type 5
XX penton, and the therapeutic product is a trophic factor, an anti-
XX apoptotic factor, gene encoding a rhodopsin protein, a wild-type
XX stargardt disease gene (STGB1), an anti-cancer agent and a protein that
XX regulates expression of a photoreceptor specific gene product. The viral
XX nucleic acid of AAV comprises ITRS and packaging signal derived from AAV
XX subgroup B or C, especially an AV type 2 or type 5. AAV is also useful
XX for targeted gene therapy, where the vector comprises an AV type 37 fiber

protein or its portion, and selectively transduces photoreceptors and
CC delivers a gene product encoded by AAV. The present sequence represents
CC the nucleotide sequence of plasmid GR5-B1-SV40-Hygro

Sequence 7607 BP, 1838 A, 1733 C, 2001 G, 2035 T, 0 U, 0 Other;

Query Match 100.0%; Score 2594; DB 6; Length 7607;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATCGATCTTACCTGCGCAGAGGCTGCTTTCCACCCAGTGAAGAGAGATGAAGAGGT 60
DB 1334 ATCGATCTTACCTGCGCAGAGGCTGCTTTCCACCCAGTGAAGAGAGATGAAGAGGT 1393
QY 61 GAGAGATTGTTGATTAATATGTGAGCAACCCGGGCAAGTTGCAAGTCTTTGATTAT 120
DB 1394 GAGAGATTGTTGATTAATATGTGAGCAACCCGGGCAAGTTGCAAGTCTTTGATTAT 1453
QY 121 CACGGAGGAATPACGGGGGACCCAGATATATATGTTGCTTTGCTATATAGAGACCTGT 180
DB 1454 CACGGAGGAATPACGGGGGACCCAGATATATATGTTGCTTTGCTATATAGAGACCTGT 1513
QY 181 GGCATGTTGTTCTACAGTAAAGTAAATTAATGAGGAGTGGTATAGATGAGTGGTTTG 240
DB 1514 GGCATGTTGTTCTACAGTAAAGTAAATTAATGAGGAGTGGTATAGATGAGTGGTTTG 1573
QY 241 GTGTGTAATTTTTTTTTTAATTTTACAGTTTGTGGTTTAAAGATTTGTATTTGTA 300
DB 1574 GTGTGTAATTTTTTTTTTAATTTTACAGTTTGTGGTTTAAAGATTTGTATTTGTA 1633
QY 301 TTTTTTAAAGGTCCTGTCTGAACTGAGACCTGAGACCCGAGCAAAACCGAGCTTG 360
DB 1534 TTTTTTAAAGGTCCTGTCTGAACTGAGACCTGAGACCCGAGCAAAACCGAGCTTG 1693
QY 361 CAAGACCTACCCGCGCTCTAAATGAGGCGCTGATCTGAGAGCGCCGATCAGCTG 420
DB 1694 CAAGACCTACCCGCGCTCTAAATGAGGCGCTGATCTGAGAGCGCCGATCAGCTG 1753
QY 421 TGTCTAGGAATGCAATAGTATGATGAGATGAGTGTGATCTGCGTCTTTCTAACACACTC 480
DB 1754 TGTCTAGGAATGCAATAGTATGATGAGATGAGTGTGATCTGCGTCTTTCTAACACACTC 1813
QY 481 CTGAGATCACCCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 1814 CTGAGATCACCCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1873
QY 541 GCGCGTCGAGGCTGTGATGATGATGAGATGATGAGATGATGAGATGATGAGATGATGAG 600
DB 1874 GCGCGTCGAGGCTGTGATGATGATGAGATGATGAGATGATGAGATGATGAGATGATGAG 1933
QY 601 ACTTGAAGCTGTAAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAG 660
DB 1934 ACTTGAAGCTGTAAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAG 1993
QY 661 GCGCTTTGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 1994 GCGCTTTGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2053
QY 721 TGCAATGGCTGTAAATGGGGGGGGCTTAAAGGATATATAATGGCGGTGGGCAACT 780
DB 2054 TGCAATGGCTGTAAATGGGGGGGGCTTAAAGGATATATAATGGCGGTGGGCAACT 2113
QY 781 TGGTTACATCTGACCTCAATGAGGCTTGGAGTGTGGAGATTTTCTGCTGTGCTGA 840
DB 2114 TGGTTACATCTGACCTCAATGAGGCTTGGAGTGTGGAGATTTTCTGCTGTGCTGA 2173
QY 841 ACTTGTCTGAACAGAGCTCTTAACAGTACCTTGTGTTTGAAGTTTCTGTGGGCTAT 900
DB 2174 ACTTGTCTGAACAGAGCTCTTAACAGTACCTTGTGTTTGAAGTTTCTGTGGGCTAT 2233
QY 901 CCCAGGCAAGTGTGCTGAGATTAAGAGGATTAACAAGTGGGATTTGAAGGCTTT 960
DB 2234 CCCAGGCAAGTGTGCTGAGATTAAGAGGATTAACAAGTGGGATTTGAAGGCTTT 2293
```

```

QY 961 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAG 1020
DB 2294 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGGGTCAACAGGCGCTTTTCCAG 2353
QY 1021 AGAAGGTACATCAAGCTTTGATTTTTCACACCGGGGGGGCTGCGGTGCTGTGCTT 1080
DB 2354 AGAAGGTACATCAAGCTTTGATTTTTCACACCGGGGGGGCTGCGGTGCTGTGCTT 2413
QY 1081 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTACTGTC 1140
DB 2414 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTACTGTC 2473
QY 1141 TGAATTTTCTGGCCATGATCTGTGAGAGGCTTGTGAACACAAGATGCTGCTAC 1200
DB 2474 TGAATTTTCTGGCCATGATCTGTGAGAGGCTTGTGAACACAAGATGCTGCTAC 2533
QY 1201 TGTGTCTTCCGTCGCGCGGCGATTAATCCGAGGAGAGAGAGAGAGAGAGAGAG 1260
DB 2534 TGTGTCTTCCGTCGCGCGGCGATTAATCCGAGGAGAGAGAGAGAGAGAGAGAGAG 2593
QY 1261 AAGCAGGCGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 2594 AAGCAGGCGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2653
QY 1321 GGGAAATGATGTTTGTACAGTGTGCTGAACTGTATCCAGAACTGAGAGCGATTTGACAT 1380
DB 2654 GGGAAATGATGTTTGTACAGTGTGCTGAACTGTATCCAGAACTGAGAGCGATTTGACAT 2713
QY 1381 TACAGAGATGGGAGAGGGGCTAAAGGGGTTAAAGGGAGAGGGGGGCTTGTGAAGCTAC 1440
DB 2714 TACAGAGATGGGAGAGGGGCTAAAGGGGTTAAAGGGAGAGGGGGGCTTGTGAAGCTAC 2773
QY 1441 AGAGAGGCTAGGAATCTAGCTTTTATGCTTATATGACAGAGACCGTCTGATGATTTAC 1500
DB 2774 AGAGAGGCTAGGAATCTAGCTTTTATGCTTATATGACAGAGACCGTCTGATGATTTAC 2833
QY 2834 TTTTCAACAGATCAAGATTAATTTGCTTAATGAGCTTATGCTGCTGCGAGAAATATTC 2893
DB 1501 TTTTCAACAGATCAAGATTAATTTGCTTAATGAGCTTATGCTGCTGCGAGAAATATTC 1560
QY 2894 CATAGAGAGCTGACCACTTATCTGCTGACAGCGGAGATGATTTTGAAGAGCTATTAAG 1620
DB 1561 CATAGAGAGCTGACCACTTATCTGCTGACAGCGGAGATGATTTTGAAGAGCTATTAAG 1680
QY 1621 GGTATATCAAGAGTGCATCTTGAAGCCAGATTTGCAAGTACAGAACTTGTAAA 1680
DB 2954 GGTATATCAAGAGTGCATCTTGAAGCCAGATTTGCAAGTACAGAACTTGTAAA 3013
QY 1681 TATCAGGAATTTGTTCAATTTCTGGGAACGGGGCCGAGGTGAGATGATACGAGAGA 1740
DB 3014 TATCAGGAATTTGTTCAATTTCTGGGAACGGGGCCGAGGTGAGATGATACGAGAGA 3073
QY 1741 TAGGTGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
DB 3074 TAGGTGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3133
QY 1801 GGTGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
DB 3134 GGTGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3193
QY 1861 CAATACCAACTTATCTTACAGGCTGTAAGCTTATAGGTTTAAACAATACCTGTGGA 1920
DB 3194 CAATACCAACTTATCTTACAGGCTGTAAGCTTATAGGTTTAAACAATACCTGTGGA 3253
QY 1921 AGCTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
DB 3254 AGCTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3313
QY 1981 GTGTGCGCCCAAAAGAGAGGCTTCAATTAAGAAATGCTCTTTGAAGGTTACCTTGGG 2040
DB 3314 GTGTGCGCCCAAAAGAGAGGCTTCAATTAAGAAATGCTCTTTGAAGGTTACCTTGGG 3373
```


Db 1934 ACTGAGCTGTAAGCCGCCAGCCATTAAGTGTAACTGTGATTTGGTGTGTATTA 1993
Qy 661 CGCCTTTGTTGCTGAATGAGTTGATGTAATTAAGGAGTAAATGTTAACT 720
Db 1994 CGCCTTTGTTGCTGAATGAGTTGATGTAATTAAGGAGTAAATGTTAACT 2053
Qy 721 TGCATGGGCTGTTAAATGGGCGGGCTTAAAGGTAATTAATGCGCGTGGGCTAACT 780
Db 2054 TGCATGGGCTGTTAAATGGGCGGGCTTAAAGGTAATTAATGCGCGTGGGCTAACT 2113
Qy 781 TGTTCACATCTGACCTCACTGAGGCTTGGAGTGTGGAGATTTTTCGTGTCGCTA 840
Db 2114 TGTTCACATCTGACCTCACTGAGGCTTGGAGTGTGGAGATTTTTCGTGTCGCTA 2173
Qy 841 ACTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTGGAGTTTCTGTGGGCTCAT 900
Db 2174 ACTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTGGAGTTTCTGTGGGCTCAT 2233
Qy 901 CCCAGGCAAAGTTAGTCTGCAAGATTTAAGAGGATTTACAGTGGGAAATTTGAAAGCTTT 960
Db 2234 CCCAGGCAAAGTTAGTCTGCAAGATTTAAGAGGATTTACAGTGGGAAATTTGAAAGCTTT 2293
Qy 961 TGAATCTGTGAGGCTGTTGATCTTGGATCTGGGTCACAGGGGCTTTCCAG 1020
Db 2294 TGAATCTGTGAGGCTGTTGATCTTGGATCTGGGTCACAGGGGCTTTCCAG 2353
Qy 1021 AGAAGTCAACAGACTTTGGAATTTTTCACACCGGGGCGCTGCGCTGTGTGCTT 1080
Db 2354 AGAAGTCAACAGACTTTGGAATTTTTCACACCGGGGCGCTGCGCTGTGTGCTT 2413
Qy 1081 TTTTGAAGTTTAAAGATTAATGAGACGAAGAAACCATCTGAGCGGGGGTACCTGC 1140
Db 2414 TTTTGAAGTTTAAAGATTAATGAGACGAAGAAACCATCTGAGCGGGGGTACCTGC 2473
Qy 1141 TGGATTTTCTGAGCATCTGTGAGAGCGGTTGTGACACAGAAATGCTGTGCTAC 1200
Db 2474 TGGATTTTCTGAGCATCTGTGAGAGCGGTTGTGAGACACAGAAATGCTGTGCTAC 2533
Qy 1201 TGTGTCTTCCGTCGCGCCGCGAGTAATACCGACGAGAGCAGACGACGACGAGAG 1260
Db 2534 TGTGTCTTCCGTCGCGCCGCGAGTAATACCGACGAGAGCAGACGACGACGAGAG 2593
Qy 1261 AAGCAGGCGCGCGGCGAGACGAGACCCAGAGCCGCGCTGCACTTC 1320
Db 2594 AAGCAGGCGCGCGGCGAGACGAGACCCAGAGCCGCGCTGCACTTC 2653
Qy 1321 GGAATGATGTTGTAAGTGGCTGAACCTGATCAGAACTGAGAGGCAATTTTGAACAT 1380
Db 2654 GGAATGATGTTGTAAGTGGCTGAACCTGATCAGAACTGAGAGGCAATTTTGAACAT 2713
Qy 1381 TACAGAGATGGGCGAGGGGTTAAAGGAGGCGGGGCTTGTGAGGCTAC 1440
Db 2714 TACAGAGATGGGCGAGGGGTTAAAGGAGGCGGGGCTTGTGAGGCTAC 2773
Qy 1441 AGAGAGGCTTGAATCTTACCTTTTAACTTAATGACCAAGACCGTCTGTAGTATAC 1500
Db 2774 AGAGAGGCTTGAATCTTACCTTTTAACTTAATGACCAAGACCGTCTGTAGTATAC 2833
Qy 1501 TTTTCAACAGATCAAGATTAATGGCTAATGAGCTTATCTGCTGGGCGAGAAATTC 1560
Db 2834 TTTTCAACAGATCAAGATTAATGGCTAATGAGCTTATCTGCTGGGCGAGAAATTC 2893
Qy 1561 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATGATTTTGAAGAGCTATTAG 1620
Db 2894 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATGATTTTGAAGAGCTATTAG 2953
Qy 1621 GGTATATGCAAAAGTGGCACTTAAGCCAGATTGCAAGTACAGCAAACTTTGTAA 1680
Db 2954 GGTATATGCAAAAGTGGCACTTAAGCCAGATTGCAAGTACAGCAAACTTTGTAA 3013
Qy 1681 TATCAGGAATTTGTTGCTACATTTCTGGGACGGGGCCAGGTGAGATGATACGAGAGA 1740
Db 1740 TATCAGGAATTTGTTGCTACATTTCTGGGACGGGGCCAGGTGAGATGATACGAGAGA 1740

Db 3014 TATCAGGAATTTGTTGCTACATTTCTGGGACGGGGCCAGGTGAGATGATACGAGAGA 3073
Qy 1741 TAGGTTGCTTTAGATGATGATGATTAATATGAGCGGGGGTCTTGGCATGAGACG 1800
Db 3074 TAGGTTGCTTTAGATGATGATGATTAATATGAGCGGGGGTCTTGGCATGAGACG 3133
Qy 1801 GGTGTTATTAATGATGTAAGTTTACGCGCCCAATTTTACGGGTATGCTTCTGCG 1860
Db 3134 GGTGTTATTAATGATGTAAGTTTACGCGCCCAATTTTACGGGTATGCTTCTGCG 3193
Qy 1861 CAATACCAACCTTATCTACACGGGTGAGTCTTATAGGATTTTAACTACCTGTGGA 1920
Db 3194 CAATACCAACCTTATCTACACGGGTGAGTCTTATAGGATTTTAACTACCTGTGGA 3253
Qy 1921 AGCCTGACCGATGTAAGGTTGCGGGCTGTGCTTTTACTGCTGCTGGAAGGGGTGCT 1980
Db 3254 AGCCTGACCGATGTAAGGTTGCGGGCTGTGCTTTTACTGCTGCTGGAAGGGGTGCT 3313
Qy 1981 GTGTGCCCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAGGTGACCTTGG 2040
Db 3314 GTGTGCCCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAGGTGACCTTGG 3373
Qy 2041 TATCTGTCTGAGGTTAACTCAGGGTGGCCCAATGTGGCTCCGACTGTGTGCTT 2100
Db 3374 TATCTGTCTGAGGTTAACTCAGGGTGGCCCAATGTGGCTCCGACTGTGTGCTT 3433
Qy 2101 CATGTAGTGAAGGCGTGTGATTTAAGCATTAACATGATGTGCAACTGCGAGA 2160
Db 3434 CATGTAGTGAAGGCGTGTGATTTAAGCATTAACATGATGTGCAACTGCGAGA 3493
Qy 2161 CAGGGCTCTCAAGTGTGACCTGTGCGAGCGCACTGTCACTGCTGGAAGCACTTCA 2220
Db 3494 CAGGGCTCTCAAGTGTGACCTGTGCGAGCGCAACTGTCACTGCTGGAAGCACTTCA 3553
Qy 2221 CGTAGCCAGCACTCTGCGAAGGCTGGCCAGTGTGAGCATTAACATGACCGGCTG 2280
Db 3554 CGTAGCCAGCACTCTGCGAAGGCTGGCCAGTGTGAGCATTAACATGACCGGCTG 3613
Qy 2281 TTCCTTGTGATTTGGGTAACAGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCA 2340
Db 3614 TTCCTTGTGATTTGGGTAACAGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCA 3673
Qy 2341 CACTTAAGTATTTGCTTGAAGCCCGAGAGCATGTCCAGGTGAACCTGAAACGGGGTGTGGA 2400
Db 3674 CACTTAAGTATTTGCTTGAAGCCCGAGAGCATGTCCAGGTGAACCTGAAACGGGGTGTGGA 3733
Qy 2401 CATGACCATGAAGATCTGGAAGTGTGAGGTAGATGAGACCCGACACAGGTGACAGC 2460
Db 3734 CATGACCATGAAGATCTGGAAGTGTGAGGTAGATGAGACCCGACACAGGTGACAGC 3793
Qy 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGTGATCGAGAGA 2520
Db 3794 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGTGATCGAGAGA 3853
Qy 2521 GCTGAGGCCCATCACTTGTGTGCTGCTGCAACCCGCGCTGAGTTTGGCTTACGAGATGA 2580
Db 3854 GCTGAGGCCCATCACTTGTGTGCTGCTGCAACCCGCGCTGAGTTTGGCTTACGAGATGA 3913
Qy 2581 AGATACAGATTGAG 2594
Db 3914 AGATACAGATTGAG 3927

RESULT 6
ADB75124
ID ADB75124 standard; DNA; 7607 BP.
XX ADB75124;
AC ADB75124;
XX
XX 04-DEC-2003 (first entry)
DT
XX
XX Chromosomal insertion pGR5-2.B1.
XX

ophthalmological; antiinflammatory; antidiabetic; gene therapy;
KM adenovirus inverted terminal repeat sequence;
KM adenovirus packaging signal; photoreceptor-specific promoter;
KM adenovirus type 37; adenovirus type D serotype; adenovirus type 2;
KM adenovirus type 5; photoreceptor; tropic factor; anti-apoptotic factor;
KM rhodopsin; wild-type Stargardt disease gene; STGD; anti-cancer agent;
KM retinal degenerative disease; retinitis pigmentosa; Stargardt's disease;
KM diabetic retinopathy; retinal vascularisation; choroideraemia;
KM gyrate atrophy; macular dystrophy; retinoblastoma;
KM photoreceptor-restricted transgene expression;
KM recombinant adenovirus vector; adenovirus type 5; E1;
KM chromosomal insertion; ds.
OS Homo sapiens.
XX US2002193327-A1.
PN 19-DEC-2002.
PD 01-MAY-2001; 2001US-00847101.
PF 01-MAY-2000; 2000US-00562934.
PR (SCRI) SCRIPPS RES INST.
PA Nemerow GR, Von Seggern DJ, Friedlander M,
PI WPI; 2003-657234/62.
PS Novel nucleic acids comprising adenovirus inverted terminal repeat
PT sequences, adenovirus packaging signals operatively linked to the
PT sequences and photoreceptor-specific promoters, useful for treating
PT retinitis pigmentosa.
PS Example 5; Page 90-93; 106pp; English.
XX The invention describes an isolated nucleic acid (I) comprising
CC adenovirus inverted terminal repeat sequence, an adenovirus packaging
CC signal operatively linked to the sequence, and a photoreceptor-specific
CC promoter. A Recombinant adenovirus vector (II) comprising (I) is useful
CC for targeted delivery of a gene product to the eye of a mammal which
CC involves administering (II) that comprises heterologous DNA encoding the
CC gene product or resulting in expression of the gene product, where the
CC recombinant virus comprises a fibre protein that specifically or
CC selectively binds to receptors that are expressed on cells which are
CC photoreceptors, in the eye. The recombinant virus comprises a fibre
CC protein which is an adenovirus type 37, from an adenovirus type D
CC serotype. The fibre is a chimeric protein containing a sufficient portion
CC of the N-terminus of an adenovirus type 2 or type 5 fibre protein for
CC interaction with an adenovirus type 2 or type 5 penton, and a sufficient
CC portion of an adenovirus serotype D knob portion of the fiber for
CC selective binding to photoreceptors in the eye of a mammal. The
CC encapsulated nucleic acid comprises a photoreceptor-specific promoter
CC operatively linked to a nucleic acid comprising the therapeutic product
CC which is chosen from tropic factor, anti-apoptotic factor, gene encoding
CC a rhodopsin protein, wild-type Stargardt disease gene (STGD), an anti-
CC cancer agent and a protein that regulates expression of a photoreceptor-
CC specific gene product. The delivery is effected for treatment of an
CC ocular disease such as retinal degenerative disease e.g., retinitis
CC pigmentosa, Stargardt's disease, diabetic retinopathies, retinal
CC vascularisation, choroideraemia, gyrate atrophy or macular dystrophy or
CC retinoblastoma inherited and acquired retinal and neovascular
CC degenerative diseases. The viral nucleic acid comprises an adenovirus
CC inverted terminal repeat (ITR) sequence, and an adenovirus packaging
CC signal operatively linked to the sequence. The ITRs and packaging signal
CC are derived from an adenovirus serotype B or C, or adenovirus type 2 or
CC 5. The viral nucleic acid further comprises a photoreceptor-specific
CC promoter. (II) includes photoreceptor promoters providing a means not
CC only for specific targeting of expression in these cells, but also for
CC photoreceptor-restricted transgene expression. This sequence represents a
CC chromosomal insertion found in adenoviral plasmids of the A549 lung
CC carcinoma cell line which provide a complement of adenoviral E1 gene
CC function.

XX Sequence 7607 BP; 1838 A; 1733 C; 2001 G; 2035 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 2594; DB 10; Length 7607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCATTTTACCTCCGACGAGGCTGCTTCCACCCTGACGACGAGATGAAGAGGT 60
DB 1334 ATGCATTTTACCTCCGACGAGGCTGCTTCCACCCTGACGAGATGAAGAGGT 1393
QY GAGGAGTTTGTTAGATTAGTTAGAGACACCCCGGACAGGTTTCAGGTCTTGTCAATTAT 120
DB 1394 GAGGAGTTTGTTAGATTAGTTAGAGACACCCCGGACAGGTTTCAGGTCTTGTCAATTAT 1453
QY 121 CACCGAGAAATACGGGGGACCCAGATATTATGTTCCTTTCCTATATAGAACCTGT 180
DB 1454 CACCGAGAAATACGGGGGACCCAGATATTATGTTCCTTTCCTATATAGAACCTGT 1513
QY 181 GGCATGTTTGCTACAGTAAGTGAATTAATGGCAGTGGGTGATAGTGGGTTTG 240
DB 1514 GGCATGTTTGCTACAGTAAGTGAATTAATGGCAGTGGGTGATAGTGGGTTTG 1573
QY 241 GTGTGTAATTTTATTTTATTTTACAGTTTGTGGTTTAAAGATTTTGTATTTGTA 300
DB 1574 GTGTGTAATTTTATTTTATTTTACAGTTTGTGGTTTAAAGATTTTGTATTTGTA 1633
QY 301 TTTTATTTTAAAGGCTCTGTGTCTGAACCTGACCTGACCCCGACACACCGAGCTTG 360
DB 1634 TTTTATTTTAAAGGCTCTGTGTCTGAACCTGACCTGACCCCGACACACCGAGCTTG 1693
QY 361 CAAGACCTACCCCGGCTTAAATGAGGCTGTATCTGAGACGCCGACATCACTTG 420
DB 1694 CAAGACCTACCCCGGCTTAAATGAGGCTGTATCTGAGACGCCGACATCACTTG 1753
QY 421 TGTCTAGAGAAATGCAATAGTATAGTACGATAGCTGTGACTCCGATCTTCTAACACACTTC 480
DB 1754 TGTCTAGAGAAATGCAATAGTATAGTACGATAGCTGTGACTCCGATCTTCTAACACACTTC 1813
QY 481 CTGAGATACACCCGGGTGCTCCGCTGTGCCCCCATTTAAACAGTTGCCGTGAGATTGGTG 540
DB 1814 CTGAGATACACCCGGGTGCTCCGCTGTGCCCCCATTTAAACAGTTGCCGTGAGATTGGTG 1873
QY 541 GGCGTCGACGAGCTGTGGAATGATTCGAGACTTGCTTAAAGAGCTGGCAACTTTGG 600
DB 1874 GGCGTCGACGAGCTGTGGAATGATTCGAGACTTGCTTAAAGAGCTGGCAACTTTGG 1933
QY 601 ACTTGAGCTGTAAACGCCACGAGCCATAGGTGTAAACCTGTGATTGCTGTGTGTTAA 660
DB 1934 ACTTGAGCTGTAAACGCCACGAGCCATAGGTGTAAACCTGTGATTGCTGTGTGTTAA 1993
QY 661 CGCCTTTGTTTCTGTAATGATGATTGATGTTTAAAGGTGAGTAATGTTTAATCT 720
DB 1994 CGCCTTTGTTTCTGTAATGATGATTGATGTTTAAAGGTGAGTAATGTTTAATCT 2053
QY 721 TGCATGGGCTGTAAATGAGGCGGGGCTTAAAGGTTATATATGCGCGTGGCTAATCT 780
DB 2054 TGCATGGGCTGTAAATGAGGCGGGGCTTAAAGGTTATATATGCGCGTGGCTAATCT 2113
QY 781 TGTTCATCATCTGACCTCATGAGAGGCTTGGAGATGTTTGGAAAGATTTTCTGTGTGCGTA 840
DB 2114 TGTTCATCATCTGACCTCATGAGAGGCTTGGAGATGTTTGGAAAGATTTTCTGTGTGCGTA 2173
QY 841 ACTTCTGGAACAGAGCTCTTAACAGTACTCTTGGTTTGGAGTTTCTGTGTGGGCTCAT 900
DB 2174 ACTTCTGGAACAGAGCTCTTAACAGTACTCTTGGTTTGGAGTTTCTGTGTGGGCTCAT 2233
QY 901 CCCAGGAAAGTTAGTCTGCAAGATTTAAGAGAGATTACAAGGGGAATTTGAAGAGCTTT 960
DB 2234 CCCAGGAAAGTTAGTCTGCAAGATTTAAGAGAGATTACAAGGGGAATTTGAAGAGCTTT 2293
QY 961 TGAATCTGTGTGTGAGCTGTTTGAATCTTTGAAATCTGGGTACACAGGCGCTTTTCAAG 1020

PI Von Seggern DJ, Nemerow GR, Hallenbeck P, Stevenson S;
PI Skripchenko Y;
XX WPI, 2003-843463/78.
XX
XX Novel isolated nucleic acid molecule useful for delivering heterologous
PT gene to human or any animal, or for producing gutless adenoviral vector
PT particle.
PS
XX Example 6; SEQ ID NO 48; 157bp; English.

XX The invention describes an isolated nucleic acid molecule (I) comprising
CC an adenovirus tripartite leader (TPL) nucleotide, the TPL nucleotide
CC sequence comprising a first and second different TPL exons or first,
CC second and third same or different TPL exons, the TPL exons chosen from
CC complete or partial TPL exon 1, complete TPL exon 2 and complete TPL exon
CC 3. (i) is useful for delivering a heterologous gene to a human or any
CC animal, or for producing a gutless adenoviral vector particle. A
CC recombinant adenovirus particle (II) is useful for delivery of an
CC exogenous gene to a target cell which involves contacting the cell with
CC an amount of (II) sufficient to infect the cell. A helper-independent
CC fiberless recombinant adenovirus vector genome (III) is useful for
CC producing an adenovirus vector particle containing (III) which involves
CC providing a packaging cell line which complements replication and
CC packaging of the genome and (III) which is deficient in expressing
CC sufficient functional fiber protein to support assembly of fiber
CC containing particles and harvesting the particle produced by the cell
CC line. (III) is useful for pseudotyping recombinant viral vectors which
CC involves complementing a missing fiber gene of (III) or helper-dependent
CC fiberless recombinant adenovirus vector genome by expressing in packaging
CC cells a fiber gene from a different adenoviral serotype than the
CC recombinant adenovirus vector. (III) is also useful for specifically
CC targeting an adenovirus vector to a cell of choice. (I) is useful for
CC gene therapy. (II) is useful for treating diseases such as hereditary
CC disorder, and for reducing proliferation of tumour cells in a subject, or
CC to disrupt HIV infection. This sequence represents construct GBS-2.B1, a
CC plasmid inserted into the chromosomal DNA of lung carcinoma line A59.

XX Sequence 7607 BP; 1838 A; 1733 C; 2001 G; 2035 T; 0 U; 0 Other;

Query Match 100.0%; Score 2594; DB 10; Length 7607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGATCTTACTCGCACGAGGCTGCTTCCACCAGTACGACGAGATGAAAGGGT 60
DB 1334 ATCGATCTTACTCGCACGAGGCTGCTTCCACCAGTACGACGAGATGAAAGGGT 1393
QY 61 GAGGAGTTGTGTAGATTATGTGAGACACCCGGGACAGTTGCAAGTCTTGTCAATT 120
DB 1394 GAGGAGTTGTGTAGATTATGTGAGACACCCGGGACAGTTGCAAGTCTTGTCAATT 1453
QY 121 CACCGGAGAAATACGGGGGACCCAGATATATGTGTGCTTGTCTATATGAGACCTGT 180
DB 1454 CACCGGAGAAATACGGGGGACCCAGATATATGTGTGCTTGTCTATATGAGACCTGT 1513
QY 181 GGCATGTTGTCTACAGTAAGTAAATATATGAGGAGTGGTATGAGATGAGTGGTTTG 240
DB 1514 GGCATGTTGTCTACAGTAAGTAAATATATGAGGAGTGGTATGAGATGAGTGGTTTG 1573
QY 241 GTGTGTAATTTTTTTTAAATTTTAAAGTTTGTGTTTAAAGATTTTGTATTGTGA 300
DB 1574 GTGTGTAATTTTTTTTAAATTTTAAAGTTTGTGTTTAAAGATTTTGTATTGTGA 1633
QY 301 TTTTTTTTAAAGTCTGTGTGTCTGAACCTGAGCCTTACGCCGACAGAAACGGAGCCCTG 360
DB 1634 TTTTTTTTAAAGTCTGTGTGTCTGAACCTGAGCCTTACGCCGACAGAAACGGAGCCCTG 1693
QY 361 CAAGACCTTACCCGCGCT 420
DB 1694 CAAGACCTTACCCGCGCT 1753
QY 421 TGTCTAGAGAAATGCAATAGTAGTACGATAGCTGTGATCTCCGCTCTTCTTACACACCTTC 480

DB 1754 TGTCTAGAGAAATGCAATAGTAGTACGATAGCTGTGATCTCCGCTCTTCTTACACACCTTC 1813
QY 481 CTGAGATACACCCGGGTGTCTCCGCTGTGCCCCATTAAACCAAGTTGCCGTGAGAGTTGGTG 540
DB 1814 CTGAGATACACCCGGGTGTCTCCGCTGTGCCCCATTAAACCAAGTTGCCGTGAGAGTTGGTG 1873
QY 541 GGGGTGCCAGGCTGTGGAATGTATGAGACCTTGTCTTAAACGAGCTGGGCAACCTTTGG 600
DB 1874 GGGGTGCCAGGCTGTGGAATGTATGAGACCTTGTCTTAAACGAGCTGGGCAACCTTTGG 1933
QY 601 ACTTGAGCTGTAAACGCCCAAGCCATTAAGTGTAAACCTGTGATTCGCTGTGTGTTAA 660
DB 1934 ACTTGAGCTGTAAACGCCCAAGCCATTAAGTGTAAACCTGTGATTCGCTGTGTGTTAA 1993
QY 661 CGCCTTGTGTGTCTGATGATGATTAAGTTTAAATTAAGGCTGAGATATGTTTAACT 720
DB 1994 CGCCTTGTGTGTCTGATGATGATTAAGTTTAAATTAAGGCTGAGATATGTTTAACT 2053
QY 721 TGCATGCGCTTTTAAATGGGGCGGGCTTAAAGGTAATATAGCGCGTGGCTAATCT 780
DB 2054 TGCATGCGCTTTTAAATGGGGCGGGCTTAAAGGTAATATAGCGCGTGGCTAATCT 2113
QY 781 TGGTTACATCTGACCTCATATGAGGCTTGGAGTGTGTAAGATTTTCTGCTGTGCGTA 840
DB 2114 TGGTTACATCTGACCTCATATGAGGCTTGGAGTGTGTAAGATTTTCTGCTGTGCGTA 2173
QY 841 ACTTGCTGAACAGAGCTCTTAACAGTACCTCTTGTGTTTGAAGTTTCTGTGGGCTCAT 900
DB 2174 ACTTGCTGAACAGAGCTCTTAACAGTACCTCTTGTGTTTGAAGTTTCTGTGGGCTCAT 2233
QY 901 CCCAGGCAAGTATAGTGTGAAGATTAAAGAGATTCAAGTGGAAATTTGAAGAGCTTT 960
DB 2234 CCCAGGCAAGTATAGTGTGAAGATTAAAGAGATTCAAGTGGAAATTTGAAGAGCTTT 2293
QY 961 TGAATCTGTGAGAGCTGTTGATCTTGTGAATCTGGTCAACAGGCTTTTCCAG 1020
DB 2294 TGAATCTGTGAGAGCTGTTGATCTTGTGAATCTGGTCAACAGGCTTTTCCAG 2353
QY 1021 AGAAGTCATCAGACCTTTGATTTTCCACACCGGGCGCGCTGCGCTCTGTGCTT 1080
DB 2354 AGAAGTCATCAGACCTTTGATTTTCCACACCGGGCGCGCTGCGCTCTGTGCTT 2413
QY 1081 TTTTGAAGTTTAAAGATTAAGTAAATGAGCGGAAGAACCATCTGAGCGGGGGTACTGCG 1140
DB 2414 TTTTGAAGTTTAAAGATTAAGTAAATGAGCGGAAGAACCATCTGAGCGGGGGTACTGCG 2473
QY 1141 TGGATTTTCTGCAATGATCTGTGAGAGCGGTTGTGAGACAAAGATTCGCTGTAC 1200
DB 2474 TGGATTTTCTGCAATGATCTGTGAGAGCGGTTGTGAGACAAAGATTCGCTGTAC 2533
QY 1201 TGTGTCTTCCGTCCGCCCGCGCATTAATCCGACGAGAGACAGACAGACGAGAGG 1260
DB 2534 TGTGTCTTCCGTCCGCCCGCGCATTAATCCGACGAGAGACAGACAGACGAGAGG 2593
QY 1261 AAGCCAGCGCGCGGAGAGAGACGCCATGGAACCCGAGACCCGAGCTGAGACCTTC 1320
DB 2594 AAGCCAGCGCGCGGAGAGAGACGCCATGGAACCCGAGACCCGAGCTGAGACCTTC 2653
QY 1321 GGGATGATGTGTGTACAGTGTGCTGAACCTGTATCAGAACTGAGACGCAATTTTGAACA 1380
DB 2654 GGGATGATGTGTGTACAGTGTGCTGAACCTGTATCAGAACTGAGACGCAATTTTGAACA 2713
QY 1381 TACAGAGATGGGCGAGGCTTAAAGGGGTAAAGGAGACCGGGGGCTTGTGAGGCTTAC 1440
DB 2714 TACAGAGATGGGCGAGGCTTAAAGGGGTAAAGGAGACCGGGGGCTTGTGAGGCTTAC 2773
QY 1441 AAGAGAGGTAGAGATCTAGCTTTAGCTTATGACAGACACCGTCTGAGTGTATTAC 1500
DB 2774 AAGAGAGGTAGAGATCTAGCTTTAGCTTATGACAGACACCGTCTGAGTGTATTAC 2833
QY 1501 TTTTCAACAGATCAAGATTAATTTGCGCTAATAGCTTGAATCTGTGGCGCAAGATTAATTC 1560

Db 2834 TTTTCAACAGATCAAGATTAATTGGCTTAATGAGCTTATCTGCTGCGCGCAAGATATTC 2893
 Qy 1561 CATAGAGAGCTGACCACTTAAGCTGCTGACAGCGGAGTATTTTGAAGAGCTATTAG 1620
 Db 2894 CATAGAGAGCTGACCACTTAAGCTGCTGACAGCGGAGTATTTTGAAGAGCTATTAG 2953
 Qy 1621 GGTATATGCAAAAGGTGGACCTTAGGCGGATTTGCAAGTACAAAGTCAAGAACTTTGTAAA 1680
 Db 2954 GGTATATGCAAAAGGTGGACCTTAGGCGGATTTGCAAGTACAAAGTCAAGAACTTTGTAAA 3013
 Qy 1681 TATCAGGAATTTGTTGCTACATTTCTGGGACGCGGCGGAGGTGAGATAGATACGAGAGA 1740
 Db 3014 TATCAGGAATTTGTTGCTACATTTCTGGGACGCGGCGGAGGTGAGATAGATACGAGAGA 3073
 Qy 1741 TAGGGTGGCTTTTGAATGATGATGATTAATATATGTTGCGCGGAGGTGCTTGGCATGAGCG 1800
 Db 3074 TAGGGTGGCTTTTGAATGATGATGATTAATATATGTTGCGCGGAGGTGCTTGGCATGAGCG 3133
 Qy 1801 GGTGGTTATTAATGAATGAATGAATTTTACGGGCGCAATTTTACGGGTACGGTTTCTTGGC 1860
 Db 3134 GGTGGTTATTAATGAATGAATGAATTTTACGGGCGCAATTTTACGGGTACGGTTTCTTGGC 3193
 Qy 1861 CAATACCAACCTTATCTTACACGCGGTGAAGCTTCTATGGGTTTAACTTCTGTTGGA 1920
 Db 3194 CAATACCAACCTTATCTTACACGCGGTGAAGCTTCTATGGGTTTAACTTCTGTTGGA 3253
 Qy 1921 AGCTTGACCGATGTAAGGTTTCGCGGCTGTGCTTTTACTGCTGCTGGAAGGCGGTGT 1980
 Db 3254 AGCTTGACCGATGTAAGGTTTCGCGGCTGTGCTTTTACTGCTGCTGGAAGGCGGTGT 3313
 Qy 1981 GTGTGCGCCCAAAAGCAAGGCTTCAATTAAGAAATGCTCTTTAAAGGTGTACTTGGG 2040
 Db 3314 GTGTGCGCCCAAAAGCAAGGCTTCAATTAAGAAATGCTCTTTAAAGGTGTACTTGGG 3373
 Qy 2041 TATCTGTCTGAGGGTAACCTTCAAGGCTGCGCCCAATGTTGCGCTCCGACTGTGTGCTT 2100
 Db 3374 TATCTGTCTGAGGGTAACCTTCAAGGCTGCGCCCAATGTTGCGCTCCGACTGTGTGCTT 3433
 Qy 2101 CATGCTAATGTAAGGCTGTGCTGATTAAGCATTAAGTATGTGGCAACTGCGAGA 2160
 Db 3434 CATGCTAATGTAAGGCTGTGCTGATTAAGCATTAAGTATGTGGCAACTGCGAGA 3493
 Qy 2161 CAGGGCTCTCAATGCTGACCTGCTGGACGCGCACTGTCACTGCTGAAGACATTTCA 2220
 Db 3494 CAGGGCTCTCAATGCTGACCTGCTGGACGCGCACTGTCACTGCTGAAGACATTTCA 3553
 Qy 2221 CGTAGCAGCCACTCTGCAAGGCTGCGGAGTGTGAGCATTAAGTATGAGCCGCTG 2280
 Db 3554 CGTAGCAGCCACTCTGCAAGGCTGCGGAGTGTGAGCATTAAGTATGAGCCGCTG 3613
 Qy 2281 TTCCTTGCAATTTGGGTAAACAGAGGGGGGTTCCTTACCTTACCAATGCAATTTGAGTCA 2340
 Db 3614 TTCCTTGCAATTTGGGTAAACAGAGGGGGGTTCCTTACCTTACCAATGCAATTTGAGTCA 3673
 Qy 2341 CACTAAGATATTTCTGAGGCGGACGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTGGA 2400
 Db 3674 CACTAAGATATTTCTGAGGCGGACGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTGGA 3733
 Qy 2401 CATGACCATGAAGATCTGAAGGTGCTGAGGTAGATGAGACCGGACCGAGTGCAGACC 2460
 Db 3734 CATGACCATGAAGATCTGAAGGTGCTGAGGTAGATGAGACCGGACCGAGTGCAGACC 3793
 Qy 2461 CTGCGAGTGTGCGGTAAACATATTAGAAACAGCCTGTGATCTGAGTGAACCGAGGA 2520
 Db 3794 CTGCGAGTGTGCGGTAAACATATTAGAAACAGCCTGTGATCTGAGTGAACCGAGGA 3853
 Qy 2521 GCTGAGGCGCGATCATTTGCTGCTGCTGCAACCGGCGTGAAGTTGGCTTACCGATGA 2580
 Db 3854 GCTGAGGCGCGATCATTTGCTGCTGCTGCAACCGGCGTGAAGTTGGCTTACCGATGA 3913
 Qy 2581 AGATACGATTTAG 2594
 Db 3914 AGATACGATTTAG 3927

RESULT 8
 AAV32373
 ID AAV32373 standard; DNA; 11152 BP.
 XX
 AC AAV32373;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-SEP-1998 (first entry)
 XX
 DE Complete sequence of the pDEX/E1 plasmid.
 XX
 KW Circular; adenovirus type 5; pMAM plasmid; structural protein;
 KW complementation; fiber protein; gene therapy; HIV; tumour; AD5;
 KW Huntington's disease; Tay-Sachs disease; early gene; sickle cell disease;
 KW E1 regulatory protein; MMTV; mouse mammary tumour virus promoter; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT 1..1454
 FT /tag= a
 FT /note= "pMAM backbone"
 FT 1460..4998
 FT /tag= b
 FT /note= "AD5 E1 regulatory gene consisting of a MMTV LTR
 FT promoter at 5' end of this gene"
 FT 5005..11152
 FT /tag= c
 FT /note= "pMAM backbone"
 XX
 PN WC9813499-A2.
 XX
 PD 02-Apr-1998.
 XX
 PF 24-SEP-1997; 97MO-EP005251.
 XX
 PR 25-SEP-1996; 96US-00719806.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (SCRI) SCRIPPS RES INST.
 PI Nemerow GR, Von Seggern DJ;
 XX
 DR WPI; 1998-230709/20.
 XX
 PT Adenoviral vectors - which lack DNA encoding for structural protein or
 PT fibre protein used particularly for gene therapy.
 XX
 PS Example 1; Page 97-111; 170pp; English.
 XX
 CC The present sequence is that of a pDEX/E1 plasmid used in the method of
 CC the invention. The plasmid contains an adenovirus type 5 (AD5) E1
 CC regulatory gene controlled by a mouse mammary tumour virus (MMTV)
 CC promoter. The invention provides adenoviral vectors having deletions of
 CC all or part of various gene sequences encoding adenoviral structural
 CC proteins and/or early region proteins. Deletions in these proteins would
 CC allow a reduced risk of wild-type virus contamination and would also
 CC allow packaging of foreign DNA in such vectors for a variety of
 CC diagnostic and therapeutic applications. The adenoviral vectors having
 CC deletions in the structural and/or early gene regions are produced by
 CC cellular complementation of these adenoviral genes. Therefore, the
 CC pDEX/E1 plasmid was used as a complementation plasmid which was
 CC introduced into a host cell line where parts of the E1 gene region would
 CC be stably inserted into the host cell chromosomes. The resulting E1 gene
 CC deficient plasmid can be used as a gene delivery vector. The vectors can
 CC be used for diagnosis or gene therapy, e.g. for treating conditions
 CC characterised by hyper-proliferative cells (e.g. tumours), genetic
 CC diseases (e.g. Huntington's disease, Tay-Sachs disease, or sickle cell
 CC disease), or infections (e.g. HIV infection). They can also be used for
 CC in vitro production of biologically active proteins. (Updated on 25-MAR-
 CC 2003 to correct PI field.)

XX	Sequence	11152 BP;	2877 A;	2520 C;	2729 G;	3026 T;	0 U;	0 Other;
SQL	Query Match	100.0%;	Score 2394;	DB 2;	Length 11152;			
	Best Local Similarity	100.0%;	Pred. No. 0;					
	Matches 2594;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps 0;
QY	1	ATCGATCTTAACCTGCGACGAGCGCTGGCTTTCCACCCAGTGCACGACGAGATGAAAGGGT	60					
DB	1825	ATCGATCTTAACCTGCGACGAGCGCTGGCTTTCCACCCAGTGCACGACGAGATGAAAGGGT	1884					
QY	61	GAGAGTTTGTGTAGATTATGTGAGCACCCCGGCGACGGTTGCAGTCTTGTCTATTAT	120					
DB	1885	GAGAGTTTGTGTAGATTATGTGAGCACCCCGGCGACGGTTGCAGTCTTGTCTATTAT	1944					
QY	121	CACCGGAGAAATCGGGGACCCAGATATTATGTGTCCGTTTGCTATATAGAGACCTGT	180					
DB	1945	CACCGGAGAAATCGGGGACCCAGATATTATGTGTCCGTTTGCTATATAGAGACCTGT	2004					
QY	181	GGCATGTTTGTCTACAGTAAAGTAAATTAAGGCACTGGGTGATAGTGTGGCTTTG	240					
DB	2005	GGCATGTTTGTCTACAGTAAAGTAAATTAAGGCACTGGGTGATAGTGTGGCTTTG	2064					
QY	241	GTGTGTAATTTTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	300					
DB	2065	GTGTGTAATTTTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	2124					
QY	301	TTTTTTTAAAGTCTGTGTCTGAACCTGAGCCTGAGCCCGAGACCGAATCCGAGCCTG	360					
DB	2125	TTTTTTTAAAGTCTGTGTCTGAACCTGAGCCTGAGCCCGAGACCGAATCCGAGCCTG	2184					
QY	361	CAAGACCTACCCGCGCTCTAAATTAAGGCGCTGCTATCTGAGACGCGCCGACATCACTG	420					
DB	2185	CAAGACCTACCCGCGCTCTAAATTAAGGCGCTGCTATCTGAGACGCGCCGACATCACTG	2244					
QY	421	TGTCTAGAGATGCAATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	480					
DB	2245	TGTCTAGAGATGCAATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT	2304					
QY	481	CTGAGATACACCCGCTGTGTCTGAGCCGCTGAGCCGCTGAGCCGCTGAGCCGCTGAG	540					
DB	2305	CTGAGATACACCCGCTGTGTCTGAGCCGCTGAGCCGCTGAGCCGCTGAGCCGCTGAG	2364					
QY	541	GGCGTGGCAGGCTGTGATGTATCGAGACTTGTCTTAAAGAGCTGTGGCACTTTTGG	600					
DB	2365	GGCGTGGCAGGCTGTGATGTATCGAGACTTGTCTTAAAGAGCTGTGGCACTTTTGG	2424					
QY	601	ACTTGAGCTGTAAAGCCGCCAGGCCATTAAGGTGTAACCTGTGATTTGCTGTGTGTTAA	660					
DB	2425	ACTTGAGCTGTAAAGCCGCCAGGCCATTAAGGTGTAACCTGTGATTTGCTGTGTGTTAA	2484					
QY	661	CGCCTTTTGTGTCTGAATGAGTGTGATGATTAATTAAGGCTGAGATATGTTTAACT	720					
DB	2485	CGCCTTTTGTGTCTGAATGAGTGTGATGATTAATTAAGGCTGAGATATGTTTAACT	2544					
QY	721	TGCATGGCGGTGTTAATGGGCGGCGCTTAAAGGATATTAATGCGCGTGGCTAATCT	780					
DB	2545	TGCATGGCGGTGTTAATGGGCGGCGCTTAAAGGATATTAATGCGCGTGGCTAATCT	2604					
QY	781	TGGTTACATCTGACCTCATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGCGTA	840					
DB	2605	TGGTTACATCTGACCTCATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGCGTA	2664					
QY	841	ACTTGTGGAACAGAGCTCTTAACAGTAACCTTGTGTTTGGAGTTTCTGTGGGCTCAT	900					
DB	2665	ACTTGTGGAACAGAGCTCTTAACAGTAACCTTGTGTTTGGAGTTTCTGTGGGCTCAT	2724					
QY	901	CCGAGGCAAGTTAGTCTGACAGATTAAGAGAGATTAACAAGTGGGATTTGAAGACTTT	960					
DB	2725	CCGAGGCAAGTTAGTCTGACAGATTAAGAGAGATTAACAAGTGGGATTTGAAGACTTT	2784					
QY	961	TGAATCTGTGTGAGCTGTGATTTTGAATCTGGGTCAACAGGCGCTTTTCAAG	1020					

DB	2785	TGAATCTGTGTGAGCTGTGATTTTGAATCTGGGTCAACAGGCGCTTTTCAAG	2844					
QY	1021	AGAGGTCAATCAAGCTTTTGATTTTTTCCACACCGGGGCGGCTGTGTGCTT	1080					
DB	2845	AGAGGTCAATCAAGCTTTTGATTTTTTCCACACCGGGGCGGCTGTGTGCTT	2904					
QY	1081	TTTTAGTTTAAAGATTAATGAGAGGAAACCATCTGAGCGGGGTACTCTG	1140					
DB	2905	TTTTAGTTTAAAGATTAATGAGAGGAAACCATCTGAGCGGGGTACTCTG	2964					
QY	1141	TGATTTTCTGCAATGATCTGTGAGAGCGGTGTGAGACACAAATTCCTCTCTAC	1200					
DB	2965	TGATTTTCTGCAATGATCTGTGAGAGCGGTGTGAGACACAAATTCCTCTCTAC	3024					
QY	1201	TGTTGTCTTCCGTCGCGCGGAGTAATACCGACGAGAGACGACGACAGAGAG	1260					
DB	3025	TGTTGTCTTCCGTCGCGCGGAGTAATACCGACGAGAGACGACGACAGAGAG	3084					
QY	1261	AGCCGAGGCGGCGGCGGACGAGACAGGCCATGAAACCGAGAGCGGCTTGACCTTC	1320					
DB	3085	AGCCGAGGCGGCGGCGGACGAGACAGGCCATGAAACCGAGAGCGGCTTGACCTTC	3144					
QY	1321	GGGAATGAATGTGTGACAGGTGCTGAATCTATCCAGAACTGAGACGATTTTGACAT	1380					
DB	3145	GGGAATGAATGTGTGACAGGTGCTGAATCTATCCAGAACTGAGACGATTTTGACAT	3204					
QY	1381	TACAGAGATGGCGAGGCTTAAGGGCGTTAAAGAGAGCGGGGGCTGTGAGGCTAC	1440					
DB	3205	TACAGAGATGGCGAGGCTTAAGGGCGTTAAAGAGAGCGGGGGCTGTGAGGCTAC	3264					
QY	1441	AGAGAGGCTAGGAATCTAGCTTTTATGCTTAATGACAGACACCGTCTGATGTATTAC	1500					
DB	3265	AGAGAGGCTAGGAATCTAGCTTTTATGCTTAATGACAGACACCGTCTGATGTATTAC	3324					
QY	1501	TTTTCAACAGATCAAGATTAATTCGCTAATGAGCTTGTGCTGGCGCAAGTATTC	1560					
DB	3325	TTTTCAACAGATCAAGATTAATTCGCTAATGAGCTTGTGCTGGCGCAAGTATTC	3384					
QY	1561	CATAGACAGCTGACCTTAATCTGTGTCGACCGAGGGAGATTTTAAAGAGCTATTAG	1620					
DB	3385	CATAGACAGCTGACCTTAATCTGTGTCGACCGAGGGAGATTTTAAAGAGCTATTAG	3444					
QY	1621	GGTATATGCAAGGTGACCTTAGAGCCAGATTGCAATGACAAATCAAGCAACTTGTAA	1680					
DB	3445	GGTATATGCAAGGTGACCTTAGAGCCAGATTGCAATGACAAATCAAGCAACTTGTAA	3504					
QY	1681	TATCAGGAATTTTCTCAATTTTCTGGAAAGGGGCGGAGGTGAGATATACGAGGA	1740					
DB	3505	TATCAGGAATTTTCTCAATTTTCTGGAAAGGGGCGGAGGTGAGATATACGAGGA	3564					
QY	1741	TAGGTGGCTTTTGAATGTAGATGATTAATATGTGCGGGGGGCTTGGCATGAGCG	1800					
DB	3565	TAGGTGGCTTTTGAATGTAGATGATTAATATGTGCGGGGGGCTTGGCATGAGCG	3624					
QY	1801	GGTGTATTATTAATGATGATTAATCTGAGCCCAATTTTAAAGCGGTATCGTTTCTGGC	1860					
DB	3625	GGTGTATTATTAATGATGATTAATCTGAGCCCAATTTTAAAGCGGTATCGTTTCTGGC	3684					
QY	1861	CAATACCAACCTTATCTTACACGCTGTAAGCTTCTAGGGTTTAACTACTGTGTGA	1920					
DB	3685	CAATACCAACCTTATCTTACACGCTGTAAGCTTCTAGGGTTTAACTACTGTGTGA	3744					
QY	1921	AGCTTGACCGATGTAAGGCTTGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGTGT	1980					
DB	3745	AGCTTGACCGATGTAAGGCTTGGGGCTGTGCTTTTAACTGCTGTGGAAGGGGTGT	3804					
QY	1981	GTGTGCGCCCAAAACAGGAGCTTCAATTAAAGAAATGCTCTTTGAAAGGTATCTTGG	2040					
DB	3805	GTGTGCGCCCAAAACAGGAGCTTCAATTAAAGAAATGCTCTTTGAAAGGTATCTTGG	3864					
QY	2041	TATCTGTCTGAGGTAATCTCCAGGGTGGCCACAATGTGCTCCGACTGTGTGCTT	2100					
DB	3865	TATCTGTCTGAGGTAATCTCCAGGGTGGCCACAATGTGCTCCGACTGTGTGCTT	3924					

QY	210.	CATGCTGTGTAAGAAAACGGTGGCTGTGATTAAGACAAATAGTATGTGGCAACCTGGCAGA	2160
Db	3925	CATGCTAGTAAAGAACGTGGCTGTGATTAAGACAAATAGTATGTGGCAACCTGGCAGA	3984
QY	2161	CAGGGCTCTCAGATGTGAACCTGGCTGGAACCGGCAACTGTCACTGTGTGAAGACCAATYCA	2220
Db	3985	CAGGGCTCTCAGATGTGAACCTGGCTGGAACCGGCAACTGTCACTGTGTGAAGACCAATYCA	4044
QY	2221	CGTAGCCAGGCAACTCTGGCAAGGCTGGCCAGTGTGGAGATTAACATCTAGACCCGCTG	2280
Db	4045	CGTAGCCAGGCAACTCTGGCAAGGCTGGCCAGTGTGGAGATTAACATCTAGACCCGCTG	4104
QY	2281	TTGCTTGACATTTGGGTAAACAGAGGGGGGTGTTCCTACCTTAACCATGTCAATTTGAATCA	2340
Db	4105	TTGCTTGACATTTGGGTAAACAGAGGGGGGTGTTCCTACCTTAACCATGTCAATTTGAATCA	4164
QY	2341	CAGTAAGATATTGTGTTAGAGCCGAGAGACATGTCCAAAGTGAACCTGAACGGGGTGTTTGA	2400
Db	4165	CAGTAAGATATTGTGTTAGAGCCGAGAGACATGTCCAAAGTGAACCTGAACGGGGTGTTTGA	4224
QY	2401	CATGACCATTGAAGATCTGGAAGGTGCTGAGGTACGATAGAACCCGCAACAGGTGTCAACC	2460
Db	4225	CATGACCATTGAAGATCTGGAAGGTGCTGAGGTACGATAGAACCCGCAACAGGTGTCAACC	4284
QY	2461	CTGCGAATGTGGCGGTAAACATATTAGAAACCAAGCTGTGTATGCTGGATGTGACCGAGGA	2520
Db	4285	CTGCGAATGTGGCGGTAAACATATTAGAAACCAAGCTGTGTATGCTGGATGTGACCGAGGA	4344
QY	2521	GCTGAGGCGCGATCACTGGTGTCTGGCTGTCAACCGCGCTGATGTTGGCTCTAGACATGA	2580
Db	4345	GCTGAGGCGCGATCACTGGTGTCTGGCTGTCAACCGCGCTGATGTTGGCTCTAGACATGA	4404
QY	2581	AGATTACAGATTGAG 2594	
Db	4405	AGATTACAGATTGAG 4418	

RESULT	9
AAAS9047	
ID	AAAS9047 brandard; DNA; 11152 BP.
AC	AAAS9047;
DT	07-NOV-2000 (first entry)
XX	
DE	Nucleotide sequence of B1-expressing plasmid pDEX/B1.
KW	Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
XX	
KW	B1 gene; ss.
XX	
OS	Synthetic.
OS	Mastadenovirus.
XX	
PN	MO200042208-A1.
PD	20-JUL-2000.
XX	
PF	14-JAN-2000; 2000WO-EP000265.
XX	
PR	14-JAN-1999; 99US-0115920P.
XX	
PA	(NOVS) NOVARTIS AG.
PA	(NOVS) NOVARTIS-BEFLINDUNGEN VERW GES MBH.
EA	(SCRI) SCRIPPS RES INST.
PI	Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC;
PI	Skripchenko Y,
DR	WPI; 2000-476068/41.
PT	New nucleic acid comprising an adenovirus tripartite leader nucleotide for producing high-capacity and targeted vectors for adenovirus-based

PT	gene therapy.
XX	
P3	Example 1, Page 156-159; 212pp; English.
XX	
CC	The specification describes a nucleic acid molecule comprising an
CC	adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence
CC	comprising two different TPL exons or three same or different TPL exons.
CC	The nucleic acid is used to produce an adenovirus vector particle,
CC	deliver an exogenous gene to a target cell, pseudotype recombinant viral
CC	vectors, target an adenovirus vector to a cell, produce a modified
CC	adenovirus, deliver a heterologous gene to an animal and produce a
CC	gates adenoviral vector particle. The present sequence represents an E1
CC	-expressing plasmid, which is used for complementation of E1-gene deleted
CC	adenoviruses
XX	
SQ	Sequence 11152 BP; 2877 A; 2520 C; 2729 G; 3026 T; 0 U; 0 Other;
Query Match:	100.0%; Score 2594; DB 3; Length 11152;
Best Local Similarity	100.0%; Prd. No. 0;
Matches 2594; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

OY	ATCATCTTACCTTCCACGAGGCTGGCTTTCACCCAGTACGACGAGAAAGAGGGT	60
Db	1825 ATCATCTTACCTTCCACGAGGCTGGCTTTCACCCAGTACGACGAGAAAGAGGGT	18844
OY	GAGAGTGTGTGTAGATTATGTGTGAGACACCCCGGGACGGTTGCAGGTCTTGCATTAT	120
Db	1885 GAGAGTGTGTGTAGATTATGTGTGAGACACCCCGGGACGGTTGCAGGTCTTGCATTAT	19444
OY	121 CACCGAGAGAAATACGGGGGACCCAGATATTATGTGTTCGCTTTCCTATATGAGACCTGT	180
Db	1945 CACCGAGAGAAATACGGGGGACCCAGATATTATGTGTTCGCTTTCCTATATGAGACCTGT	20044
OY	181 GGCATGTTTGCTACAGTAAGTGAATTTATGCGGCACTGGGTGTATAGTGGTGGTTTG	240
Db	2005 GGCATGTTTGCTACAGTAAGTGAATTTATGCGGCACTGGGTGTATAGTGGTGGTTTG	20644
OY	241 GTGTGTATTTTTTTTTTAAATTTTTCACGTTTTGTGTGTTAAAGAAATTTTGTATTTGTGA	300
Db	2065 GTGTGTATTTTTTTTTTAAATTTTTCACGTTTTGTGTGTTAAAGAAATTTTGTATTTGTGA	21244
OY	301 TTTTTTTTAAAAAGTCTGTGTCTTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG	360
Db	2125 TTTTTTTTAAAAAGTCTGTGTCTTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG	21844
OY	361 CAAGACCTACCCGCGCTCTAAAAATGGGGCTGTATCTCGAGAGCGGCCAGATCACTG	420
Db	2185 CAAGACCTACCCGCGCTCTAAAAATGGGGCTGTATCTCGAGAGCGGCCAGATCACTG	22444
OY	421 TGTCTAGAGATGCATAAGTAGTAGACGATAGCTGTGACTCCGGTCTTCTTAAACAACCTC	480
Db	2245 TGTCTAGAGATGCATAAGTAGTAGACGATAGCTGTGACTCCGGTCTTCTTAAACAACCTC	23044
OY	481 CTGAGATACACCCGGTGTCCCGTGTGCCCATTTAAACAAGTTGCCGTGAGAGTTGGT	540
Db	2305 CTGAGATACACCCGGTGTCCCGTGTGCCCATTTAAACAAGTTGCCGTGAGAGTTGGT	23644
OY	541 GGGCTCGCCAGAGCTGTGTGAAATGTATTCGAGACCTTGCTTAAAGAGCTTGGGCAACTTTGG	600
Db	2365 GGGCTCGCCAGAGCTGTGTGAAATGTATTCGAGACCTTGCTTAAAGAGCTTGGGCAACTTTGG	24244
OY	601 ACTTGACCTGTAAACGCCCAGGCGCATTAAGGTGTAAACCTGTGATTCGTTGTGTGTTAA	660
Db	2425 ACTTGACCTGTAAACGCCCAGGCGCATTAAGGTGTGTAAACCTGTGATTCGTTGTGTTAA	24844
OY	661 CGCCTTGTGTGCTGAATGAGTTGATGTAAAGTTTAAATAAGGGTGAATATGTTTAACT	720
Db	2485 CGCCTTGTGTGCTGAATGAGTTGATGTAAAGTTTAAATAAGGGTGAATATGTTTAACT	25444
OY	721 TGCATGCGCGTAAATATGGGGCGGGGCTTAAAGGGTATATAATATGCGCCGCGGGCTAATC	780
Db	2545 TGCATGCGCGTAAATATGGGGCGGGGCTTAAAGGGTATATAATATGCGCCGCGGGCTAATC	26044


```

PF 30-APR-2001, 2001WO-EP004863.
XX
XX 01-MAY-2000, 2000US-00562934.
XX
XX (NOVS ) NOVARTIS AG.
XX (SCRI ) SCRIPPS RES INST.
XX (NEME) NEMEROW G R.
XX (VESE) VON SEGGERN D J.
XX (FRIE) FRIEDLANDER M.
XX
XX Nemerow GR, Von Seggern DJ, Friedlander M;
XX WPI, 2002-082846/11.
XX
XX Polynucleotide for making vectors, useful for treating ocular diseases,
XX e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat
XX sequences, packaging signal and photoreceptor-specific promoter.
XX
XX Example 1, Page 110-113, 149pp; English.
XX
XX The invention provides an isolated polynucleotide comprising adenovirus
XX (AV) inverter terminal repeat sequences (ITRS), AV packaging signal
XX operatively linked to ITRS and a photoreceptor-specific promoter. A
XX recombinant AV vector (AVV) comprising the polynucleotide is useful for
XX targeted delivery of a gene product to the eye (especially to the
XX vitreous cavity), for treating an ocular disease, e.g., retinal
XX degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic
XX retinopathy, retinal vascularizations, and retinoblastoma, of a mammal
XX preferably human. The AVV comprises a fiber protein that specifically or
XX selectively binds to receptors that are expressed on cells (preferably
XX photoreceptors in the eye). Preferably, the recombinant virus comprises a
XX fiber protein from an adenovirus type D subgroup or is a chimeric protein
XX containing a portion of the N-terminus of an adenovirus type 2 or type 5
XX penton, and the therapeutic product is a trophic factor, a wild-type
XX apoptotic factor, gene encoding a rhodopsin protein, a wild-type
XX Stargardt disease gene (STGD1), an anti-cancer agent and a protein that
XX regulates expression of a photoreceptor specific gene product. The viral
XX nucleic acid of AVV comprises ITRS and packaging signal derived from AVV
XX subgroup B or C, especially an AV type 2 or type 5. AVV is also useful
XX for targeted gene therapy, where the vector comprises an AV type 37 fiber
XX protein or its portion, and selectively transduces photoreceptors and
XX delivers a gene product encoded by AVV. The present sequence represents
XX an expression plasmid pDex/BI containing the adenovirus BI gene
XX
XX
XX Sequence 11152 BP, 2877 A; 2520 C; 2729 G; 3026 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2594; DB 6; Length 11152;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGGATTTAAGTTCACGAGAGCTGCGCTTTTCACCCAGTGAACGAGATGAAGAGGT 60
XX 1825 ATGATCTTACCTGCGACGAGAGCTGCGCTTTTCACCCAGTGAACGAGATGAAGAGGT 1884
XX
XX 61 GAGAGAGTTGTGTTAGTTATGTGAGACACCCCGGGGACGCTTTCATTTAT 120
XX 1885 GAGAGAGTTGTGTTAGTTATGTGAGACACCCCGGGGACGCTTTCATTTAT 1944
XX
XX 121 CACCGAGAGATACGGGGGACCCAGATATTATGTGCTTTCATTTATGAGAGCTGT 180
XX 1945 CACCGAGAGATACGGGGGACCCAGATATTATGTGCTTTCATTTATGAGAGCTGT 2004
XX
XX 181 GGCATGTTTGTCTACATTAAGTAAATTAATGAGCAGTGGGTATGAGTGGTGGTTTG 240
XX 2005 GGCATGTTTGTCTACATTAAGTAAATTAATGAGCAGTGGGTATGAGTGGTGGTTTG 2064
XX
XX 241 GTGGGATTTTGTCTACATTTTATTTTACAGTTTGTGTTTAAAGATTTTGTATTTGA 300
XX 2065 GTGGGATTTTGTCTACATTTTATTTTACAGTTTGTGTTTAAAGATTTTGTATTTGA 2124
XX
XX 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCGAGACCGAGAGCTGT 360
XX 2125 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCGAGACCGAGAGCTGT 2184

```

```

QY 361 CAAGACCTACCCGCGCTCTTAAAAATGCGCGCTGCTATCTTGAGACGCCGCAATACCTTG 420
DB 2185 CAAGACCTACCCGCGCTCTTAAAAATGCGCGCTGCTATCTTGAGACGCCGCAATACCTTG 2244
QY 421 TGTCTTAAGAAATGCAATATGTAATGTAACGATAGCTGTGACTCGGTCCTTTTAAACACTTC 480
DB 2245 TGTCTTAAGAAATGCAATATGTAATGTAACGATAGCTGTGACTCGGTCCTTTTAAACACTTC 2304
QY 481 CTGAGATTAACCCCGGTGATCCCGCTGTCGCCCACTTAAACAGTGGCCGTGAGAGTGGTG 540
DB 2305 CTGAGATTAACCCCGGTGATCCCGCTGTCGCCCACTTAAACAGTGGCCGTGAGAGTGGTG 2364
QY 541 GCGCTGCGCAGGCTGTGGAATGTAATGAGAGCTTGTAAAGAGCTTGAGCAACTTTTG 600
DB 2365 GCGCTGCGCAGGCTGTGGAATGTAATGAGAGCTTGTAAAGAGCTTGAGCAACTTTTG 2424
QY 601 ACTTGAGCTGTAAACGCCGCCAGGCAATAGGTGTAAACCTGTATTCCTGTGTGTTAA 660
DB 2425 ACTTGAGCTGTAAACGCCGCCAGGCAATAGGTGTAAACCTGTATTCCTGTGTGTTAA 2484
QY 661 GCGCTTGTGTTGCTGATAGTATGTAATGTAATTAAGAGGTAATGTTTAACT 720
DB 2485 GCGCTTGTGTTGCTGATAGTATGTAATGTAATTAAGAGGTAATGTTTAACT 2544
QY 721 TGCATGCGGTGTAAATGAGGCGGGGCTTAAAGGGTATATATGCGCGTGAGCTAACT 780
DB 2545 TGCATGCGGTGTAAATGAGGCGGGGCTTAAAGGGTATATATGCGCGTGAGCTAACT 2604
QY 781 TGTCTTAATCTGACCTTATGAGAGCTTGGGAGTGTGGAAGATTTTTCCTGTGCTGA 840
DB 2605 TGTCTTAATCTGACCTTATGAGAGCTTGGGAGTGTGGAAGATTTTTCCTGTGCTGA 2664
QY 841 ACTTGCTGAAACAGAGCTTAAACAGTACTCTTGTTTGAAGGTTTCTGTGGGCTCAT 900
DB 2665 ACTTGCTGAAACAGAGCTTAAACAGTACTCTTGTTTGAAGGTTTCTGTGGGCTCAT 2724
QY 901 CCCAGCGAAAGTTATGCTGCAAGATTAAGAGATTAACAATGGAATTTGAAGAGCTTT 960
DB 2725 CCCAGCGAAAGTTATGCTGCAAGATTAAGAGATTAACAATGGAATTTGAAGAGCTTT 2784
QY 961 TGAATTCCTGTGTGAGCTTGTGATTTTGAATCTGAGTCAACAGGCGCTTTCCAG 1020
DB 2785 TGAATTCCTGTGTGAGCTTGTGATTTTGAATCTGAGTCAACAGGCGCTTTCCAG 2844
QY 1021 AGAAGGTCATCAAGACTTTGATTTTTCACACCGGGGCGCGCTGCGCTGTGCTT 1080
DB 2845 AGAAGGTCATCAAGACTTTGATTTTTCACACCGGGGCGCGCTGCGCTGTGCTT 2904
QY 1081 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTAACTGTC 1140
DB 2905 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTAACTGTC 2964
QY 1141 TGAATTTTCTGGCAATGCAATCTGTGAGAGCGGTTGTGAACACAGAAATTCGCTGTAC 1200
DB 2965 TGAATTTTCTGGCAATGCAATCTGTGAGAGCGGTTGTGAACACAGAAATTCGCTGTAC 3024
QY 1201 TGTGTCTTCCGTCGCGCGCGGCGATTAATACCAAGAGAGAGAGAGAGAGAGAGAGG 1260
DB 3025 TGTGTCTTCCGTCGCGCGCGGCGGCAATTAATACCAAGAGAGAGAGAGAGAGAGAGG 3084
QY 1261 AAGCCAGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 1320
DB 3085 AAGCCAGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 3144
QY 1321 GGGAAATGAAATGTTGTAAGAGTGTGCTGAATCTGTATCCAGAACTGAAGAGCAATTTTGA 1380
DB 3145 GGGAAATGAAATGTTGTAAGAGTGTGCTGAATCTGTATCCAGAACTGAAGAGCAATTTTGA 1440
QY 1381 TACAGAGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 1440
DB 3205 TACAGAGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 3264

```


1441 AGAGGAGGCTAGGATCTAGCTTTAGCTTAATGACAGACCGCTCTGAGTATTAAC 1500
1501 TTTTCAACGATCAGAGATTAATTCGCTAAATGAGCTTTGATCTCTGGCCGAGAAATTC 1560
1561 CATAGAGGAGCTACCACTTACTGGCTGACGCGAGGGAGTATTTGAGGAGCTATTAG 1620
1621 GGTATATGCAAGAGGTGACCTTAGGCGCAGATTGCAGATCAAGATCAGCAACTTGTAAA 1680
1681 TATCAGGAATTTGTTGCTACATTTCTGGGAAACGGGGCCGAGGTGAGATTAATACGAGGA 1740
1741 TAGGGTGGCTTTTATGATGATGATGATTAATATGATGAGCGGGGTGCTTGGCATGAGCG 1800
1801 GGTGTTATTATGAATGATGAAGGTTTACTGCGCCCAATTTTACGGTACGGTTTCTGGC 1860
1861 CAATACCAACTTATCTTACACGGGTGTAAGCTTTATGAGGTTTAAACAATACCTGTGGA 1920
1921 AGCTTGACCGATGTAAGGGTTCGGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGTGCT 1980
1981 GTGTGCGCCCAAAAGCAGGGCTTCAATTAGAATGCTCTTTGAAAGGTGATCTTGGG 2040
2041 TATCTGTCTGAGGTAATCTCCAGGGTGGCCCAATGTGGCTCCGACTGCTGTTGGCTT 2100
2101 CATGCTATGAAAGCGTGGCTGTGATTAAAGCATTAACGTGATGCAACTGCGAGGA 2160
2161 CAGGCGCTCTCAGATGCTGACCTGTGCGACGGCAACTGTCACTGCTGGAAGACCAATTA 2220
2221 CGTAGCCACCACTCTCGCAAGGCTGCGCACTGTTTGAAGCATTAATCAACCGGCTG 2280
2281 TTCCTTGAATTTGGGTAACAGAGGGGGGGTTCCTTCACTTACCAATGCAATTTGAGTCA 2340
2341 CACTAAGATATTGCTTGAAGCCCGAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTTCGA 2400
2401 CATGACCATGAAAGATCTGGAAGGTGCTGAGGTGCAATGAGACCCGACCAAGGTGAGACC 2460
2461 CTTGCGAGTGTGGGTAACATATTAGGAACGAGCTGTGATCTGATGTGACCGAGGA 2520
2521 GCTGAGGCCGATCACTGTGTGCTGCGCTGACACCGCGCTGAAGTTGGCTTACGCAATGA 2580

4345 GCTGAGGCCGATCACTTGTGCTGCTGACCGCGCTGAGTTGGCTTACGATGA 4404
2581 AGATACAGATTGAG 2594
4405 AGATACAGATTGAG 4418
RESULT 11
ADB75153
ID ADB75153 standard; DNA; 11152 BP.
XX
AC ADB75153;
XX
DT 04-DEC-2003 (first entry)
XX
DE Plasmid pDEX/EI DNA sequence.
KW ophthalmological; antiinflammatory; antidiabetic; gene therapy;
KW adenovirus inverted terminal repeat sequence;
KW adenovirus packaging signal; photoreceptor-specific promoter;
KW adenovirus type 37; adenovirus type D serotype; adenovirus type 2;
KW adenovirus type 5; photoreceptor; trophic factor; anti-apoptotic factor;
KW rhodopsin; wild-type Stargardt disease gene; STBD1; anti-cancer agent;
KW retinal degenerative disease; retinitis pigmentosa; Stargardt's disease;
KW diabetic retinopathy; retinal vascularisation; choroideraemia;
KW gyrate atrophy; macular dystrophy; retinoblastoma;
KW photoreceptor-restricted transgene expression;
KW recombinant adenovirus vector; adenovirus type 5; E1a; E1b; pDEX/E1;
KW plasmid; cyclic; circular; db.
XX
XX Synthetic.
OS Human adenovirus type 6.
XX
XX US2002193327-A1.
XX
XX 19-DEC-2002.
XX
XX 01-MAY-2001; 2001US-00847101.
XX
XX 01-MAY-2000; 2000US-00562934.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Nemerow GR, Von Seggern DJ, Friedlander M;
XX
XX MPI; 2003-657234/62.
XX
XX Novel nucleic acids comprising adenovirus inverted terminal repeat
XX sequences, adenovirus packaging signals operatively linked to the
XX PT sequences and photoreceptor-specific promoters, useful for treating
XX PT retinitis pigmentosa.
XX
XX Example 1; Page 45-50; 106pp; English.
XX
XX The invention describes an isolated nucleic acid (I) comprising
XX CC adenovirus inverted terminal repeat sequence, an adenovirus packaging
XX CC signal operatively linked to the sequence, and a photoreceptor-specific
XX CC promoter. A Recombinant adenovirus vector (II) comprising (I) is useful
XX CC for targeted delivery of a gene product to the eye of a mammal which
XX CC involves administering (II) that comprises heterogeneous DNA encoding the
XX CC gene product or resulting in expression of the gene product, where the
XX CC recombinant virus comprises a fibre protein that specifically or
XX CC selectively binds to receptors that are expressed on cells which are
XX CC photoreceptors, in the eye. The recombinant virus comprises a fibre
XX CC protein which is an adenovirus type 37, from an adenovirus type D
XX CC serotype. The fibre is a chimeric protein containing a sufficient portion
XX CC of the N-terminus of an adenovirus type 2 or type 5 penton, and a sufficient
XX CC interaction with an adenovirus type 2 or type 5 penton, and a sufficient
XX CC portion of an adenovirus serotype D knob portion of the fiber for
XX CC selective binding to photoreceptors in the eye of a mammal. The
XX CC encapsulated nucleic acid comprises a photoreceptor-specific promoter
XX CC operatively linked to a nucleic acid comprising the therapeutic product

CC which is chosen from trophic factor, anti-apoptotic factor, gene encoding
CC a rhodopsin protein, wild-type Stargardt disease gene (STGB1), an anti-
CC cancer agent and a protein that regulates expression of a photoreceptor-
CC specific gene product. The delivery is effected for treatment of an
CC ocular disease such as retinal degenerative disease e.g., retinitis
CC pigmentosa, Stargardt's disease, diabetic retinopathies, retinal
CC vascularisation, choroideremia, gyrate atrophy or macular dystrophy or
CC retinoblastoma inherited and acquired retinal and neovascular
CC degenerative diseases. The viral nucleic acid comprises an adenovirus
CC inverted terminal repeat (ITR) sequences, and an adenovirus packaging
CC signal operatively linked to the sequence. The ITRs and packaging signal
CC are derived from an adenovirus serotype B or C, or adenovirus type 2 or
CC 5. The viral nucleic acid further comprises a photoreceptor-specific
CC promoter. (ii) includes photoreceptor promoters providing a means not
CC only for specific targeting of expression in these cells, but also for
CC photoreceptor-restricted transgene expression. This sequence represents
CC an adenovirus E1-expressing plasmid for complementation of an E1-gene-
CC deleted adenovirus.
CC
XX

Sequence 11152 BP; 2877 A; 2520 C; 2729 G; 3026 T; 0 U; 0 Other;

Query Match 100.0%; Score 2594; DB 10; Length 11152;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATCGATCTTACCTGCGACGAGGCTGCTTCCACCGAGTGAAGAGATGAAGGGT	60
DB	1825	ATCGATCTTACCTGCGACGAGGCTGCTTCCACCGAGTGAAGAGATGAAGGGT	1884
QY	61	GAGGATTTGTGTTAGATTATGAGAGACCCCGGGCAGGTTGACGCTTGTCTAT	120
DB	1885	GAGGATTTGTGTTAGATTATGAGAGACCCCGGGCAGGTTGACGCTTGTCTAT	1944
QY	121	CACCGAGAAATACGGGGAGCCAGATATTATGTTGCTTGTCTATATGAGACCTGT	180
DB	1945	CACCGAGAAATACGGGGAGCCAGATATTATGTTGCTTGTCTATATGAGACCTGT	2004
QY	181	GCCATGTTTGTCTACAGTAAAGTAAATATGAGGCGATGAGTGTGAGTGGTTTG	240
DB	2005	GCCATGTTTGTCTACAGTAAAGTAAATATGAGGCGATGAGTGTGAGTGGTTTG	2064
QY	241	GGTGGTAAATTTTTTTTAACTTTTACAGTTTGTGTTTAAAGAAATTTGATTTG	300
DB	2065	GGTGGTAAATTTTTTTTAACTTTTACAGTTTGTGTTTAAAGAAATTTGATTTG	2124
QY	301	TTTTTTTAAAGGCTCTGTCTGAACCTGAGCTGAGCCGAGCCAGAACCGAGCTTG	360
DB	2125	TTTTTTTAAAGGCTCTGTCTGAACCTGAGCTGAGCCGAGCCAGAACCGAGCTTG	2184
QY	361	CAGAGCTTACCCCGGCTCTTAAATGCGCGCTGCTATCTTGAAGCGCCGACATCACTG	420
DB	2185	CAGAGCTTACCCCGGCTCTTAAATGCGCGCTGCTATCTTGAAGCGCCGACATCACTG	2244
QY	421	TGTCTAGAAATGCAATAGTAGTAGGATGAGCTGAGCTCGGCTCTTACACACCTC	480
DB	2245	TGTCTAGAAATGCAATAGTAGTAGGATGAGCTGAGCTCGGCTCTTACACACCTC	2304
QY	481	CTGAGATACACCCGGTGTCCGCTGTGCCATTAAACCACTTGGCCGTGAGATTTGGT	540
DB	2305	CTGAGATACACCCGGTGTCCGCTGTGCCATTAAACCACTTGGCCGTGAGATTTGGT	2364
QY	541	GCGCTGCGCAGGCTGTGAAATGATGAGGACTTGTCTTAAAGAGCTTGGGCAACTTTGG	600
DB	2365	GCGCTGCGCAGGCTGTGAAATGATGAGGACTTGTCTTAAAGAGCTTGGGCAACTTTGG	2424
QY	601	ACTTAGAGCTTAAAGCCCGCAGGCAATAGTGAACCTGTGATTTGAGTGTGGTTAA	660
DB	2425	ACTTAGAGCTTAAAGCCCGCAGGCAATAGTGAACCTGTGATTTGAGTGTGGTTAA	2484
QY	661	GCGCTTGTGTTGCTGAATGATTTGATTAATTAAGGATGAGATTAATTTAACT	720
DB	2485	GCGCTTGTGTTGCTGAATGATTTGATTAATTAAGGATGAGATTAATTTAACT	2544

QY	721	TGCATGCGCTGTTAAATGCGCGGCGCTTAAAGGATATATATGCGCGTGGCTAATCT	780
DB	2545	TGCATGCGCTGTTAAATGCGCGGCGCTTAAAGGATATATATGCGCGTGGCTAATCT	2604
QY	781	TGATTACATCTACCTCATGAGAGGCTTGGAGGTTTGGAGATTTTTCGCTGTCGTA	840
DB	2605	TGATTACATCTACCTCATGAGAGGCTTGGAGGTTTGGAGATTTTTCGCTGTCGTA	2664
QY	841	ACTTGTGGAACAGAGCTCTTAAACATGACTCTTGTGTTGAGGTTCTGTGGGCTCAT	900
DB	2665	ACTTGTGGAACAGAGCTCTTAAACATGACTCTTGTGTTGAGGTTCTGTGGGCTCAT	2724
QY	901	CCGAGCAAAAGTTAGTCTGCAAAATTTAAGAGATTTCAAGTGGGAATTTGAAGACTTT	960
DB	2725	CCGAGCAAAAGTTAGTCTGCAAAATTTAAGAGATTTCAAGTGGGAATTTGAAGACTTT	2784
QY	961	TGAATTCCTGTGTGAGCTGTTTGAATCTTTGAATCTGGGTCACCGAGGCTTTTCAAG	1020
DB	2785	TGAATTCCTGTGTGAGCTGTTTGAATCTTTGAATCTGGGTCACCGAGGCTTTTCAAG	2844
QY	1021	AGAAGGTCAATCAAGACTTTGATTTTCCACACCGGAGCGCTGTGGCTGTGTTGCTT	1080
DB	2845	AGAAGGTCAATCAAGACTTTGATTTTCCACACCGGAGCGCTGTGGCTGTGTTGCTT	2904
QY	1081	TTTTGAGTTTATTAAGATTAATGAGCGAAGAAACCATCTGACCGGGGCTACCTGC	1140
DB	2905	TTTTGAGTTTATTAAGATTAATGAGCGAAGAAACCATCTGACCGGGGCTACCTGC	2964
QY	1141	TGGAATTTCTGCGCATGCACTGTGTGAGAGCGGTTGTGAGACAAAGATTCGCTGCTAC	1200
DB	2965	TGGAATTTCTGCGCATGCACTGTGTGAGAGCGGTTGTGAGACAAAGATTCGCTGCTAC	3024
QY	1201	TGTTGCTTCCGTCGCGCCGCGGATTAATCCGACGAGAGGACGACGACGACGAGAG	1260
DB	3025	TGTTGCTTCCGTCGCGCCGCGGATTAATCCGACGAGAGGACGACGACGACGAGAG	3084
QY	1261	MAGCAGGCGGCGGCGGCGGACGAGGAGCCATGGAACCCGAGAGCGCGCTGACCTTC	1320
DB	3085	MAGCAGGCGGCGGCGGCGGACGAGGAGCCATGGAACCCGAGAGCGCGCTGACCTTC	3144
QY	1321	GGAATGAAATGTTTGAACAGGTGCTGAACCTGTATCAAGACTGAGACGATTTTGA	1380
DB	3145	GGAATGAAATGTTTGAACAGGTGCTGAACCTGTATCAAGACTGAGACGATTTTGA	3204
QY	1381	TACAGAGATGCGGCGGCTTAAAGCGGCTTAAAGAGGACCGGCGGCTTGTGAAGCTAC	1440
DB	3205	TACAGAGATGCGGCGGCTTAAAGCGGCTTAAAGAGGACCGGCGGCTTGTGAAGCTAC	3264
QY	1441	AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACCAAGACCGTCTGATGTTAC	1500
DB	3265	AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACCAAGACCGTCTGATGTTAC	3324
QY	1501	TTTTCAACAGATCAAGGATTAATTTGCGCTAATGAGCTTATGCTGGGCGAAGATTC	1560
DB	3325	TTTTCAACAGATCAAGGATTAATTTGCGCTAATGAGCTTATGCTGGGCGAAGATTC	3384
QY	1561	CATAGAGAGCTGACCACTTACTGTGCTGACGACGAGGAGTGAATTTTGAAGAGCTATTAG	1620
DB	3385	CATAGAGAGCTGACCACTTACTGTGCTGACGACGAGGAGTGAATTTTGAAGAGCTATTAG	3444
QY	1621	GGTATATGCAAAAGGTGGCACTTAAGCCAGATTGCAAGTACCAAGATCAGCAACTTTG	1680
DB	3445	GGTATATGCAAAAGGTGGCACTTAAGCCAGATTGCAAGTACCAAGATCAGCAACTTTG	3504
QY	1681	TATCAGGAATTTGCTCATTTCTGAGGAACGGGCGCAGAGGTGAGATAGATACGAGGA	1740
DB	3505	TATCAGGAATTTGCTCATTTCTGAGGAACGGGCGCAGAGGTGAGATAGATACGAGGA	3564
QY	1741	TAGGTTGACCTTTAGATGATGATTAATATGTTGACCGGGGCTTGTGGCATGACCG	1800
DB	3565	TAGGTTGACCTTTAGATGATGATTAATATGTTGACCGGGGCTTGTGGCATGACCG	3624
QY	1801	GGTGTTATATGATATGAAGTTTACGCGCCCAATTTTACCGGATACGGTTTCTGCG	1860

```
DB 3625 GGTGGTTATTAAGATGTAAGTTTAACTGCGCCCAATTTTACGGTCTTCTGCG 3684
|||
DB 1861 CAATACCAACCTTATCTTACACGGTGAAGCTTTATGCGTTTAACTATCTGTGTGA 1920
|||
DB 3685 CAATACCAACCTTATCTTACACGGTGAAGCTTTATGCGTTTAACTATCTGTGTGA 3744
|||
DB 1921 AGCCGTGACCGGATGTAAGGTTTCCGGGCGTGTGCTTTTATCTGTGTGAAGGGGTTGT 1980
|||
DB 3745 AGCCGTGACCGGATGTAAGGTTTCCGGGCGTGTGCTTTTATCTGTGTGAAGGGGTTGT 3804
|||
DB 1981 GTGTGCGCCCAAGACGGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTAACCTTGGG 2040
|||
DB 3805 GTGTGCGCCCAAGACGGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTAACCTTGGG 3864
|||
DB 2041 TATCTGTCTGAGGGTACTCCAGGGTGGCCCAATGTGGCTCCGACTGTGTGTTGCTT 2100
|||
DB 3865 TATCTGTCTGAGGGTACTCCAGGGTGGCCCAATGTGGCTCCGACTGTGTGTTGCTT 3924
|||
DB 2101 CATGCTAGTGAAGAAAGCGTGGCTGTGATTAAGCATTAACATGTATGTGGCACTGGGAGGA 2160
|||
DB 3925 CATGCTAGTGAAGAAAGCGTGGCTGTGATTAAGCATTAACATGTATGTGGCACTGGGAGGA 3984
|||
DB 2161 CAGGGGCTCTCAGATGCTGACCTGTGCGACGGCAACTGTCACTGTGTGAAGACCAATTCA 2220
|||
DB 3985 CAGGGGCTCTCAGATGCTGACCTGTGCGACGGCAACTGTCACTGTGTGAAGACCAATTCA 4044
|||
DB 2221 CGTAGCCACCACTCTCGCAAGGCTGCGCAAGTGTGTAAGCATATCTGACCCGCTG 2280
|||
DB 4045 CGTAGCCACCACTCTCGCAAGGCTGCGCAAGTGTGTAAGCATATCTGACCCGCTG 4104
|||
DB 2281 TTCCTTGTGATTTGGGTAACAGAGAGGGGGGTTCCTCACTTCCAAATGCAATTTGAGTGA 2340
|||
DB 4105 TTCCTTGTGATTTGGGTAACAGAGAGGGGGGTTCCTCACTTCCAAATGCAATTTGAGTGA 4164
|||
DB 2341 CACTAAGATATTTGCTTGTAGCCCGAGAGCATGTTCMAAGTGAACCTGMAACGGGGTGTTTGA 2400
|||
DB 4165 CACTAAGATATTTGCTTGTAGCCCGAGAGCATGTTCMAAGTGAACCTGMAACGGGGTGTTTGA 4224
|||
DB 2401 CATGACCATGAAGATTTGGAAGGTGCTGAGAGTACGATGAGAACCCGCAACGAGTGCAGACC 2460
|||
DB 4225 CATGACCATGAAGATTTGGAAGGTGCTGAGAGTACGATGAGAACCCGCAACGAGTGCAGACC 4284
|||
DB 2461 CTGCGAGTGTGGCGGTAACATATTTAGGAACCAAGCGCTGTGAGTGTGACCGAGGA 2520
|||
DB 4285 CTGCGAGTGTGGCGGTAACATATTTAGGAACCAAGCGCTGTGAGTGTGACCGAGGA 4344
|||
DB 2521 GCTGAGGCCCGCATCACTTGTGTGCTGTGCAACCCGCGCTGAGTTTGGCTTAGCGATGA 2580
|||
DB 4345 GCTGAGGCCCGCATCACTTGTGTGCTGTGCAACCCGCGCTGAGTTTGGCTTAGCGATGA 4404
|||
DB 2581 AGATACAGATTGAG 2594
|||
DB 4405 AGATACAGATTGAG 4418
|||
RESULT 12
ADF48798 standard; DNA; 11152 BP.
ID ADF48798
AC ADF48798;
XX
XX
DT 12-FEB-2004 (first entry)
XX
XX
DE E1 expressing plasmid pEA/Hygro.
DE
DE cytolethal; anti-HIV; gene therapy; HIV gene expression inhibitor;
KM HIV gene expression activation; adenovirus tripartite leader; TPL;
KM guinea adenovirus vector particle;
KM helper-independent fiberless recombinant adenovirus vector;
KM packaging cell line; pseudotyping; adenovirus vector; gene therapy;
KM hereditary disorder; tumour; HIV infection; E1 transcription unit;
KM E1-gene-deleted adenoviruses; hygromycin resistance; ds; circular;
```

```
KM cyclic.
XX
OS Synthetic.
OS Human adenovirus type 5.
XX
XX US2003157688-A1.
XX
XX 21-AUG-2003.
XX
XX 14-JAN-2000; 2000US-00482682.
XX
XX 14-JAN-1999; 99US-0115920P.
PR 26-JUN-2000; 2000US-00423783.
XX
XX (VSEK/) VON SEGGERN D J.
PA (NEMER/) NEMEROW G R.
PA (HALL/) HALLENBECK P.
PA (STEV/) STEVENSON S.
PA (SKRI/) SKRIPCHENKO Y.
XX
XX Von Seggern DJ, Nemerow GR, Hallenbeck P, Stevenson S;
PI Skripchenko Y;
XX
XX WPI; 2003-843463/78.
XX
XX Novel isolated nucleic acid molecule useful for delivering heterologous
PT gene to human or any animal, or for producing gutless adenoviral vector
PT particle.
PT
PS Example 1; SEQ ID NO 12; 157pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I) comprising
CC an adenovirus tripartite leader (TPL) nucleotide, the TPL nucleotide
CC sequence comprising a first and second different TPL exons or first,
CC second and third, same or different TPL exons, the TPL exons chosen from
CC complete or partial TPL exon 1, complete TPL exon 2 and complete TPL exon
CC 3. (I) is useful for delivering a heterologous gene to a human or any
CC animal, or for producing a gutless adenoviral vector particle. A
CC recombinant adenovirus particle (II) is useful for delivery of an
CC exogenous gene to a target cell which involves contacting the cell with
CC an amount of (II) sufficient to infect the cell. A helper-independent
CC fiberless recombinant adenovirus vector genome (III) is useful for
CC producing an adenovirus vector particle containing (III) which involves
CC providing a packaging cell line which complements replication and
CC packaging of the genome and (III) which is deficient in expressing
CC sufficient functional fiber protein to support assembly of fiber
CC containing particles and harvesting the particle produced by the cell
CC line. (III) is useful for pseudotyping recombinant viral vectors which
CC involves complementing a missing fiber gene of (III) or helper-dependent
CC fiberless recombinant adenovirus vector genome by expressing in packaging
CC cells a fiber gene from a different adenoviral serotype than the
CC recombinant adenovirus vector. (III) is also useful for specifically
CC targeting an adenovirus vector to a cell of choice. (I) is useful for
CC gene therapy. (II) is useful for treating diseases such as hereditary
CC disorder, and for reducing proliferation of tumour cells in a subject, or
CC to disrupt HIV infection. This sequence represents the pDEX/E1 plasmid,
CC an adenovirus E1 expressing plasmid containing a hygromycin resistance
CC gene for complementation of E1-gene-deleted adenoviruses.
XX
XX SQ Sequence 11152 BP; 2877 A; 2520 C; 2729 G; 3026 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2594; DB 10; Length 11152;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
DB 1 ATCGATCTTACTGCGCACGAGGCTGGCTTCCACCCAGTACGACGAGATGAAGGGT 60
|||
DB 1825 ATCGATCTTACTGCGCACGAGGCTGGCTTCCACCCAGTACGACGAGATGAAGGGT 1884
|||
DB 61 GAGGAGTTGTGTTGATTAATGTGAGACACCCCGGCGACGAGTTGACGAGCTTGTCTTAT 120
|||
DB 1885 GAGGAGTTGTGTTGATTAATGTGAGACACCCCGGCGACGAGTTGACGAGCTTGTCTTAT 1944
|||
```

QY	121	CACCGGAGGAATATACGGGGAGACCCAGATATATATGTTGTGGCTTTGCTATATAGACACTCTGT	180
DB	1945	CACCGGAGGAATATACGGGGAGACCCAGATATATATGTTGTGGCTTTGCTATATAGACACTCTGT	2004
QY	181	GGCATGTTTGTCTACAGATAGTAAATAATATGGGCAATGGGATGATAGATGATGGGTTTG	240
DB	2005	GGCATGTTTGTCTACAGATAGTAAATAATATGGGCAATGGGATGATAGATGATGGGTTTG	2064
QY	241	GTGTGGTAATTTTTTTTTTAATTTTTTACAGTTTGTGGTTTAAAGAAATTTTGTATTTGTGA	300
DB	2065	GTGTGGTAATTTTTTTTTTAATTTTTTACAGTTTGTGGTTTAAAGAAATTTTGTATTTGTGA	2124
QY	301	TTTTTTTTTAAAGGTCCTGTGTCTGAACCTGAAGCTGAGCCGAGACCCGAGACCTG	360
DB	2125	TTTTTTTTTAAAGGTCCTGTGTCTGAACCTGAAGCCGAGACCCGAGACCTG	2184
QY	361	CAGAAGCTACCGCGGCTCTTAAATAAGGGGCGCTGATCTCTAGACGCGCGGACATACCTG	420
DB	2185	CAGAAGCTACCGCGGCTCTTAAATAAGGGGCGCTGATCTCTAGAGCGCGGACATACCTG	2244
QY	421	TGCTAGAGAAATGCATAATAGTATAGTACGATAGCTGTGACTCCGATCTCTTAAACACCTC	480
DB	2245	TGCTAGAGAAATGCATAATAGTATAGTATAGTATAGCTGTGACTCCGATCTCTTAAACACCTC	2304
QY	481	CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAACAACATTTGCCGTGAGTTGGTG	540
DB	2305	CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAACAACATTTGCCGTGAGTTGGTG	2364
QY	541	GGCGTCGCGAGGCTGTGGAAATGATATCGAGAGACTGTCTTAAGAGCTGTGGGCAACTTTGG	600
DB	2365	GGCGTCGCGAGGCTGTGGAAATGATATCGAGAGACTGTCTTAAGAGCTGTGGGCAACTTTGG	2424
QY	601	ACTTGAGCTGTAAACGCCCCAGGCCATATAGGTGTAAACCTGTGATGGGTGTGGTTAA	660
DB	2425	ACTTGAGCTGTAAACGCCCCAGGCCATATAGGTGTAAACCTGTGATGGGTGTGGTTAA	2484
QY	661	CGCCTTTGTTTGTGTAATGAGTTGATGTATAGTTTAAATTAAGGGTGAGATTAATGTTTAACT	720
DB	2485	CGCCTTTGTTTGTGTAATGAGTTGATGTATAGTTTAAATTAAGGGTGAGATTAATGTTTAACT	2544
QY	721	TGCATATGGGTGTAAATATGGGCGGGGCTTAAAGGATATATATATGCGCTGTGGCTAACT	780
DB	2545	TGCATATGGGTGTAAATATGGGCGGGGCTTAAAGGATATATATATGCGCTGTGGCTAACT	2604
QY	781	TGGTTACATCTGACCTCAATGAGAGGCTTGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA	840
DB	2605	TGGTTACATCTGACCTCAATGAGAGGCTTGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA	2664
QY	841	ACTTGCTGGAACAGAGCTCTAACAGTACTCTTGTGTTTGTGAGGTTTCTGTGCGGCTCAT	900
DB	2665	ACTTGCTGGAACAGAGCTCTAACAGTACTCTTGTGTTTGTGAGGTTTCTGTGCGGCTCAT	2724
QY	901	CCGAGGCAAAAGTTAGTCTGCAAGATTTAAGAGAGATTAACAAGTGGGAATTTGAAGACTTT	960
DB	2725	CCGAGGCAAAAGTTAGTCTGCAAGATTTAAGAGAGATTAACAAGTGGGAATTTGAAGACTTT	2784
QY	961	TGAATATCTGTGTGAGGCTGTTTGAATCTTTTGAATCTGGGTCACAGGCGCTTTTCCAG	1020
DB	2785	TGAATATCTGTGTGAGGCTGTTTGAATCTTTTGAATCTGGGTCACAGGCGCTTTTCCAG	2844
QY	1021	AGAAAGTCATCAAGACTTTTGAATTTTTTACACCGGGGCGGCTGTGCGCTGTGTTGCTT	1080
DB	2845	AGAAAGTCATCAAGACTTTTGAATTTTTTACACCGGGGCGGCTGTGCGCTGTGTTGCTT	2904
QY	1081	TTTTTGAATTTTATTAAGATTAATATGAGACGAAGAAACCATCTGAGCGGGGGGTAACTGTC	1140
DB	2905	TTTTTGAATTTTATTAAGATTAATATGAGACGAAGAAACCATCTGAGCGGGGGGTAACTGTC	2964
QY	1141	TGATATTTTCTGGCCATGATCTGTGTGAGAGGCGGTTGTGAGACACAAGAAATGCGCTGTGAC	1200
DB	2965	TGATATTTTCTGGCCATGATCTGTGTGAGAGGCGGTTGTGAGACACAAGAAATGCGCTGTGAC	3024
QY	1201	TGTTGTCTTCGTCGCGCCGCGGATATATACGAGCGAGAGACAGACAGCAGCAGAGAGG	1260

Db	3025	TTGTTGCTCTTCGTCGCGCCGGCGATTAATCCGAGCGAGGACACAGACGACGAGGAGG	3084
QY	1261	AAGCAGCGCGCGCGCGGCGAGAGACAGACCATGAAACCCGAGAGCCGGCTCGAACCTC	1320
Db	3085	AAGCCAGCGCGCGCGCGGAGAGACGACGACCCATGGAAACCGAGAGCCGGCTCGAACCTC	3144
QY	1321	GGGAATGAATGTGTACAGGTGGCTGAACTGTATCCAGAACCTGACGCAATTTTGACAAAT	1380
Db	3145	GGGAATGAATGTGTACAGGTGGCTGAACTGTATCCAGAACCTGACGCAATTTTGACAAAT	3204
QY	1381	TACAGAGATGGCGACAGGGGCTTAAGGGGGGTAAAGGGAGGGGGGGGCTTGTGAGGCTAC	1440
Db	3205	TACAGAGATGGCGAGGGGCTTAAGGGGGGTAAAGGGAGGGGGGGCTTGTGAGGCTAC	3264
QY	1441	AGAGAGGCTTGAAGATCTAGCTTTTATAGCTTAATACACGACACCGTCCCTGATGTAAATAC	1500
Db	3265	AGAGAGGCTTGAAGATCTAGCTTTTATAGCTTAATACACGACACCGTCCCTGATGTAAATAC	3324
QY	1501	TTTTCAACAGATCAAGATAATATTCGCTAATAGCTTGATCTGCTGGCGCAGAAATATTC	1560
Db	3325	TTTTCAACAGATCAAGATAATATTCGCTAATAGCTTGATCTGCTGGCGCAGAAATATTC	3384
QY	1561	CATGAGGAGCTGACCACTTACTGTGGCTGACCCAGGGGATGTATTTTGAGAGGCTAATTAG	1620
Db	3385	CATGAGGAGCTGACCACTTACTGTGGCTGACCCAGGGGATGTATTTTGAGAGGCTAATTAG	3444
QY	1621	GATATATCAAAAGGAGGCACTTAGCCGAGATTGCAAGTCAAGATTCAGCAACTGTGAAA	1680
Db	3445	GATATATCAAAAGGAGGCACTTAGCCGAGATTGCAAGTCAAGATTCAGCAACTGTGAAA	3504
QY	1681	TATCAGGAATGTGTCTACTATTTCTGGGACGGGGCGAGGTGAGATAGATACGAGGA	1740
Db	3505	TATCAGGAATGTGTCTACTATTTCTGGGAAAGGGGCGAGGTGAGATAGATACGAGGA	3564
QY	1741	TAGGGTGCCCTTTAGATGTAGCATGATTAATATGTGGCCGGGGGTGCTTGCATGACGCG	1800
Db	3565	TAGGGTGCCCTTTAGATGTAGCATGATTAATATGTGGCCGGGGGTGCTTGCATGACGCG	3624
QY	1801	GGTGGTTATTAATGATGTAGAGTTTACTGGGCCCAATTTTAAAGCGGTACGGTTTCTGGCC	1866
Db	3625	GGTGGTTATTAATGATGTAGAGTTTACTGGGCCCAATTTTAAAGCGGTACGGTTTCTGGCC	3684
QY	1861	CAATACCAACTTATCTCTACACAGGTGTAGCTTATAGGGTTTAAACAATACCTGTGTGA	1920
Db	3685	CAATACCAACTTATCTCTACACAGGTGTAGCTTATAGGGTTTAAACAATACCTGTGTGA	3744
QY	1921	AGCCTGACCGATGTAAAGGGTTCGGGGCTGTGCTTTTACTGTGCTGGAAGGGGGTGT	1980
Db	3745	AGCCTGACCGATGTAAAGGGTTCGGGGCTGTGCTTTTACTGTGCTGGAAGGGGGTGT	3804
QY	1981	GTTGTCGCCCCAAAAGCAGGGGTTCAATTAAAGAAATGCTCTTTGAAAGGTGTACTGGG	2040
Db	3805	GTTGTCGCCCCAAAAGCAGGGGTTCAATTAAAGAAATGCTCTTTGAAAGGTGTACTGGG	3864
QY	2041	TATCTGTGCTGAGGGTAACTCAGAGGTGCGCACAATGTGGCTCCGACTGTGTGTTCTT	2100
Db	3865	TATCTGTGCTGAGGGTAACTCAGAGGTGCGCACAATGTGGCTCCGACTGTGTGTTCTT	3924
QY	2101	CATCTAGTGAAGAAAGCGTGTGTGATTAAAGCATTAACATGTATGTGGCAACTGCGAGGA	2160
Db	3925	CATCTAGTGAAGAAAGCGTGTGTGATTAAAGCATTAACATGTATGTGGCAACTGCGAGGA	3984
QY	2161	CAGGGGCTCTTCAGATGTGTACCTGTGCTGGACCGGAACCTGTCAACCTGCTGAAAGACATTTCA	2220
Db	3985	CAGGGGCTCTTCAGATGTGTGTGACTGTGACCGGAACCTGTCAACCTGCTGAAAGACATTTCA	4044
QY	2221	CGTAGACGACCACTCTGCGCAAGGCTGTGGCAAGTGTTTGAGCATTAACATCTGACCCGCTG	2280
Db	4045	CGTAGACGACCACTCTGCGCAAGGCTGTGGCAAGTGTTTGAGCATTAACATCTGACCCGCTG	4104
QY	2281	TTCTTTCGATTGGGTAAACAGAGGGGGGTGTCTTACTTTACCAATGCAATTTGAGTCA	2340

Qy 721 TGCAAGGCGGTGTAATAGGGGCGGGGCTTAAAGGTAATATATGCGCCGTGGAATCT 780
Db 2345 TGCAAGGCGGTGTAATAGGGGCGGGGCTTAAAGGTAATATATGCGCCGTGGAATCT 2604
Qy 781 TGGTAACTCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGCGTA 840
Db 2605 TGGTAACTCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGCGTA 2664
Qy 841 ACTTGCTGGAACAGAGCTCTAACAGTACCTTGGTTTGGAGGTTTCTGCGGCTCAT 900
Db 2665 ACTTGCTGGAACAGAGCTCTAACAGTACCTTGGTTTGGAGGTTTCTGCGGCTCAT 2724
Qy 901 CCGAGGCAAGTGTGTCGAGAAATTAAGAGAAATTAAGTGGAAATTTGAAGCTTT 960
Db 2725 CCGAGGCAAGTGTGTCGAGAAATTAAGAGAAATTAAGTGGAAATTTGAAGCTTT 2784
Qy 961 TGAATCTGTGTGAGCTGTTGATCTTTGAACTGGGTCAACAAGGCGCTTTTCCAG 1020
Db 2785 TGAATCTGTGTGAGCTGTTGATCTTTGAACTGGGTCAACAAGGCGCTTTTCCAG 2844
Qy 1021 AGAAGTCAATCAAGACTTTGGATTTTTCACACCGGGGCGGCTGCGCTGTGCTT 1080
Db 2845 AGAAGTCAATCAAGACTTTGGATTTTTCACACCGGGGCGGCTGCGCTGTGCTT 2904
Qy 1081 TTTGAGTTTATTAAGATTAATAGAGCGAAGAAACCATCTGAGCGGGGGTAACTGC 1140
Db 2905 TTTGAGTTTATTAAGATTAATAGAGCGAAGAAACCATCTGAGCGGGGGTAACTGC 2964
Qy 1141 TGGATTTTCTGCGCATCTGTGAGAGAGGTTGTGAGACACAGAAATGACCTGTAC 1200
Db 2965 TGGATTTTCTGCGCATCTGTGAGAGAGGTTGTGAGACACAGAAATGACCTGTAC 3024
Qy 1201 TGTGTCTTCCGTCGCCCGCGGCAATATACCGACGAGAGCAGACAGACAGAGAG 1260
Db 3025 TGTGTCTTCCGTCGCCCGCGGCAATATACCGACGAGAGCAGACAGACAGAGAG 3084
Qy 1261 AAGGCAAGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 3085 AAGGCAAGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3144
Qy 1321 GGGAAATGATTTGTTTACAGGTGCTGAACTGTATCCAGAACTGAGACGATTTTGA 1380
Db 3145 GGGAAATGATTTGTTTACAGGTGCTGAACTGTATCCAGAACTGAGACGATTTTGA 3204
Qy 1381 TACAGAGATGAGGAGGAGGCTTAAAGGGGTAAAGAGAGAGAGAGAGAGAGAGAG 1440
Db 3205 TACAGAGATGAGGAGGAGGCTTAAAGGGGTAAAGAGAGAGAGAGAGAGAGAGAG 3264
Qy 1441 AGAGAGGCTAGAGAACTAGCTTTTAAATGACAGACACCGTCTGTAGTGTATTAC 1500
Db 3265 AGAGAGGCTAGAGAACTAGCTTTTAAATGACAGACACCGTCTGTAGTGTATTAC 3324
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGATCTGCTGGGCGAGAGTATTC 1560
Db 3325 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGATCTGCTGGGCGAGAGTATTC 3384
Qy 1561 CATAGACAGCTGACCACTTACTGCTGACAGCGAGGAGTATTTTGAAGAGCTATTAG 1620
Db 3385 CATAGACAGCTGACCACTTACTGCTGACAGCGAGGAGTATTTTGAAGAGCTATTAG 3444
Qy 1621 GGTATATGCAAAAGGTGCACTTAGCCAGATTGACAGTAAAGATCAAGAACTTTGTA 1680
Db 3445 GGTATATGCAAAAGGTGCACTTAGCCAGATTGACAGTAAAGATCAAGAACTTTGTA 3504
Qy 1681 TATCAGAAATTTGTTGCTACATTTCTGGGAGCGGGGCGAGGTGAGATAGATAGAGA 1740
Db 3505 TATCAGAAATTTGTTGCTACATTTCTGGGAGCGGGGCGAGGTGAGATAGATAGAGA 3564
Qy 1741 TAGGGTGGCTTTAGATGATGATGATTAATATATGTGCGCGGGGCTGCTTGACATGAC 1800
Db 3565 TAGGGTGGCTTTAGATGATGATGATTAATATATGTGCGCGGGGCTGCTTGACATGAC 3624
Qy 1801 GGTTGGTTATTAATGATGATGATTAATGATGATTTTGAAGGCTTCTGCTGCTG 1860

Db 3625 GGTGTTATTAATGATGATGATTAATGATGATTTTGAAGGCTTCTGCTGCTGCTG 3684
Qy 1861 CAATACCAACCTTATCTTACACAGGTGTAAGCTTCTATGAGTTTAAACATACCTGTGGA 1920
Db 3685 CAATACCAACCTTATCTTACACAGGTGTAAGCTTCTATGAGTTTAAACATACCTGTGGA 3744
Qy 1921 AGCTGGAACGATGTAAGGGTTGCGGGCTGTGCTTTTACTGTCTGTGGAAGGGGCTGT 1980
Db 3745 AGCTGGAACGATGTAAGGGTTGCGGGCTGTGCTTTTACTGTCTGTGGAAGGGGCTGT 3804
Qy 1981 GTGTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTGAAGGTGTAACCTTGG 2040
Db 3805 GTGTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTGAAGGTGTAACCTTGG 3864
Qy 2041 TATCTGTCTGAGGGTAACTTCAAGGTGCGCACAAATGTGCTCCGACTGTGTGCTT 2100
Db 3865 TATCTGTCTGAGGGTAACTTCAAGGTGCGCACAAATGTGCTCCGACTGTGTGCTT 3924
Qy 2101 CATGCTAGTAAAGCGTGTGATTAAGCATPAACATGTAATGTGCAACTGTGAGGA 2160
Db 3925 CATGCTAGTAAAGCGTGTGATTAAGCATPAACATGTAATGTGCAACTGTGAGGA 3984
Qy 2161 CAGGGGCTCTGAGATGCTGACCTGTGAGAGGGAACGTGACCTGTGAGAGACATTC 2220
Db 3985 CAGGGGCTCTGAGATGCTGACCTGTGAGAGGGAACGTGACCTGTGAGAGACATTC 4044
Qy 2221 CGTAGCAGACCACTCTGCAAGGCTGTGCAAGTGTGAGCATTAACATCTGACCCGCTG 2280
Db 4045 CGTAGCAGACCACTCTGCAAGGCTGTGCAAGTGTGAGCATTAACATCTGACCCGCTG 4104
Qy 2281 TTCTTGATTTGGGTAAACAGAGAGGGGCTGTCTTACTTAACATCAATGCAATTTGATCA 2340
Db 4105 TTCTTGATTTGGGTAAACAGAGAGGGGCTGTCTTACTTAACATCAATGCAATTTGATCA 4164
Qy 2341 CACTAAGATATTTGTTAGCCCGAGAGATGTCGAAGGTGAACCTGAACGGGGTGTGGA 2400
Db 4165 CACTAAGATATTTGTTAGCCCGAGAGATGTCGAAGGTGAACCTGAACGGGGTGTGGA 4224
Qy 2401 CATGACCATGAAAGATCTGGAAGGTGTGAGTGAAGATGAGATGAGATGAGATGAGATG 2460
Db 4225 CATGACCATGAAAGATCTGGAAGGTGTGAGTGAAGATGAGATGAGATGAGATGAGATG 4284
Qy 2461 CTGCGAGTGTGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGAGATGAGATG 2520
Db 4285 CTGCGAGTGTGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGAGATGAGATG 4344
Qy 2521 GCTGAGGCCGATCACTTGTGCTGCGCTGCAACCGGCGTGAAGTTGGCTTACGAGATGA 2580
Db 4345 GCTGAGGCCGATCACTTGTGCTGCGCTGCAACCGGCGTGAAGTTGGCTTACGAGATGA 4404
Qy 2581 AGATACAGATTGAG 2594
Db 4405 AGATACAGATTGAG 4418

RESULT 14
AAAS9050
ID AAAS9050 standard; DNA, 14455 BP.
XX
AC AAAS9050;
XX
DT 07-NOV-2000 (first entry)
XX
Nucleotide sequence of the EI/fiber-expressing plasmid pEI/fiber.
DE Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
KW EI gene; fiber gene; se.
XX
OS Synthetic.
XX Human adenovirus type 5.
XX
PN W0200042208-A1.

XX 20-JUL-2000.
PD 14-JAN-2000; 2000MO-EP000265.
XX 14-JAN-1999; 99US-0115920P.
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERN GRS MBH.
PA (SCRI) SCRIPPS RES INST.
XX Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC,
PI Skripchenko Y;
XX WPI; 2000-476068/41.
XX New nucleic acid comprising an adenovirus tripartite leader nucleotide
PT for producing high-capacity and targeted vectors for adenovirus-based
PT gene therapy.

PS Example 1; Page 160-164; 212pp; English.

XX The specification describes a nucleic acid molecule comprising an
CC adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence
CC comprising two different TPL exons or three same or different TPL exons.
CC The nucleic acid is used to produce an adenovirus vector particle,
CC deliver an exogenous gene to a target cell, pseudotype recombinant viral
CC vectors, target an adenovirus vector to a cell, produce a modified
CC adenovirus, deliver a heterologous gene to an animal and produce a
CC E1/fiber-expressing plasmid, which was used for complementation of
CC E1/fiber-gene deleted adenoviruses

XX Sequence 14455 BP; 3698 A; 3271 C; 3565 G; 3921 T; 0 U; 0 Other;

Query Match 100.0%; Score 2594; DB 3; Length 14455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCATCTTACTCCACGAGGCTGGCTTCCACCCAGTACGACGAGATGAAGAGGT 60
DB 1825 ATGCATCTTACTCCACGAGGCTGGCTTCCACCCAGTACGACGAGATGAAGAGGT 1884
QY 61 GAGAGTTTGTGTAGATTTATGTGAGACACCCGGGACGAGTTGCAAGTCTTGCATTAT 120
DB 1885 GAGAGTTTGTGTAGATTTATGTGAGACACCCGGGACGAGTTGCAAGTCTTGCATTAT 1944
QY 121 CACCGAGAAATACGGGGACCCAGATATTATGTGCTTGTCTATATGAGACCTGT 180
DB 1945 CACCGAGAAATACGGGGACCCAGATATTATGTGCTTGTCTATATGAGACCTGT 2004
QY 181 GCGATTTTGTCTACAGTAATGAAAAATTATGGCAGTGGGTATAGTGTGGTTTG 240
DB 2005 GCGATTTTGTCTACAGTAATGAAAAATTATGGCAGTGGGTATAGTGTGGTTTG 2064
QY 241 GTGTGTAATTTTATTTTATTTTACAGTTTGTGTGTTTAAAGATTTTGTATTTGA 300
DB 2065 GTGTGTAATTTTATTTTATTTTACAGTTTGTGTGTTTAAAGATTTTGTATTTGA 2124
QY 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCTGAGCCGAGCCAGAACCGAGCCTG 360
DB 2125 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCTGAGCCGAGCCAGAACCGAGCCTG 2184
QY 361 CAAGACCTACCCGCGCTCTAAATGAGCGCTGTCTATCTGAGACGCCGACATCACCTG 420
DB 2185 CAAGACCTACCCGCGCTCTAAATGAGCGCGCTGTCTATCTGAGACGCCGACATCACCTG 2244
QY 421 TGTCTAGAGATGCAATAGTAGTACGAGTAGCTGTGATCCGCGTCTTCTACACACCTC 480
DB 2245 TGTCTAGAGATGCAATAGTAGTACGAGTAGCTGTGATCCGCGTCTTCTACACACCTC 2304
QY 481 CTGAGATACACCCGGTGTCTCCGCTGTGCCCATTTAAACAGTTGCCGTGAGAGTTGTG 540

DB 2305 CTGAGATACACCCGGTGTCTCCGCTGTGCCCATTTAAACAGTTGCCGTGAGAGTTGTG 2364
QY 541 GCGGTGCCAGGCTGTGGAATGTATGAGGACTTGTCTTAAGAGCTGGGCAACTTTGG 600
DB 2365 GCGGTGCCAGGCTGTGGAATGTATGAGGACTTGTCTTAAGAGCTGGGCAACTTTGG 2424
QY 601 ACTTGAGCTGTAAACGCCAGGCGCATTAAGTGTAAACCTGTGATTCGTGTGTTAA 660
DB 2425 ACTTGAGCTGTAAACGCCAGGCGCATTAAGTGTAAACCTGTGATTCGTGTGTTAA 2484
QY 661 GCGCTTTGTTGCTGAATGATGTATTAATTAAAGGTGAGATTAATTTAACT 720
DB 2485 GCGCTTTGTTGCTGAATGATGTATTAATTAAAGGTGAGATTAATTTAACT 2544
QY 721 TGCAATGCGTGTAAATGAGGCGGGCTTAAAGGCTATTAATGAGCGCGGTAAATCT 780
DB 2545 TGCAATGCGTGTAAATGAGGCGGGCTTAAAGGCTATTAATGAGCGCGGTAAATCT 2604
QY 781 TGCTTACATCTGACCTCATGAGGCTTGGAGTGTGTAAGATTTTCTGTGCGTA 840
DB 2605 TGCTTACATCTGACCTCATGAGGCTTGGAGTGTGTAAGATTTTCTGTGCGTA 2664
QY 841 ACTTGTGAAACAGAGCTCTTAACATACCTTGTGTTTGGAGTCTGTGGGCTCAT 900
DB 2665 ACTTGTGAAACAGAGCTCTTAACATACCTTGTGTTTGGAGTCTGTGGGCTCAT 2724
QY 901 CCCAGGCAAGTTAGTGTGAGATTAAGAGAGATTCAAGTGGGAATTTGAAAGCTTT 960
DB 2725 CCCAGGCAAGTTAGTGTGAGATTAAGAGAGATTCAAGTGGGAATTTGAAAGCTTT 2784
QY 961 TGAATCTGTGTGAGCTGTGATTTCTTGAATCTGGGTACACAGGCGCTTTCCAG 1020
DB 2785 TGAATCTGTGTGAGCTGTGATTTCTTGAATCTGGGTACACAGGCGCTTTCCAG 2844
QY 1021 AGAAGTCAATCAAGACTTTGATTTTCCACACCGGGCGCGCTGCGCTCTGTGTT 1080
DB 2845 AGAAGTCAATCAAGACTTTGATTTTCCACACCGGGCGCGCTGCGCTCTGTGTT 2904
QY 1081 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTAACTGCG 1140
DB 2905 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTAACTGCG 2964
QY 1141 TGAATTTTCCGCGCATCTGTGAGAGCGTGTGAGACACAGAAATGCGCTGTAC 1200
DB 2965 TGAATTTTCCGCGCATCTGTGAGAGCGTGTGAGACACAGAAATGCGCTGTAC 3024
QY 1201 TGTGTCTTCCGTCCGCCCGCGCATTAATCCGACGAGACAGACAGACAGAGG 1260
DB 3025 TGTGTCTTCCGTCCGCCCGCGCATTAATCCGACGAGACAGACAGACAGAGG 3084
QY 1261 AAGCCAGGCGGCGCGCAGAGAGAGCCCATGGAACCCGAGAGCGGCTGAGACCTC 1320
DB 3085 AAGCCAGGCGGCGCGCAGAGAGAGCCCATGGAACCCGAGAGCGGCTGAGACCTC 3144
QY 1321 GGGATGAATGTTGTACAGGTGCTGAACGTATCCAGAACTGAGACGCAATTTTGACAT 1380
DB 3145 GGGATGAATGTTGTACAGGTGCTGAACGTATCCAGAACTGAGACGCAATTTTGACAT 3204
QY 1381 TACAGAGATGAGGAGGCGCTAAAGGGGCTAAAGGAGAGCGGGGGCTTGTAGGCTAC 1440
DB 3205 TACAGAGATGAGGAGGCGCTAAAGGGGCTAAAGGAGAGCGGGGGCTTGTAGGCTAC 3264
QY 1441 AGAGAGAGCTAGGAATGTAGCTTTAGCTTAATGACAGACAGCAGTCTGAGTATTAAC 1500
DB 3265 AGAGAGAGCTAGGAATGTAGCTTTAGCTTTATATACAGACAGCAGTCTGAGTATTAAC 3324
QY 1501 TTTTCAACAGATCAAGATTAATGCGCTAAATGAGCTTGTCTGCGCAGAAATATTC 1560
DB 3325 TTTTCAACAGATCAAGATTAATGCGCTAAATGAGCTTGTCTGCGCAGAAATATTC 3384
QY 1561 CATAGAGAGCTGACCACTTAATCTGCTGACAGCAGGGGATGATTTTGTAGAGGCTATTAG 1620
DB 3385 CATAGAGAGCTGACCACTTAATCTGCTGACAGCAGGGGATGATTTTGTAGAGGCTATTAG 3444

[illegible]

XX ABA94259;
XX
XX 13-MAR-2002 (first entry)
XX
XX
XX Nucleotide sequence of expression plasmid pBI/Fiber.
DE
XX
XX Adenovirus: inverter terminal repeat sequence; ITRS; ocular disease;
KW fiber protein; photoreceptor; rhodopsin; stargardt disease gene; STGD1;
KW ophthalmological; antiinflammatory; antidiabetic; cyostatic;
KW gene therapy; ss.
XX
XX Synthetic.
OS
XX WO200183729-A2.
XX
XX 08-NOV-2001.
XX
XX 30-APR-2001; 2001WO-EP004863.
XX
XX 01-MAY-2000; 2000US-00562934.
XX
XX (NOVS) NOVARTIS AG.
XX (SCRI) SCRIPPS RES INST.
XX (NEME/) NEMEROW G R.
XX (VSEB/) VON SEGGERN D J.
XX (FRIE/) FRIEDLANDER M.
XX
XX Nemerow GR, Von Seggern DJ, Friedlander M;
PI WPI: 2002-082846/11.
XX
XX Polynucleotide for making vectors, useful for treating ocular diseases,
PT e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat
PT sequences, packaging signal and photoreceptor-specific promoter.
XX
XX
XX Example 1, Page 114-118; 149pp; English.
XX
XX The invention provides an isolated polynucleotide comprising adenovirus
XX (AV) inverter terminal repeat sequences (ITRS), AV packaging signal
XX operatively linked to ITRS and a photoreceptor-specific promoter. A
XX recombinant AV vector (AAV) comprising the polynucleotide is useful for
XX targeted delivery of a gene product to the eye (especially to the
XX vitreous cavity), for treating an ocular disease, e.g., retinal
XX degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic
XX retinopathies, retinal vascularizations, and retinoblastoma, of a mammal
XX preferably human. The AAV comprises a fiber protein that specifically or
XX selectively binds to receptors that are expressed on cells (preferably
XX photoreceptors in the eye). Preferably, the recombinant virus comprise a
XX fiber protein from an adenovirus type D subgroup or is a chimeric protein
XX containing a portion of the N-terminus of an adenovirus type 2 or type 5
XX penton, and the therapeutic product is a trophic factor, an anti-
XX apoptotic factor, gene encoding a rhodopsin protein, a wild-type
XX stargardt disease gene (STGD1), an anti-cancer agent and a protein that
XX regulates expression of a photoreceptor specific gene product. The viral
XX nucleic acid of AAV comprises ITRS and packaging signal derived from AAV
XX subgroup B or C, especially an AV type 2 or type 5. AAV is also useful
XX for targeted gene therapy, where the vector comprises an AV type 37 fiber
XX protein or its portion, and selectively transduces photoreceptors and
XX delivers a gene product encoded by AAV. The present sequence represents
XX an expression plasmid pBI/Fiber containing the adenovirus EI and Fiber
XX gene
XX
XX Sequence 14455 BP; 3698 A; 3271 C; 3565 G; 3921 T; 0 U; 0 Other;

RESULT 15	
ABA94259	
ID ABA94259	standard; DNA; 14455 BP.

Query Match	100.0%	Score 2594	DB 6	Length 14455
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2594	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1	ATCATCTTACCTGCGCCAGAGCGTCTTTCCACCCAGTACCAACGAGATGAAGAAGGT	60
Db	1925	ATCATATCTTACCTGCGCCAGAGCGTCTTTCCACCCAGTACCAACGAGATGAAGAAGGT	1884

QY	61	GAGAGATTGTTGTTAGATTATATGTGAGACACCCCGGAGCA	CGGTTGCAGGTCCTTGTCATTTAT	120
Db	1885	GAGGAGTTTGTTGTTAGATTATATGTGAGACACCCCGGAGCA	CGGTTGCAGGTCCTTGTCATTTAT	1944
QY	121	CACCGAGAAATACGGGGGAGCCACAGATTTATATGTTGCTTG	CTATATAGAGACCTGT	180
Db	1945	CACCGAGAAATACGGGGGAGCCACAGATTTATATGTTGCTTG	CTATATAGAGACCTGT	2004
QY	181	GGCATGTTTGTCTACAGTAAGTGAAAATTAATGGCAGTGGGT	TGATAGAGTGGGTTTG	240
Db	2005	GGCATGTTTGTCTACAGTAAGTGAAAATTAATGGCAGTGGGT	TGATAGAGTGGGTTTG	2064
QY	241	GTTGTGTAATTTTTTTTTTAATTTTTTACAGTTTGTGTGTTAA	GAATTTTTGTATTTGTGA	300
Db	2065	GTTGTGTAATTTTTTTTTTAATTTTTTACAGTTTGTGTGTTAA	GAATTTTTGTATTTGTGA	2124
QY	301	TTTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCGAGCCGAG	CCAGAACCGGAGCCTG	360
Db	2125	TTTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCGAGCCGAG	CCAGAACCGGAGCCTG	2184
QY	361	CAGAAGCTTACCGCGCGCTCTAAATATGCGCGCTGATCTGA	GACGCGGCATACACTG	420
Db	2185	CAGAAGCTTACCGCGCGCTCTAAATATGCGCGCTGATCTGA	GACGCGGCATACACTG	2244
QY	421	TGTCATAGAGATGCATATGTAGTACGATAGCTGTGACTCCG	GGTCCTTTACACACTTC	480
Db	2245	TGTCATAGAGATGCATATGTAGTACGATAGCTGTGACTCCG	GGTCCTTTACACACTTC	2304
QY	481	CTGAAATACACCCGGATGGTCCCGCTGTGCCCCCATTAAC	CAAGTTGCGGTGAGATGGTG	540
Db	2305	CTGAAATACACCCGGATGGTCCCGCTGTGCCCCCATTAAC	CAAGTTGCGGTGAGATGGTG	2364
QY	541	GCGCTGCGCAGGCTGTGATATGTATCGAGACTTGCTTTAC	AGAGCTTGCGCAACTTTGG	600
Db	2365	GCGCTGCGCAGGCTGTGATATGTATCGAGACTTGCTTTAC	AGAGCTTGCGCAACTTTGG	2424
QY	601	ACTTAGCTGTAAACGCCCGAGGCCATAAAGTTTAACTGTAT	TGCTGTGTGGTTTAA	660
Db	2425	ACTTAGCTGTAAACGCCCGAGGCCCATAAAGTTTAACTGTAT	TGCTGTGTGGTTTAA	2484
QY	661	GCGCTTGTGTTGCTGAATAGTGTATGTATTAATTAAGGTG	AGATATATGTTTAACT	720
Db	2485	GCGCTTGTGTTGCTGAATAGTGTATGTATTAATTAAGGTG	AGATATATGTTTAACT	2544
QY	721	TGCATGCGGTGTTTAATGCGGCGGGGCTTAAAGGTTATAT	GATATGCGCGGCTTAACT	780
Db	2545	TGCATGCGGTGTTTAATGCGGCGGGGCTTAAAGGTTATAT	GATATGCGCGGCTTAACT	2604
QY	781	TGGTTACATCTGACCTCATATGAGGCTTGAGAGTGTGTAAG	ATTTTTTCTGCTGTGCGTA	840
Db	2605	TGGTTACATCTGACCTCATATGAGGCTTGAGAGTGTGTAAG	ATTTTTTCTGCTGTGCGTA	2664
QY	841	ACTTGTCTGGAACAGAGCTCTAACATCTACTCTTGTTTGT	GAGTTTCTGTGGGGCTCAT	900
Db	2665	ACTTGTCTGGAACAGAGCTCTAACATCTACTCTTGTTTGT	GAGTTTCTGTGGGGCTCAT	2724
QY	901	CCCAGGCAAAAGTTAATCTGCAGAAATTAAGAGAGATTA	CAAGTGGGAATTTGAAGCTTT	960
Db	2725	CCCAGGCAAAAGTTAATCTGCAGAAATTAAGAGAGATTA	CAAGTGGGAATTTGAAGCTTT	2784
QY	961	TGAAAATCCGTGTGAGAGCTGTTTGAATCTTGAGATCTGG	AGTCAACGAGCGCTTTTCAAG	1020
Db	2785	TGAAAATCCGTGTGAGAGCTGTTTGAATCTTGAGATCTGG	AGTCAACGAGCGCTTTTCAAG	2844
QY	1021	AGAAAGTCATCAAGACTTTTGAATTTTTTCAACACCGGG	CGCGCTGTGCTGTGTGCTT	1080
Db	2845	AGAAAGTCATCAAGACTTTTGAATTTTTTCAACACCGGG	CGCGCTGTGCTGTGTGCTT	2904
QY	1081	TTTTAGTTTTTAAAGATAAATGAGAGGAAACCATCTGAG	CGGGGGGTATACCTGC	1140
Db	2905	TTTTAGTTTTTAAAGATAAATGAGAGGAAACCATCTGAG	CGGGGGGTATACCTGC	2964
QY	1141	TGGATTTTTCTGGCATGCACTGTGTGAGAGCGGTTGTGAG	ACACAAAGATCGCTGTCTAC	1200

Db	2965	TGATATTTCTGGCCATGCATCTGTGGAGAGCGGGTGTGAACAACAAATTCGGCTGTAC	3024
Qy	1201	TGTTGTTCTTCGTCCTCCGCCCGCATTAATACCGACGAGAGACAGCAGCAGCAGAGG	1260
Db	3025	TGTTGTTCTTCGTCCTCCGCCCGCATTAATACCGACGAGAGACAGCAGCAGCAGAGG	3084
Qy	1261	AAGCCAGGCGCGCGCGCGCAGAGACAGAGCCCATGAAACCCGAGAGCCGCGCTGACCTC	1320
Db	3085	AAGCCAGGCGCGCGCGCGCAGAGACAGAGCCCATGAAACCCGAGAGCCGCGCTGACCTC	3144
Qy	1321	GGGAATGAATGTTGTAACGGTGGCTGAACGTATCCAGAACTGAGACGCAATTTTGAACAT	1380
Db	3145	GGGAATGAATGTTGTAACGGTGGCTGAACGTATCCAGAACTGAGAGCAATTTTGAACAT	3204
Qy	1381	TACAGAGATAGGCGCAGGGGCTAAAGGGGGTTAAAGAGGAGCGGGGGCTTGTGAGGCTAC	1440
Db	3205	TACAGAGATAGGCGCAGGGGCTAAAGGGGGTTAAAGAGGAGCGGGGGCTTGTGAGGCTAC	3264
Qy	1441	AGAGAGGCTTAGAGAACTTACCTTTTACCTTAAATGACCAACACCGTCTGAGTATTAAC	1500
Db	3265	AGAGAGGCTTAGAGAACTTACCTTTTACCTTAAATGACCAACACCGTCTGAGTATTAAC	3324
Qy	1501	TTTTTCAACATATCAAGGATTAATGGCGTATATGAGCTTGAATCTGCGCGAGAAATTC	1560
Db	3325	TTTTTCAACATATCAAGGATTAATGGCGTATATGAGCTTGAATCTGCGCGAGAAATTC	3384
Qy	1561	CATAGAGCAGCTGCACACTTACTGCTGCAGACGAGGGATGATTTTTCAGAGGCTATTAAG	1620
Db	3385	CATAGAGCAGCTGCACACTTACTGCTGCAGACGAGGGATGATTTTTCAGAGGCTATTAAG	3444
Qy	1621	GGTATATGCAAAAGGTGGCACTTAAGCCAGATTGCAGATCAAGATCAGCAACTTGTAA	1680
Db	3445	GGTATATGCAAAAGGTGGCACTTAAGCCAGATTGCAGATCAAGATCAGCAACTTGTAA	3504
Qy	1681	TATCAGGAATTTGTTGCTACATTTCTGGGAAACGGGGCCGAGTGGAGATATATCCGAGGA	1740
Db	3505	TATCAGGAATTTGTTGCTACATTTCTGGGAAACGGGGCCGAGTGGAGATATATCCGAGGA	3564
Qy	1741	TAGGGTGGGCTTTTATGATGTAGCATGATTAATATATGTGGCCGGGGGCTTGGCATGACGG	1800
Db	3565	TAGGGTGGGCTTTTATGATGTAGCATGATTAATATATGTGGCCGGGGGCTTGGCATGACGG	3624
Qy	1801	GGTGGTATTAATGATGTAAAGTTTACTGGCCCCCAATTTTACGGGTACGGTTCCTGCGC	1860
Db	3625	GGTGGTATTAATGATGTAAAGTTTACTGGCCCCCAATTTTACGGGTACGGTTCCTGCGC	3684
Qy	1861	CAATACCAACCTTATCTTAACAGGTGTAACTTCTATAGGTTTAAACAATACCTGTGTGA	1920
Db	3685	CAATACCAACCTTATCTTAACAGGTGTAACTTCTATAGGTTTAAACAATACCTGTGTGA	3744
Qy	1921	AGCTGTGACGATGTAAAGGTTGCGGGCTGTGCTTTTACTGCTGTGAAAGGGGGGTGT	1980
Db	3745	AGCTGTGACGATGTAAAGGTTGCGGGCTGTGCTTTTACTGCTGTGAAAGGGGGGTGT	3804
Qy	1981	GTTGTGCCCCCAAAAGCAGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGG	2040
Db	3805	GTTGTGCCCCCAAAAGCAGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTACCTTGGG	3864
Qy	2041	TATCTCTGTGAGGGTAACTTCCAGGGTGGCCACAAATGTGGCTTCCGACTGTGTGCTT	2100
Db	3865	TATCTCTGTGAGGGTAACTTCCAGGGTGGCCACAAATGTGGCTTCCGACTGTGTGCTT	3924
Qy	2101	CATCTATGTGAAAAGCGTGGCTGTGATTAAGCAATTAATGTTATGTGGCAATGCGAGGA	2160
Db	3925	CATCTATGTGAAAAGCGTGGCTGTGATTAAGCAATTAATGTTATGTGGCAATGCGAGGA	3984
Qy	2161	CAGGGCTCTTCAGATGCTGACTGTGCGACGGCAACTGTCACTGCTGTGAAGACCATTCA	2220
Db	3985	CAGGGCTCTTCAGATGCTGACTGTGCGACGGCAACTGTCACTGCTGTGAAGACCATTCA	4044
Qy	2221	CGTACCAACCACTCTTCGCAAGGCTTGGCAATGTTTGAACATTAATTAACCTGACCGCTG	2280

```
Db 4045 CGTAGCCAGCCACTCTGCGAAGGCGTGGCCAGTGTGAGCATTAACATCTGACCCGCTG 4104
QY 2281 TTCCTTGCAATTTGGGTAAACAGAGAGGGGGTGTTCCTACCTTAACCAATGCAATTGAGTCA 2340
Db 4105 TTCCTTGCAATTTGGGTAAACAGAGAGGGGGTGTTCCTACCTTAACCAATGCAATTGAGTCA 4164
QY 2341 CACTAAGATATTGCTTGAGCCCGAGAGAGATGTCCAAAGTGAACCTGAAACGGGGTGTGGA 2400
Db 4165 CACTAAGATATTGCTTGAGCCCGAGAGAGATGTCCAAAGTGAACCTGAAACGGGGTGTGGA 4224
QY 2401 CATGACCATGAAGATCTGGAAGTGTCTGAGGTAGATGAGACCCGACACAGGTGAGACC 2460
Db 4225 CATGACCATGAAGATCTGGAAGTGTCTGAGGTAGATGAGACCCGACACAGGTGAGACC 4284
QY 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGGA 2520
Db 4285 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGGA 4344
QY 2521 GCTGAGGCCCGATGACTTGGTGTGCTGGCCTGCAACCCGCGCTGAGTTGGCTCTAGCGATGA 2580
Db 4345 GCTGAGGCCCGATGACTTGGTGTGCTGGCCTGCAACCCGCGCTGAGTTGGCTCTAGCGATGA 4404
QY 2581 AGATACAGATTGAG 2594
Db 4405 AGATACAGATTGAG 4418
```

Search completed: October 30, 2005, 19:47:44
Job time : 1364 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 18:47:03 ; Search time 8240 Seconds
(without alignments)
11982.854 Million cell updates/sec

Title: US-10-790-562-33_COPY_459_3052

Sequence: 1 atgcatcttactctgcacga.....cgatgaagatcacagatgag 2594

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_est4:
5: gb_est5:
6: gb_est6:
7: gb_est7:
8: gb_est8:
9: gb_est9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	615.8	23.7	648	4	BM655780 170006873
2	592.8	22.9	625	7	CK624194 m18c08.y
3	476	18.4	726	6	CA307899 UI-H-FT1-
4	476	18.4	750	6	CD370352 UI-H-FT1-
5	476	18.4	766	6	CD742927 UI-H-FT1-
6	469.4	18.1	743	6	CA306892 UI-H-FT1-
7	460	17.9	602	6	CD370856 UI-H-FT1-
8	335.4	12.9	337	2	BM591710 170006873
9	249.8	9.6	347	2	BF915148 IL3-UT011
10	224.2	8.6	321	2	BF914577 IL3-UT011
11	223.8	8.6	321	2	BF915126 IL3-UT011
12	223.4	8.6	741	6	CD366021 UI-H-FT1-
13	173.6	6.7	667	6	CD742922 UI-H-FT1-
14	167	6.4	661	6	CD365243 UI-H-FT1-
15	162	6.2	173	4	BM600614 170006870
16	131.8	5.1	229	2	BF915892 IL3-UT011
17	100.8	3.9	198	2	BF914321 IL3-UT011
18	50.2	1.9	884	9	CNS006060 Drosophila
19	48.6	1.9	942	9	CNS006061 Drosophila
20	48.2	1.9	940	9	CNS03004 Drosophila
21	47.6	1.8	1101	9	CNS00100 Drosophila
22	47.2	1.8	732	7	CK305430 SB02029B1
23	46.8	1.8	1220	6	CD504965 CDA71-A08
24	46.6	1.8	1032	9	CL505993 SAIL_759_

25	46.4	1.8	519	4	BM439574 pgtc.pko
26	46.2	1.8	1101	9	CNS017M2 Drosophila
27	46	1.8	670	9	CNS04K72 Tetraodon
28	46	1.8	807	9	CNS0128R Drosophila
29	46	1.8	1511	9	CG753350 P048-2-F0
30	45.8	1.8	662	5	BU303489 AGENCOURT
31	45.8	1.8	891	5	BU842949 AGENCOURT
32	45.6	1.8	556	9	CR336545 Medicago
33	45.6	1.8	1003	9	CNS017UQ Drosophila
34	45.6	1.8	1042	9	CNS0039B Drosophila
35	45.4	1.8	922	9	CNS0073W Drosophila
36	45.4	1.8	1101	9	CNS00UT2 Drosophila
37	45	1.7	861	9	CNS0075A Drosophila
38	45	1.7	1098	9	CNS015EM Drosophila
39	45	1.7	1101	9	CNS000D1 Drosophila
40	44.8	1.7	564	9	CNS00711 Drosophila
41	44.8	1.7	768	7	CK306519 SB02034A2
42	44.6	1.7	455	2	BE208710 Mus muscu
43	44.6	1.7	713	9	AGS06778 Mus muscu
44	44.6	1.7	939	9	CNS00CNG Drosophila
45	44.6	1.7	1101	9	CNS0100X Drosophila

ALIGNMENTS

RESULT 1
BM655780 648 bp mRNA linear EST 26-FEB-2002
LOCUS 17000687386917 A.Gam.ad.cdna1 Anopheles gambiae cdna clone
DEFINITION 19600449669374 5', mRNA sequence.

ACCESSION BM655780
VERSION BM655780.1 GI:18955291

KEYWORDS Anopheles gambiae (African malaria mosquito)
SOURCE Anopheles gambiae

ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.

REFERENCE 1 (bases 1 to 648)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)

TITLE JOURNAL
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404531151
Fax: 2404534580

FEATURES
source
1. 648
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
/clone="19600449669374"
/dev_stage="Adult"
/lab_host="DHI10B"
/clone_lib="A.Gam.ad.cdna1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

ORIGIN

Query Match 23.7%; Score 615.8; DB 4; Length 648;
Best Local Similarity 97.7%; Pred. No. 8.7e-156;

	Matches	636,	Conservative	0;	Mismatches	12;	Indels	3;	Gaps	1;
QY	668	GTTCGCTGAATGAGATTGATGTAAAGTTTAAATAAAGGTGAGATTAATGTTTAACTTGCATG	727							
Db	1	GTTCGCTGAATGAGATTGATGTAAAGTTTAAATAAAGGTGAGATTAATGTTTAACTTGCATG	60							
QY	728	CGTGTAAATGAGGCGGGGCTTAAAGGATATAATAATGCGCGTGGGCTAAATCTTGATAC	787							
Db	61	CGTGTAAATGAGGCGGGGCTTAAAGGATATAATAATGCGCGTGGGCTAAATCTTGATAC	120							
QY	788	ATCTGACCTCATTGAGAGCTTGGAGTGTGGTGGAAAGATTTTTCTGCTGTGCGTAATTGCT	847							
Db	121	ATCTGACCTCATTGAGAGCTTGGAGTGTGGTGGAAAGATTTTTCTGCTGTGCGTAATTGCT	180							
QY	848	GGAAACAGAGCTCTTAACAGTACTCTCTGGTTTTGAGAGTTTCTGAGGGGCTATCCAGAG	907							
Db	181	GGAAACAGAGCTCTTAACAGTACTCTCTGGTTTTGAGAGTTTCTGAGGGGCTATCCAGAG	240							
QY	908	AAAGTTAGTCTGCAGAAATTAAAGAGATTAACAAGTGGAAATTGGAAGACTTTTGAAATC	967							
Db	241	AAAGTTAGTCTGCAGAAATTAAAGAGATTAACAAGTGGAAATTGGAAGACTTTTGAAATC	300							
QY	968	CTGTGCTGAGCTGTGTTGATTTCTTTGAATCTGGGTACCAAGGCGCTTTTCCAAGAGAAAGT	1022							
Db	301	CTGTGCTGAGCTGTGTTGATTTCTTTGAATCTGGGTACCAAGGCGCTTTTCCAAGAGAAAGT	360							
QY	1028	CATCAAGACTTTGGATTTTTTCCACACCGGGGCGCGCTCGCTGTGTGCTTTTGTAG	1087							
Db	361	CATCAAGACTTTGGATTTTTTCCACACCGGGGCGCGCTCGCTGTGTGCTTTTGTAG	420							
QY	1088	TTTTTAATAAGATTAATGAGCGGAAGAAACCCATCTGAGCGGGGGGATACCTGTGAGATT	1147							
Db	421	TTTTTAATAAGATTAATGAGCGGAAGAAACCCATCTGAGCGGGGGGATACCTGTGAGATT	480							
QY	1148	TCTGGGCAATGATCTGTGAGAGCGGTTGTAGACACAAGAAATGCGCTGACTAGTTGTC	1207							
Db	481	TCTGGGCAATGATCTGTGAGAGCGGTTGTAGACACAAGAAATGCGCTGACTAGTTGTC	540							
QY	1208	TTCCGTCGCCCGCGATTAATACCGACGAGAGAGCAGCAGCAGCAGCAGCAGAGAGAACCG	1267							
Db	541	TTCCGTCGCCCGCGATTAATACCGACGAGAGAGCAGCAGCAGCAGCAGCAGAGAGAACCG	597							
QY	1268	GCGGCGGCGGAGAGAGCAGAGCCCATATGAAATCCGAGAGCCCGGCTTGAAGCC	1318							
Db	598	GCGGCGGCGGAGAGAGCAGAGCCCATATGAAATCCGAGAGCCCGGCTTGAAGCC	648							

[illegible]

FEATURES		location/Qualifiers
SOURCE		1. 625
		/organism="Mus musculus"
		/mol_type="mRNA"
		/strain="C57Bl6J"
		/db_xref="taxon:10090"
		/clone="m18c08"
		/sex="Male"
		/tissue_type="RPE/choroid"
		/dev_stage="Adult"
		/lab_host="EMDH10B"
		/clone_lib="Mouse RPE/choroid, unamplified: ml/mj"
		/note="Organ: Eye; Vector: pSPoriT; 64ug total RNA was extracted from 200 adult male mouse RPE/choroids. A directionally cloned cDNA library in the pSPoriT vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGATGATGCTGATGATGCGAGCGCGCC(1)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
ORIGIN		
Query Match	22.9%;	Score 592.8; DB 7; Length 625;
Best Local Similarity	97.6%;	Pred. No. 1.6e-149;
Matches 613;	Conservative 0;	Mismatches 12; Indels 3; Gaps 1;
QY	669	TTTGCCTGAATGAGCTGTGAATGTTAAATTAAGGGTCAGATTAATGTTAACTTGCAATGC 728
DB	1	TTTGCCTGAATGAGCTGTGAATGTTAAATTAAGGGTCAGATTAATGTTAACTTGCAATGC 60
QY	729	GTTGTTAAATGGGGGGGGCTTAAAGGGTATATATATGCGCGCTTAATCTTGTTATCA 788
DB	61	GTTGTTAAATGGGGGGGGCTTAAAGGGTATATATATGCGCGCTTAATCTTGTTATCA 120
QY	789	TCTGACCTCATGAGAGCGTTGGAGTGTGTTGAAAGATTTTCTGCTGTGGCTAACTTGCTG 848
DB	121	TCTGACCTCATGAGAGCGTTGGAGTGTGTTGAAAGATTTTCTGCTGTGGCTAACTTGCTG 180
QY	849	GAAACAGAGCTTAAACAGTACTCTTGCTTTTGGAGTTTCTGTGGGCTCATCCACAGCA 908
DB	181	GAAACAGAGCTTAAACAGTACTCTTGCTTTTGGAGTTTCTGTGGGCTCTCTCCACAGCA 240
QY	909	AAGTTAGCTGCAGAAATTAAGAGGATTTACAGGCGGAATTTGAAGACTTTTGAATTC 968
DB	241	AAGTTAGCTGCAGAAATTAAGAGGATTTACAGTGGGAATTTGAAGACTTTTGAATTC 300
QY	969	TGTGTGAGCTGTTTGAATCTTTGAATCTTGAGTCAACAGCGCTTTTCAAGAGAGGTC 1028
DB	301	TGTGTGAGCTGTTTGAATCTTTGAATCTTGAGTCAACAGCGCTTTTCAAGAGAGGTC 360
QY	1029	ATCAAGACTTTTGATTTTTCACACACCGGGGCGGCTGCTGCTGTGCTTTTGAAT 1088
DB	361	ATCAAGACTTTTGATTTTTCACACACCGGGGCGGCTGCTGCTGTGCTTTTGAAT 420
QY	1089	TTTATAAGATTAATAGAGGAAAGAACCATCTGACCGGGGGGTACCTGCTGGATTTT 1148
DB	421	TTTATAAGATTAATAGAGGAAAGAACCATCTGACCGGGGGGTACCTGCTGGATTTT 480
QY	1149	CTGGCCATGATCTGTGGAGAGCGGTGTGAGACACAAAGATGCGCTGTAATGTTGCT 1208
DB	481	CTGGCCATGATCTGTGGAGAGCGGTGTGAGACACAAAGATGCGCTGTAATGTTGCT 540
QY	1209	TCCGTCGCGCCCGGCGATTAATCCGACGGAGAGCAGACGACGACGAGAGAAACCAAG 1268
DB	541	TCCGTCGCGCCCGGCGATTAATCCGACGGAGG---AGCAACGACGAGAGAGCAAGCGG 597
QY	1269	CGGGGGGCGACGAGACGAGCCCATGGA 1296

Db 598 CGCGGGCGCAGAGCAGAGCCCATGGA 625

RESULT 3
LOCUS CA307899 726 bp mRNA linear EST 05-AUG-2004DEFINITION UT-H-FT1-b1b-a-23-0-UI.61 NCI CGAP_FTI Homo sapiens cDNA clone
UT-H-FT1-b1b-a-23-0-UI 3', mRNA sequence.ACCESSION CA307899
VERSION CA307899.1 GI:24470953

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 726)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapdb-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@iowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-21, >AT rich#low_complexity (matched complement)
Seq primer: M13 FORWARD
PolyA-yes.FEATURES
source

1..726
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UT-H-FT1-b1b-a-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FTI"
/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP_FTI is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; LPS 100 ng/ml; 24
hours; LPS 100 ng/ml; 3 hours; PMA 10 ng/ml; 24 hours;
PMA 10 ng/ml; 3 hours; PMA 10 ng/ml; 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ads CMV egfp), moi 500, 3 hours; Adenoviral vector
(Ads CMV egfp), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pRTT3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCATGCGG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.

ORIGIN

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCGCATGCGGQuery Match 18.4%; Score 476; DB 6; Length 726;
Best Local Similarity 83.8%; Pred. No. 9.7e-118;
Matches 602; Conservative 0; Mismatches 0; Indels 116; Gaps 1;

1 ATGCATCTTACTCTCCAGCAGAGCTGGCTTCCACCCAGTAGACGAGAGATGAAGAGGT 60
618 ATGCATCTTACTCTCCAGCAGAGCTGGCTTCCACCCAGTAGACGAGAGATGAAGAGGT 559
61 GAGGAGTTGTGTAGATTATGTGAGACCCCGGACCGGTTGCAAGCTTGTCAATTAT 120
558 GAGGAGTTGTGTAGATTATGTGAGACCCCGGACCGGTTGCAAGCTTGTCAATTAT 499
121 CACCGAGGAATAGGGGGACCCAGATATTATGTGCTTGTGCTATATAGACCTGT 180
498 CACCGAGGAATAGGGGGACCCAGATATTATGTGCTTGTGCTATATAGACCTGT 439
181 GGCACTTTTGTCTACAGTAAGTAAATTAATGGCAGTGGGTATAGATGGTGGTTTG 240
438 GGCACTTTTGTCTACAGTAAGTAAATTAATGGCAGTGGGTATAGATGGTGGTTTG 423
241 GTGTGTAAATTTTTTTTAAATTTTACAGTTTGTGTTAAAGATTTTGTATGTA 300
422 ----- 423
301 TTTTAAAGATCTGTGCTGTAACCTGAGCCTGAGCCCGACGAGACCGAGCCTG 360
422 -----GTCCTGTGCTGAACTGAGCCTGAGCCCGACGAGACCGAGCCTG 375
361 CAAGACCTACCCGCGCTCTTAAATGAGCGCTGTATCTGAGAGCGCCGACATACCTG 420
374 CAAGACCTACCCGCGCTCTTAAATGAGCGCTGTATCTGAGAGCGCCGACATACCTG 315
421 TGTCTAGAAATGCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 480
314 TGTCTAGAAATGCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 255
481 CTGAGATACACCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
254 CTGAGATACACCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 195
541 GGCGTCCGACGAGCTGTGAAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 600
194 GGCGTCCGACGAGCTGTGAAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 135
601 ACTGAGCTGTAAGCGCCGACGATGAGTGAATGTAATGTAATGTAATGTAATGTA 660
134 ACTGAGCTGTAAGCGCCGACGATGAGTGAATGTAATGTAATGTAATGTAATGTA 75
661 CGCTTTGTTTCTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 718
74 CGCTTTGTTTCTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 17

RESULT 4
LOCUS CD370352 750 bp mRNA linear EST 05-AUG-2004
DEFINITION UT-H-FT1-bkb-j-17-0-UI.61 NCI CGAP_FTI Homo sapiens cDNA clone
UT-H-FT1-bkb-j-17-0-UI 3', mRNA sequence.

ACCESSION CD370352
VERSION CD370352.1 GI:31154442
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 750)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Stransberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Humminghake, U of I
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

SOURCE

Location/Qualifiers
1..750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bkb-j-17-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FTI"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ads CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ads CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCATGCCG. The tissue was provided by Dr. Gary W. Humminghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCATGCCG"

ORIGIN

Query Match 18.4%; Score 476; DB 6; Length 750;
Best Local Similarity 83.8%; Pred. No. 9.8e-11;
Matches 602; Conservative 0; Mismatches 0; Indels 116; Gaps 1;

QY 1 ATCGATCTTACCTGACGAGGCTGGCTTCCACCCAGTACGACGAGGAGGAGGCT 60
Db 618 ATCGATCTTACCTGACGAGGCTGGCTTCCACCCAGTACGACGAGGAGGAGGCT 559
QY 61 GAGGAGTTTGTGATGATGATGAGACACCCGGGACGAGTTCAGGCTTGTCTATAT 120
Db 558 GAGGAGTTTGTGATGATGATGAGACACCCGGGACGAGTTCAGGCTTGTCTATAT 499
QY 121 CACCGAGAGATACGGGGAGCCAGATATATATGTTGCTTATATAGACCTGT 180
Db 498 CACCGAGAGATACGGGGAGCCAGATATATATGTTGCTTATATAGACCTGT 439

QY 181 GGCATGTTTGTGCTACAGTAAGTAAATTAATGGCAGTGGGTGATAGAGTGTGGGTTTG 240
Db 438 GGCATGTTTGTGCTACAGTAAGTAAATTAATGGCAGTGGGTGATAGAGTGTGGGTTTG 423
QY 241 GTGTGTAATATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTGA 300
Db 422 ----- 423
QY 301 TTTTAAAAAGTTCCTGTGCTGTAACCTGAGCTTGAGCCCGAGACCGAGGACTTG 360
Db 422 -----GTCCGTGTCTGAACTGAGCTTGAGCCCGAGACCGAGGACTTG 375
QY 361 CAAGACCTACCCGCGCCTTAAATGAGGCGCTGTATCTGAGAGCGCCGACATCACCTG 420
Db 374 CAAGACCTACCCGCGCCTTAAATGAGGCGCTGTATCTGAGAGCGCCGACATCACCTG 315
QY 421 TGCTAGAGATGCAATAGTATGATAGATAGCTGTGATCTCGCTCTTAAACACCTC 480
Db 314 TGCTAGAGATGCAATAGTATGATAGATAGCTGTGATCTCGCTCTTAAACACCTC 255
QY 481 CTGAGATACACCCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 254 CTGAGATACACCCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 195
QY 541 GGCCTGCGCAGGCTGTGGAATGTATGAGGACTTGAACGAGCTTGAGCACTTGG 600
Db 194 GGCCTGCGCAGGCTGTGGAATGTATGAGGACTTGAACGAGCTTGAGCACTTGG 135
QY 601 ACTGAGCTGTAAAGCCGCCAGCCATAGGTGTAACTGTGATTCGTGTGTGTAA 660
Db 134 ACTGAGCTGTAAAGCCGCCAGCCATAGGTGTAACTGTGATTCGTGTGTGTAA 75
QY 661 GGCCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 718
Db 74 GGCCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 17

RESULT 5

CD742927/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

FEATURES

SOURCE

Location/Qualifiers
1..766
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

clone="UI-H-PT11-Bkx-m-09-0-UY"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_idb="NCI CGAP P11"
/clone_Organ="Lung; Vector: pT713-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP P11 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella mol 10, 3 hours; Klebsiella mol 10, 24 hours; Staph aureus mol 10, 3 hours; Staph aureus mol 10, 24 hours; Adenoviral vector (Ad5 CMV EGFP), mol 500, 3 hours; Adenoviral vector (Ad5 CMV EGFP), mol 500, 24 hours; wt adenovirus mol 500, 3 hours; wt adenovirus mol 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lemon and Soares, Genomes Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT713-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATCCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-PT11
TAG_SEQ=GGCCATCCCG"

Query Match	18.4%	Score 476;	DB 6;	Length 766;
Best Local Similarity	83.8%	Pred. No. 9.9e-118;		
Matches 602;	Conservative 0;	Indels 116;	Gaps 1;	
1 ATGATCTTACCTGCGCACGAGCGCTGCTTCCACCCAGTGCAGCAGAGATGAAGAGCGT	60			
618 ATGATCTTACCTGCGCACGAGCGCTGCTTCCACCCAGTGCAGCAGAGATGAAGAGCGT	559			
61 GAGAGTTTGTGTAAATTATGTGAGACACCCGGGCACGGTTGCAGGCTTGTCAATTAT	120			
558 GAGAGTTTGTGTAAATTATGTGAGACACCCGGGCACGGTTGCAGGCTTGTCAATTAT	499			
121 CACCGGAGAAATACGGGGGACCCGATATTATGTGCTTGCTTCTATATAGAGACCTGT	180			
498 CACCGGAGAAATACGGGGGACCCGATATTATGTGCTTGCTTCTATATAGAGACCTGT	439			
181 GGCATGTTGTCTACAGTAAGTGAATAATTATGGCAGTGGGTGATAGAGTGTGGTTTG	240			
438 GGCATGTTGTCTACA-----	423			
241 GTGTGGTAATTTTTTTTTTAATTTTACAGTTTGTGTGTTAAAGAAATTTGTATGTGA	300			
422 -----	423			
301 TTTTTTAAAGGCTCTGTGTCTGAACCTGAGCCGAGCCAGAACCGAGGCTGT	360			
422 -----GTCTGTGTCTGAACCTGAGCCGAGCCAGAACCGAGGCTGT	375			
361 CAAGACCTACCGCGGCTCTPAAATGCGGCTGTATCTGTAGACGCCCGACATCACTGT	420			
374 CAAGACCTACCGCGGCTCTPAAATGCGGCTGTATCTGTAGACGCCCGACATCACTGT	315			

OY	421	TGTCAGAGATGCAATGTAGTACGAGTACTGGAATCCGGTCTCTTAACAACCTC	480
Db	314	TGTCAGAGATGCAATGTAGTACGAGTACTGGAATCCGGTCTCTTAACAACCTC	255
OY	481	CTGAGATACACCCGGTGTCCCGCTGTGCCCATTAACAAGATTGCCGTGAGATTGGT	540
Db	254	CTGAGATACACCCGGTGTCCCGCTGTGCCCATTAACAAGATTGCCGTGAGATTGGT	195
OY	541	GGCGTCGCACAGCTGTGGATGTATTCAGAGACTTGCTTAACGAGCTGAGCAACTTTGG	600
Db	194	GGCGTCGCACAGCTGTGGATGTATTCAGAGACTTGCTTAACGAGCTGAGCAACTTTGG	135
OY	601	ACTTGAGCTGAACGCCACAGCCCATTAAGTGTAAACCTGTGATTGCGTGTGGTTAA	660
Db	134	ACTTGAGCTGAACGCCACAGCCCATTAAGTGTAAACCTGTGATTGCGTGTGGTTAA	75
OY	661	GGCCTTTGTTGCAGATAGTATGTAATGAATTTAAATAAAGGTGAGATTAATGTTAA	718
Db	74	GCCCTTTTGTCTGATAGATTATGTATGTTATTAATAAGGTGAGATTAATGTTAA	17

RESULT 6	CA306892/c	CA306892	743 bp	mRNA	linear	EST 05-AUG-2004
LOCUS						
DEFINITION		UI-H-FT1-bhc-p-24-0-UI.s1 NCI_CGAP_FTI Homo sapiens cDNA clone				
		UI-H-FT1-bhc-p-24-0-UI 3', mRNA sequence.				
ACCESSION		CA306892				
VERSION		CA306892.1	GI:2446946			
KEYWORDS		EST.				
SOURCE		Homo sapiens				
ORGANISM		Homo sapiens (human)				
		Homo sapiens				

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 743)	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
PolyA=yes.

FEATURES	Location/Qualifiers
source	1. .743

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="U1-H-F11-bht-p-24-0-U1"
/clisue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1id="NCI CGAP F11"
/notes="Organ: Lung; Vector: PT73-Pac (Pharmacia) with a
modified polylinker; Site 1: Scór I; Site 2: Not I;
NCI CGAP F11 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral

```

vector (Ad5 CMV eGFP), moi 500, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hummingake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 18.1%; Score 469.4; DB 6; Length 743;
Best Local Similarity 83.7%; Pred. No. 6;le-116;
Matches 607; Conservative 0; Mismatches 1; Indels 117; Gaps 2;

```
QY      1 ATCGATCTTACCTGCGACGAGCTGCTTCCACCCAGGACGACGAGATGAGAGGAT 60
DB      1 ATCGATCTTACCTGCGACGAGCTGCTTCCACCCAGGACGACGAGATGAGAGGAT 60
QY      625 ATCGATCTTACCTGCGACGAGCTGCTTCCACCCAGGACGACGAGATGAGAGGAT 566
DB      625 ATCGATCTTACCTGCGACGAGCTGCTTCCACCCAGGACGACGAGATGAGAGGAT 566
QY      61 GAGGAGTTTGTTAGATTATGTGAGACACCCCGGCGACGTTTGACGTTTGTCTATTAT 120
DB      61 GAGGAGTTTGTTAGATTATGTGAGACACCCCGGCGACGTTTGACGTTTGTCTATTAT 120
QY      565 GAGGAGTTTGTTAGATTATGTGAGACACCCCGGCGACGTTTGACGTTTGTCTATTAT 506
DB      565 GAGGAGTTTGTTAGATTATGTGAGACACCCCGGCGACGTTTGACGTTTGTCTATTAT 506
QY      121 CACCGGAGAGATACCGGGGACCCAGATATTATGTGTGCTTTGCTATATAGACCTGT 180
DB      121 CACCGGAGAGATACCGGGGACCCAGATATTATGTGTGCTTTGCTATATAGACCTGT 180
QY      505 CACCGGAGAGATACCGGGGACCCAGATATTATGTGTGCTTTGCTATATAGACCTGT 446
DB      505 CACCGGAGAGATACCGGGGACCCAGATATTATGTGTGCTTTGCTATATAGACCTGT 446
QY      181 GGCATGTTTGTCTACAGTAAGTAAGAAATTATGGGAGTGGGTATAGATGAGTGGGTTTG 240
DB      181 GGCATGTTTGTCTACAGTAAGTAAGAAATTATGGGAGTGGGTATAGATGAGTGGGTTTG 240
QY      445 GGCATGTTTGTCTACAGTAAGTAAGAAATTATGGGAGTGGGTATAGATGAGTGGGTTTG 430
DB      445 GGCATGTTTGTCTACAGTAAGTAAGAAATTATGGGAGTGGGTATAGATGAGTGGGTTTG 430
QY      241 GTGTGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 300
DB      241 GTGTGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 300
QY      429 -----GTCTGTGTCTGTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 430
DB      429 -----GTCTGTGTCTGTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 430
QY      301 TTTTAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 360
DB      301 TTTTAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 360
QY      429 -----GTCTGTGTCTGTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 382
DB      429 -----GTCTGTGTCTGTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 382
QY      361 CAAGACCTACCCGCGCTCTAAATATGGGCGCTGATCTTGAAGACGCGGACATCACTG 420
DB      361 CAAGACCTACCCGCGCTCTAAATATGGGCGCTGATCTTGAAGACGCGGACATCACTG 420
QY      381 CAAAGCTTACCCGCGCTCTAAATATGGGCGCTGATCTTGAAGACGCGGACATCACTG 322
DB      381 CAAAGCTTACCCGCGCTCTAAATATGGGCGCTGATCTTGAAGACGCGGACATCACTG 322
QY      421 TGTCTAGAGAAATGCAATAGTAGTAGAGTAGCTGAGTCCGCTCTTCTAACAACCTC 480
DB      421 TGTCTAGAGAAATGCAATAGTAGTAGAGTAGCTGAGTCCGCTCTTCTAACAACCTC 480
QY      321 TGTCTAGAGAAATGCAATAGTAGTAGAGTAGCTGAGTCCGCTCTTCTAACAACCTC 262
DB      321 TGTCTAGAGAAATGCAATAGTAGTAGAGTAGCTGAGTCCGCTCTTCTAACAACCTC 262
QY      481 CTGAGATACACCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB      481 CTGAGATACACCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY      261 CTGAGATACACCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 202
DB      261 CTGAGATACACCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 202
QY      541 GGCCTGCGCAGGCTGTGAATGTATCGAGACTTCTTAAACGAGCCTGAGCAACCTTTGG 600
DB      541 GGCCTGCGCAGGCTGTGAATGTATCGAGACTTCTTAAACGAGCCTGAGCAACCTTTGG 600
QY      201 GGCCTGCGCAGGCTGTGAATGTATCGAGACTTCTTAAACGAGCCTGAGCAACCTTTGG 142
DB      201 GGCCTGCGCAGGCTGTGAATGTATCGAGACTTCTTAAACGAGCCTGAGCAACCTTTGG 142
QY      601 ACTTAGAGCTGTAAACGCGCCAGCCATTAAGGTGTAAACCTGTGTGTGTGTGTAA 660
DB      601 ACTTAGAGCTGTAAACGCGCCAGCCATTAAGGTGTAAACCTGTGTGTGTGTGTAA 660
QY      141 ACTTAGAGCTGTAAACGCGCCAGCCATTAAGGTGTAAACCTGTGTGTGTGTGTAA 82
DB      141 ACTTAGAGCTGTAAACGCGCCAGCCATTAAGGTGTAAACCTGTGTGTGTGTGTAA 82
QY      661 GGCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAA 719
DB      661 GGCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAA 719
QY      81 GGCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAA 22
DB      81 GGCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAA 22
```

QY 720 TTGCA 724
DB 21 TTGAA 17

RESULT 7

CD370856/c

LOCUS

DEFINITION

UI-H-FT1-bj2-n-11-0-UI s1 NCI CGAP_FTI Homo sapiens CDNA clone

UI-H-FT1-bj2-n-11-0-UI 3', mRNA sequence.

CD370856

CD370856

CD370856.1

GI:31154946

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 602)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-roman1.nih.gov

Tissue Procurement: Dr. Gary W. Hummingake, U of I

CDNA library preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/cgap.html>

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

location/Qualifiers

1..602

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-FT1-bj2-n-11-0-UI"

/tissue_type="Alveolar Macrophage"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/note="Organ: Lung; Vector: pRT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_FTI is a normalized CDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; wt adenovirus + LPS 24 hours; The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hummingake of the University of Iowa.

ORIGIN

TNG_TISSUE=Human Lung Alveolar Macrophage
TAG_Lib=UI-H-FTI
TAG_SEQ=GGCCATGCCG"

Query Match 17.7% Score 460; DB 6; Length 602;
Best Local Similarity 83.5%; Pred. No. 2.1e-113; Indels 116; Gaps 1;
Matches 586; Conservative 0; Mismatches 0;

17 ACAGAGCTGCTTTCCACCCAGTGCAGACGAGATGAAGAGGTGAGAGTTGTGTAG 76
17 ACAGAGCTGCTTTCCACCCAGTGCAGACGAGATGAAGAGGTGAGAGTTGTGTAG 76
602 ACAGAGCTGCTTTCCACCCAGTGCAGACGAGATGAAGAGGTGAGAGTTGTGTAG 543
77 ATTATGTGAGACACCCGGGCAAGGTTCAGAGTCTTTCATTTATCAACCGAATACGG 136
77 ATTATGTGAGACACCCGGGCAAGGTTCAGAGTCTTTCATTTATCAACCGAATACGG 136
542 ATTATGTGAGACACCCGGGCAAGGTTCAGAGTCTTTCATTTATCAACCGAATACGG 483
137 GGGAGCCGATATTAATGTTGCTTGTATATGAGACCTGTGAGCAGTTGTCTACA 196
137 GGGAGCCGATATTAATGTTGCTTGTATATGAGACCTGTGAGCAGTTGTCTACA 196
482 GGGAGCCGATATTAATGTTGCTTGTATATGAGACCTGTGAGCAGTTGTCTACA 423
197 GTAAGTGAATAATTAGGCAAGTGTGATAGAGTGTGGTGTGTATATTTT 256
422 -----
257 TTTATTTTTCACAGTTTGTGTGTTAAAGAAATTTGTATTTTAAAAAGTCC 316
422 -----
317 TGTGCTGAACCTGAGCTGAGCCGAGCCAGAACCGAGGCTGCAAGACCTACCCGCG 376
317 TGTGCTGAACCTGAGCTGAGCCGAGCCAGAACCGAGGCTGCAAGACCTACCCGCG 376
418 TGTGCTGAACCTGAGCTGAGCCGAGCCAGAACCGAGGCTGCAAGACCTACCCGCG 359
377 TCTTAAATGCGCGCTGCTATCTGAGACGCGCCGACATCACCTGTGTCTAGAGATGCA 436
377 TCTTAAATGCGCGCTGCTATCTGAGACGCGCCGACATCACCTGTGTCTAGAGATGCA 436
358 TCTTAAATGCGCGCTGCTATCTGAGACGCGCCGACATCACCTGTGTCTAGAGATGCA 299
437 TAGTAGTACGATAGCTGTGACTCGGTCTTCTTAACAACCTCTGAGATACACCGGT 496
437 TAGTAGTACGATAGCTGTGACTCGGTCTTCTTAACAACCTCTGAGATACACCGGT 496
298 TAGTAGTACGATAGCTGTGACTCGGTCTTCTTAACAACCTCTGAGATACACCGGT 239
497 GGTCCCGCTGAGCCCATTAACAGTGCCTGAGTGAAGTGTGGGCGTCCGAGGCTGT 556
497 GGTCCCGCTGAGCCCATTAACAGTGCCTGAGTGAAGTGTGGGCGTCCGAGGCTGT 556
238 GGTCCCGCTGAGCCCATTAACAGTGCCTGAGTGAAGTGTGGGCGTCCGAGGCTGT 179
557 GGAATGTATCGAGACTGTCTTAACGAGCCTGTGGCAACCTTTGAGCTGTAAACG 616
557 GGAATGTATCGAGACTGTCTTAACGAGCCTGTGGCAACCTTTGAGCTGTAAACG 616
178 GGAATGTATCGAGACTGTCTTAACGAGCCTGTGGCAACCTTTGAGCTGTAAACG 119
617 CCCAGAGCCATTAAGGTGAACCTGTGATTCGCTGTGTGTTAACGCCCTTTGTGCTGA 676
617 CCCAGAGCCATTAAGGTGAACCTGTGATTCGCTGTGTGTTAACGCCCTTTGTGCTGA 676
118 CCCAGAGCCATTAAGGTGAACCTGTGATTCGCTGTGTGTTAACGCCCTTTGTGCTGA 59
677 ATGAGTTGATGATTAATTAAGGCTGAGATATGTTAA 718
58 ATGAGTTGATGATTAATTAAGGCTGAGATATGTTAA 17

RESULT 8
BMS91710 337 bp mRNA linear EST 25-FEB-2002
LOCUS BMS91710
DEFINITION 1700687388831 A.Gam.ad.cdna.blood1 Anopheles gambiae cdna clone
19600449695952 5', mRNA sequence.
ACCESSION BMS91710
VERSION BMS91710.1 GI:18887571
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 337)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,

TITLE

Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltR@celera.com
Plate: N01004AB8 row: P column: 18
Seq primer: M13 Reverse.

FEATURES

source

1..337
location/qualifiers

/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"

/db_xref="taxon:7165"
/clone="19600449695952"
/dev_stage="Adult"

/lab_host="DHI0b"

/clone_1lb="A.Gam.ad.cdna.blood1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
hours after human blood feeding. CDNA inserts >500 bp
cloned directionally into pSport 1. Not 1 site is 3'.
Clones available through the Malaria Research and
Reference Reagent Resource Center (www.malaria.mr4.org)"

ORIGIN

Query Match 12.9% Score 335.4; DB 4; Length 337;
Best Local Similarity 99.7%; Pred. No. 1.4e-79;
Matches 336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

668 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 727
1 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
728 CGTGTAAATGAGGCGGCGCTTAAAGGATATTAATGCGCGGTGCTAATCTTGTTAC 787
61 CGTGTAAATGAGGCGGCGCTTAAAGGATATTAATGCGCGGTGCTAATCTTGTTAC 120
788 ATTCGACCTCATGAGAGCTTGGAGAGCTTGGAGATTTTCTGCTGCGCTAATCTTCT 847
121 ATTCGACCTCATGAGAGCTTGGAGAGCTTGGAGATTTTCTGCTGCGCTAATCTTCT 180
848 GGAACAGAGCTCTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 907
181 GGAACAGAGCTCTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
908 AAAGTTAGTCTGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGAT 967
241 AAAGTTAGTCTGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGAT 300
968 CTGTGTGAGCTGTTGATTTCTTGAATCTGCGTCAC 1004
301 CTGTGTGAGCTGTTGATTTCTTGAATCTGCGTCAC 337

RESULT 9
BP915148/c 347 bp mRNA linear EST 18-JAN-2001
LOCUS BP915148
DEFINITION IL3-UT0114-041200-328-H03_1 UT0114 Homo sapiens CDNA, mRNA
sequence.
ACCESSION BP915148
VERSION BP915148.1 GI:12306606
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 347)
Dias Neto,E., Garcia Correa,R., Veijovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.P., Matsumura,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL
MEDLINE
PUBMED
20202663
10737800
TITLE
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-
041200-3&t3=H03_1&t3=2000-12-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 329.
Location/Qualifiers
1. .347
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="UT0114"
/note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 9.6%; Score 249.8; DB 2; Length 347;
Best Local Similarity 95.5%; Pred. No. 2.8e-56;
Matches 257; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY CCGACATACCTGCTCTAGAGCAATGCACTAGTACGATAGCTGACCTCCGCTCT 467
DB CCGACATACCTGCTCTAGAGCAATGCACTAGTACGATAGCTGACCTCCGCTCT 288
QY TCTTAACACACCTCTGATACACCCGGTGGTCCGCTGTCGCCCATTAACCAAGTCC 527
DB TCTTAACACACCTCTGATACACCCGGTGGTCCGCTGTCGCCCATTAACCAAGTCC 228
QY 528 GTGAGAGTGTGGGGCGTGCACAGGCTGTGAAATGATTCAGAGACTTCTTAACGAGCT 587
DB 227 GTGAGAGTGTGGGGCGTGCACAGGCTGTGAAATGATTCAGAGACTTCTTAACGAGCT 168
QY 588 GGGCAACCTTTGAGATTGAGCTGTAAAGCCCCAGGCCATTAAGCTGTAAACCTTGATG 647
DB 167 GGGCAACCTTTGAGATTGAGCTGTAAAGCCCCAGGCCATTAAGCTGTGATG 108
QY 648 CGTGTGTGTTAACGCTTTGTGTTGCTGA 676
DB 107 CGTGTGTGTTCTTGTATTATGCAAGCTTA 79
RESULT 10
BF914577/c 323 bp mRNA linear EST 18-JAN-2001
LOCUS IL3-UT0114-011200-3&t2-G09_1 UT0114 Homo sapiens cDNA, mRNA
DEFINITION
Sequence.
ACCESSION BF914577
VERSION BF914577.1 GI:12306035
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 323)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.P., Matsumura,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL
MEDLINE
PUBMED
20202663
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-
011200-3&t2-G09_1&t3=2000-12-01&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 322.
Location/Qualifiers
1. .323
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="UT0114"
/note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 8.6%; Score 224.2; DB 2; Length 323;
Best Local Similarity 94.7%; Pred. No. 2.5e-49;
Matches 232; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 432 TGCATATGTAGTACGATAGCTGACCTCGGCTCTTACACACCTCGAGTACAC 491
DB 323 TGCATATGTAGTACGATAGCTGACCTCGGCTCTTACACACCTCGAGTACAC 264
QY 492 CCGGTGGTCCGCTGTGTCATTAACCAAGTTCCGCTGAGAGTGTGGGCGTGCAG 551
DB 263 CCGGTGGTCCGCTGTGTCATTAACCAAGTTCCGCTGAGAGTGTGGGCGTGCAG 204
QY 552 GCTGTGAATGATTCAGAGACTTCTTAACGAGCTGGGCAACTTGTGACTTGACTGT 611
DB 203 GCTGTGAATGATTCAGAGACTTCTTAACGAGCTGGGCAACTTGTGACTTGACTGT 144
QY 612 AAAGCCCCAGGCCATTAAGCTGTAAAGCTGTGATGTGCTGTAAACCTTTGTTT 671
DB 143 AAAGCCCCAGGCCATTAAGCTGTAAAGCTGTGATGTGCTGTGTTATTGCA 84
QY 672 GCTGA 676
DB 83 GCTTA 79
RESULT 11
BF915126/c

LOCUS BP915126 321 bp mRNA linear EST 18-JAN-2001
 DEFINITION IL3-UT0114-041200-328-A10_1 UT0114 Homo sapiens cDNA, mRNA
 ACCESSION BP915126
 VERSION BP915126
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 321)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.P., Goldman, G.H., Carvalho, A.F., Matsumura, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPBP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=IL3&l2=IL3:UT0114-041200-328-A10_1&l3=2000-12-04&l4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 159.
 Location/Qualifiers
 1..321
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="UT0114"
 /note="Organ: uterus, tumor; Vector: puc18; Site_1: Smal; Site_2: SmaI; A mini-library was made by cloning products derived from ORBSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 ORIGIN
 Query Match 8.6%; Score 223.8; DB 2; Length 321;
 Best Local Similarity 95.1%; Pred. No. 3.3e-49;
 Matches 231; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Oy 434 CAATAGTAGTACGATAGCTGTGACTCCGGTCTTCTTAACACACCTCTGAGATACACC 493
 Db 321 CAATAGTAGTACGATAGCTGTGACTCCGGTCTTCTTAACACACCTCTGAGATACACC 262
 Oy 494 GGTGTCTCCCGCTGTCCTTAAACGAGTTCCTGAGAGTGTGGGCGCTCCGACAGC 553
 Db 261 GGTGTCTCCCGCTGTCCTTAAACGAGTTCCTGAGAGTGTGGGCGCTCCGACAGC 202
 Oy 554 TGTGATATATATCGAGACTTGCTTAACGAGCTGGCAACTTTGAGCTGATTA 613
 Db 201 TGTGATATATATCGAGACTTGCTTAACGAGCTGGCAACTTTGAGCTGATTA 142
 Oy 614 AGCCCGACGACCATTAAGGTGTAACCTGTGATGGGTGTGTGTTACGCCCTTTGTTGC 673
 Db 141 AGCCCGACGACCATTAAGGTGTAACCTGTGATGGGTGTGTGTTATTTGACAGC 82
 Oy 674 TGA 676

Db 81 TTA 79
 RESULT 12
 LOCUS CD366021/c
 DEFINITION UI-H-F11-bjs-k-22-0-UI-81 NCI CGAP_F11 Homo sapiens cDNA clone
 UI-H-F11-bjs-k-22-0-UI 3', mRNA sequence.
 ACCESSION CD366021
 VERSION CD366021
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 741)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 JOURNAL COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
 Seq primer: M13 FORWARD
 Polya+Yes.
 Location/Qualifiers
 1..741
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-F11-bjs-k-22-0-UI"
 /tissue_type="Alveolar Macrophage"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP F11"
 /note="Organ: lung; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP_F11 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/mL, 3 hours; LPS 10 ng/mL, 24 hours; PMA 10 ng/mL, 3 hours; PMA 10 ng/mL, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 3 hours; Adenoviral vector (Ad5 CMV egfp), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drr)18 tail. The sequence tag for this library is GGCATGCGG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
 TAG_TISSUE=Human Lung Alveolar Macrophage

ORIGIN TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

Query Match 8.6%; Score 222.4; DB 6; Length 741;
Best Local Similarity 98.7%; Pred. No. 9.8e-49;
Matches 234; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2358 AGCCGAGAGCATGTCGCAAGGTAACCTGAAACGGGGTCTTTGACATGACATGAAGACT 2417
Db AGCCGAGAGCATGTCGCAAGGTAACCTGAAACGGGGTCTTTGACATGACATGAAGACT 672
QY 2418 GGAAGTCTGAGTACATGATGAGACCCGACAGGTGAGACCTCTGCAAGTGTGGCGTA 2477
Db GGAAGTCTGAGTACATGATGAGACCCGACAGGTGAGACCTCTGCAAGTGTGGCGTA 612
QY 2478 AACATATTAGAACACGACCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2537
Db AACATATTAGAACACGACCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 552
QY 2538 TGGTGTGCTGCTGACCGCGGCTGAGTTGGCTCAGAGTAAGATACAGATTGAG 2594
Db TGGTGTGCTGCTGACCGCGGCTGAGTTGGCTCAGAGTAAGATACAGATTGAG 495

RESULT 13
LOCUS CD742922 667 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bka-k-23-0-UI.81 NCI CGAP_F11 Homo sapiens cDNA clone
CD742922
VERSION CD742922
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 667)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 546-595, >(CAG)nSimple_repeat (matched complement).
Seq primer: M13 FORWARD
POLY-A=yes.

FEATURES
source Location/Qualifiers
1..667
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bka-k-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP F11"
/note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI-CGAP F11 is a normalized cDNA library constructed from
a pool of 61 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to

incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/mL, 3 hours; LPS 100 ng/mL, 24 hours;
PMA 10 ng/mL, 3 hours; PMA 10 ng/mL, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an Ecor I adaptor,
digested with Not I, and cloned directionally into
pT773-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 6.7%; Score 173.6; DB 6; Length 667;
Best Local Similarity 97.8%; Pred. No. 1.8e-35;
Matches 176; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1165 GGAAGGCGGTGTGAGACACAAAGATCGCTCTACTCTTCTCCGCGCGGCGGA 1224
Db GGAAGGCGGTGTGAGACACAAAGATCGCTCTACTCTTCTCCGCGCGGCGGA 608
QY 1225 TAATACGAGCGAGC 1284
Db TAATACGAGCGAGC 548
QY 1285 AGAGCCCATGGAACCCGAGAGCCGCGCTGACCCCTCGGGAATGATGTTGTACAGGTGC 1344
Db AGAGCCCATGGAACCCGAGAGCCGCGCTGACCCCTCGGGAATGATGTTGTACAGGTGC 488

RESULT 14
LOCUS CD365243 661 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT2-bj1-c-23-0-UI.81 NCI CGAP_F12 Homo sapiens cDNA clone
CD365243
VERSION CD365243
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 661)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 19:12:23 ; Search time 429 Seconds
(without alignments)
9893.944 Million cell updates/sec

Title: US-10-790-562-33_COPY_459_3052

Perfect score: 2594
Sequence: 1 atcgattctaccctgcacga.....cgatgaagatcacagatcgag 2594

Scoring table:
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2594	100.0	7090	4 US-09-714-550-18	Sequence 18, Appl
2	2594	100.0	35935	2 US-08-735-609-1	Sequence 1, Appl
3	2594	100.0	35935	2 US-08-735-609-1	Sequence 1, Appl
4	2594	100.0	35935	2 US-08-735-609-1	Sequence 1, Appl
5	2594	100.0	35935	3 US-09-315-372-1	Sequence 1, Appl
6	2594	100.0	35935	3 US-09-244-752-1	Sequence 1, Appl
7	2594	100.0	35935	3 US-09-244-752-1	Sequence 1, Appl
8	2594	100.0	35935	3 US-09-409-670-43	Sequence 43, Appl
9	2594	100.0	35935	3 US-09-562-919-1	Sequence 1, Appl
10	2594	100.0	35978	4 US-09-956-335-1	Sequence 1, Appl
11	2582	99.5	35871	4 US-09-956-335-2	Sequence 2, Appl
12	2161	83.3	34303	2 US-08-735-609-4	Sequence 4, Appl
13	2161	83.3	34303	2 US-08-735-609-4	Sequence 4, Appl
14	2161	83.3	34303	3 US-09-315-372-4	Sequence 4, Appl
15	2161	83.3	34303	3 US-09-244-752-4	Sequence 4, Appl
16	2161	83.3	34303	3 US-09-244-752-4	Sequence 4, Appl
17	2161	83.3	34303	3 US-09-244-752-4	Sequence 4, Appl
18	714	27.5	1356	1 US-08-562-919-4	Sequence 1, Appl
19	714	27.5	1356	1 US-08-143-497-1	Sequence 1, Appl
20	714	27.5	1356	1 US-08-461-666-1	Sequence 1, Appl
21	714	27.5	1356	1 US-08-461-184-1	Sequence 1, Appl
22	714	27.5	1356	1 US-08-461-675-1	Sequence 1, Appl
23	714	27.5	1356	1 US-08-757-300-1	Sequence 1, Appl
24	682.4	26.3	36519	3 US-08-464-589-1	Sequence 1, Appl
25	644.8	24.9	35524	3 US-08-923-137-2	Sequence 2, Appl
26	634	24.4	1000	1 US-07-960-112B-1	Sequence 1, Appl
27	634	24.4	1000	1 US-07-960-112B-1	Sequence 3, Appl

28	634	24.4	1000	1 US-08-301-316B-1	Sequence 1, Appl
29	634	24.4	1000	1 US-08-301-316B-3	Sequence 3, Appl
30	634	24.4	1000	2 US-08-473-399B-1	Sequence 1, Appl
31	634	24.4	1000	2 US-08-473-399B-3	Sequence 3, Appl
32	634	24.4	1000	3 US-08-853-831-1	Sequence 1, Appl
33	634	24.4	1000	3 US-08-853-831-3	Sequence 3, Appl
34	634	24.4	1000	4 US-09-510-885-1	Sequence 1, Appl
35	634	24.4	1000	4 US-09-510-885-3	Sequence 3, Appl
36	634	24.4	1000	5 PCT-US93-09774-1	Sequence 1, Appl
37	634	24.4	1000	5 PCT-US93-09774-3	Sequence 3, Appl
38	618.2	23.8	34794	4 US-09-713-678-39	Sequence 39, Appl
39	599.6	23.1	35081	2 US-08-752-760A-1	Sequence 1, Appl
40	546.8	21.1	7507	4 US-08-653-114A-1	Sequence 1, Appl
41	463	17.8	1800	4 US-08-540-077-4	Sequence 4, Appl
42	458.2	17.7	1796	1 US-08-540-077-2	Sequence 2, Appl
43	308.6	11.9	315	3 US-08-945-424-1	Sequence 1, Appl
44	308.6	11.9	315	4 US-09-718-865-1	Sequence 1, Appl
45	183.8	7.1	216	4 US-09-714-550-5	Sequence 5, Appl

ALIGNMENTS

```
RESULT 1
US-09-714-550-18
Sequence 18, Application US/09714550
Patent No. 6558948
GENERAL INFORMATION:
APPLICANT: Schindler, Stefan
TITLE OF INVENTION: Permanent amniocytic cell line, its
TITLE OF INVENTION: Production and use for the production of gene transfer
FILE REFERENCE: 50125/007002
CURRENT APPLICATION NUMBER: US/09/714,550
CURRENT FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/167,439
PRIOR FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 7090
TYPE: DNA
ORGANISM: Plasmid STK146
US-09-714-550-18

Query Match 100.0%; Score 2594; DB 4; Length 7090;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCGATCTTACTGCGACGAGGCTGCTTCCACCGATGACGAGATGAAGAGGT 60
DB 3165 ATCGATCTTACTGCGACGAGGCTGCTTCCACCGATGACGAGATGAAGAGGT 3224

QY 61 GAGGAGTTGTGTAGATTAATATGTCGAGACCCCGGCGACCGTTGCAAGTCTTGCATTAT 120
DB 3225 GAGGAGTTGTGTAGATTAATATGTCGAGACCCCGGCGACCGTTGCAAGTCTTGCATTAT 3284

QY 121 CACCGAGAGATATACGGGGGACCCGATATTAATGTCGATTAATGAGACCTGT 180
DB 3285 CACCGAGAGATATACGGGGGACCCGATATTAATGTCGATTAATGAGACCTGT 3344

QY 181 GCGATGTTGTCTACAGTAAGTAAATTAATGCGACAGTGGTGTATAGTGGGTTTG 240
DB 3345 GCGATGTTGTCTACAGTAAGTAAATTAATGCGACAGTGGTGTATAGTGGGTTTG 3404

QY 241 GTGCGTAATTTTATTTTATTTTACAGTTGTGTGTTTAAAGATTTTGTATTGGA 300
DB 3405 GTGCGTAATTTTATTTTATTTTACAGTTGTGTGTTTAAAGATTTTGTATTGGA 3464

QY 301 TTTTAAAGGCTGTGTCTGAACCTGAGCTGAGCCGAGACCGAGAGCTG 360
DB 3465 TTTTAAAGGCTGTGTCTGAACCTGAGCTGAGCCGAGACCGAGAGCTG 3524
```

OY 361 CAAGACCTACCCGCGCTCTTAAATGGGCGCTGCMATCTGAGACGCCCGACATCACTG 420
DB 3525 CAAGACCTACCCGCGCTCTTAAATGGGCGCTGCMATCTGAGACGCCCGACATCACTG 3584
OY 421 TGTCTAGAAATGCAATAGTATGATACGGAATAGCTGATCTCGGATCTTCTTAACAACACTC 480
DB 3585 TGTCTAGAAATGCAATAGTATGATACGGAATAGCTGATCTCGGATCTTCTTAACAACACTC 3644
OY 481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCATTTAAACCAAGTTGCCGTGAGAGTTGGTG 540
DB 3645 CTGAGATACACCCGGTGGTCCCGCTGTGCCCATTTAAACCAAGTTGCCGTGAGAGTTGGTG 3704
OY 541 GGCGCTGCGCAGAGCTGTGGAATGTATCGAGAGCTTGCTTAACGAGCTGGGCAACTTTGG 600
DB 3705 GGCGCTGCGCAGAGCTGTGGAATGTATCGAGAGCTTGCTTAACGAGCTGGGCAACTTTGG 3764
OY 601 ACTTGAAGCTGTAAACGCCCGACAGGCCATTAAGGTGTAAACCTGTGATTTGCCGTGTGTAA 660
DB 3765 ACTTGAAGCTGTAAACGCCCGACAGGCCATTAAGGTGTAAACCTGTGATTTGCCGTGTGTAA 3824
OY 661 CGCCTTTGTTTGTCTGAATGATGTATGATTTAATAAGGTGAGATTAATGTTTAATCT 720
DB 3825 CGCCTTTGTTTGTCTGAATGATGTATGATTTAATAAGGTGAGATTAATGTTTAATCT 3884
OY 721 TGCATGCGGTGTAAATGGGGCGGGGCTTAAAGGGTATATATGCGCGGTGCTAATCT 780
DB 3885 TGCATGCGGTGTAAATGGGGCGGGGCTTAAAGGGTATATATGCGCGGTGCTAATCT 3944
OY 781 TGGTTCACATCTGACCTCAATGAGGCTTGGAGTGTGGAAAGATTTTCTGCTGTGCTA 840
DB 3945 TGGTTCACATCTGACCTCAATGAGGCTTGGAGTGTGGAAAGATTTTCTGCTGTGCTA 4004
OY 841 ACTTGTCTGAAACAGAGCTCTTAACAGTACTCTTGTGTTTGGAGTTTCTGTGGGCTCAT 900
DB 4005 ACTTGTCTGAAACAGAGCTCTTAACAGTACTCTTGTGTTTGGAGTTTCTGTGGGCTCAT 4064
OY 901 CCCAGGCAAGTTGATGTGAGAAATTAAGAGAGATTAAGAGGGAAATTTGAAAGCTTT 960
DB 4065 CCCAGGCAAGTTGATGTGAGAAATTAAGAGAGATTAAGAGGGAAATTTGAAAGCTTT 4124
OY 961 TGAATCTGTGTGAGAGCTGTGTTGATTTTGAATCTGGGTCAACGAGCGCTTTTCCAG 1020
DB 4125 TGAATCTGTGTGAGAGCTGTGTTGATTTTGAATCTGGGTCAACGAGCGCTTTTCCAG 4184
OY 1021 AGAAGGTATCAAGACTTTGGAATTTTCCACACCGGGGCGGCTGCGCTGTGTGCTT 1080
DB 4185 AGAAGGTATCAAGACTTTGGAATTTTCCACACCGGGGCGGCTGCGCTGTGTGCTT 4244
OY 1081 TTTTGAAGTTTATTAAGATTAATGAGAGCAAGAAACCATCTGAGCGGGGATTAAGCTGC 1140
DB 4245 TTTTGAAGTTTATTAAGATTAATGAGAGCAAGAAACCATCTGAGCGGGGATTAAGCTGC 4304
OY 1141 TGAATTTTCTGGCCATGTCATCTGTGAGAGCGGTTGTGACAACAAGATGCGCTGTAC 1200
DB 4305 TGAATTTTCTGGCCATGTCATCTGTGAGAGCGGTTGTGACAACAAGATGCGCTGTAC 4364
OY 1201 TGTGTCTTCCGCTCGCGCGCGGATTAATCCGACGGAAGAGACAGACAGACAGAGAGG 1260
DB 4365 TGTGTCTTCCGCTCGCGCGCGGATTAATCCGACGGAAGAGACAGACAGACAGAGAGG 4424
OY 1261 AAGCGAGCGCGGCGGAGG 1320
DB 4425 AAGCGAGCGCGGCGGAGG 4484
OY 1321 GGAATGATATGTTGATCAAGTGTGCTGAATCTGTATCAAGACTGAGACGCAATTTGACAT 1380
DB 4485 GGAATGATATGTTGATCAAGTGTGCTGAATCTGTATCAAGACTGAGACGCAATTTGACAT 4544
OY 1381 TACAGAGATGAGGAGGCTTAAGAGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 1440
DB 4545 TACAGAGATGAGGAGGCTTAAGAGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 4604

OY 1441 AGAAGAGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGCTCTGAGTATTAAC 1500
DB 4605 AGAAGAGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGCTCTGAGTATTAAC 4664
OY 1501 TTTTCAACAGATCAAGATTAATGCGCTTAATGAGCTTGTGCTGCGCAGAGATATTC 1560
DB 4665 TTTTCAACAGATCAAGATTAATGCGCTTAATGAGCTTGTGCTGCGCAGAGATATTC 4724
OY 1561 CATGAGACACTGACCACTTAAGTGGCTGACAGCGAGGGAGATTTTGAAGGCTAATTAAG 1620
DB 4725 CATGAGACACTGACCACTTAAGTGGCTGACAGCGAGGGAGATTTTGAAGGCTAATTAAG 4784
OY 1621 GGTATATGCAAGGTGCGCACTTGAAGCCAGATTGCAATGACATCAAGATCAGCAACTTGTAA 1680
DB 4785 GGTATATGCAAGGTGCGCACTTGAAGCCAGATTGCAATGACATCAAGATCAGCAACTTGTAA 4844
OY 1681 TATCAGGAATTTGTTCTTACATTTCTGGGAAACGGGGCCGAGGTGAGATATGATACGAGGA 1740
DB 4845 TATCAGGAATTTGTTCTTACATTTCTGGGAAACGGGGCCGAGGTGAGATATGATACGAGGA 4904
OY 1741 TAGGGTGGCCCTTGAATGATGATGATTAATATGATGGCCGGGGGTGCTTGGCATGAGACGG 1800
DB 4905 TAGGGTGGCCCTTGAATGATGATGATTAATATGATGGCCGGGGGTGCTTGGCATGAGACGG 4964
OY 1801 GGTTGTTATTAATGATGATGATTAAGGTTTACTGGCCCAATTTTAAGCGGTACGGTTTCTGGC 1860
DB 4965 GGTTGTTATTAATGATGATGATTAAGGTTTACTGGCCCAATTTTAAGCGGTACGGTTTCTGGC 5024
OY 1861 CAATACCAACCTTATCTTACACGAGGTGATGCTTATGAGTTTAACAATACCTGTGTGGA 1920
DB 5025 CAATACCAACCTTATCTTACACGAGGTGATGCTTATGAGTTTAACAATACCTGTGTGGA 5084
OY 1921 AGCTGGAACGATGATGAGGTTGGGGGCTGTGCTTTTACGCTGCTGGAAGGGGGTGT 1980
DB 5085 AGCTGGAACGATGATGAGGTTGGGGGCTGTGCTTTTACGCTGCTGGAAGGGGGTGT 5144
OY 1981 GTGTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTACCTTGGG 2040
DB 5145 GTGTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTACCTTGGG 5204
OY 2041 TATCTGTCTGAGGGTAACTTCAGAGGTGCGCACATATGTGCTCCGACTGTGTGCTT 2100
DB 5205 TATCTGTCTGAGGGTAACTTCAGAGGTGCGCACATATGTGCTCCGACTGTGTGCTT 5264
OY 2101 CATGCTAGTAAAGCGGTGCTGATTAAGCATTAACATGATGTGGAACCTGCGAGGA 2160
DB 5265 CATGCTAGTAAAGCGGTGCTGATTAAGCATTAACATGATGTGGAACCTGCGAGGA 5324
OY 2161 CAGGGCTCTCAGATGCTGACCTGCTCGACCGGCACTGTCACTGTGAGAGACCATTTCA 2220
DB 5325 CAGGGCTCTCAGATGCTGACCTGCTCGACCGGCACTGTCACTGTGTGAGAGACCATTTCA 5384
OY 2221 CGTAGCCAGCCACTCTGCGAAGGCTTGGCCAGTGTGTTGAGCATTAACATATGACCCGCTG 2280
DB 5385 CGTAGCCAGCCACTCTGCGAAGGCTTGGCCAGTGTGTTGAGCATTAACATATGACCCGCTG 5444
OY 2281 TTCTTTCATTTGGGTAAACAGAGGGGGGTGTTCTTACCTTAACAATGCAATTTGAGTCA 2340
DB 5445 TTCTTTCATTTGGGTAAACAGAGGGGGGTGTTCTTACCTTAACAATGCAATTTGAGTCA 5504
OY 2341 CACTAAGATATTTGCTTGAAGCCGAGACATGTCCAGAGTGAACCTGAAACGGGGTGTTTGA 2400
DB 5505 CACTAAGATATTTGCTTGAAGCCGAGACATGTCCAGAGTGAACCTGAAACGGGGTGTTTGA 5564
OY 2401 CATGACATGAAGATCTGGAAGGTGTGAGGTACGATGAGACCCGCAACAGGTGCAAGCC 2460
DB 5565 CATGACATGAAGATCTGGAAGGTGTGAGGTACGATGAGACCCGCAACAGGTGCAAGCC 5624
OY 2461 CTGCGAGGTGGCGGTAAACAATTAAGAAACCAAGCTGTGATGCTGGAATGAGACGAGAGA 2520
DB 5625 CTGCGAGGTGGCGGTAAACAATTAAGAAACCAAGCTGTGATGCTGGAATGAGACGAGAGA 5684
OY 2521 GCTGAGGCCGATCACTTGTGTGCTGAGCTGCAACCGGCTGAGTTTGGCTTACGATGA 2580

Db 5685 GCTAGAGCCCATCATCTTGCTGCTGCTGCACTCCGCTGAGTTGGCTCTAGCGATGA 5744
Qy 2581 AGATACAGATTGAG 2594
Db 5745 AGATACAGATTGAG 5758

RESULT 2

US-08-735-609-1
Sequence 1, Application US/08735609
Patent No. 5953360

GENERAL INFORMATION:

APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735, 609
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 35935 base pairs
TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

US-08-735-609-1

Query Match 100.0%; Score 2594; DB 2; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCATCTTACTCCAGAGGCTGCTTTCCACCAAGTGAAGAGAGGCT 60
Db 917 ATGCATCTTACTCCAGAGGCTGCTTTCCACCAAGTGAAGAGAGGCT 976
Qy 61 GAGAGTTTGTGTTAGATTATGTGAGACACCCGGGCGACGGTTGCAAGCTTGTCAATTAT 120
Db 977 GAGAGTTTGTGTTAGATTATGTGAGACACCCGGGCGACGGTTGCAAGCTTGTCAATTAT 1036
Qy 121 CACCGAGGAATTAAGGGGAGCCAGATTAATTATGTGCTTGTCTATATAGAACCTGT 180
Db 1037 CACCGAGGAATTAAGGGGAGCCAGATTAATTATGTGCTTGTCTATATAGAACCTGT 1096
Qy 181 GGCATGTTTGTCTACAGTAAGTGAATAATTATGGGAGTGGTGAATAGATGGTGGTTTG 240
Db 1097 GGCATGTTTGTCTACAGTAAGTGAATAATTATGGGAGTGGTGAATAGATGGTGGTTTG 1156

Qy 241 GTGTGTATATTTTTTTTAAATTTTACAGTTTGTGTGTTAAAGATTTGTATGTGA 300
Db 1157 GTGTGTATATTTTTTTTAAATTTTACAGTTTGTGTGTTAAAGATTTGTATGTGA 1216
Qy 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCGAGCCGAGCAGAACCGAGGCTTG 360
Db 1217 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCGAGCCGAGCAGAACCGAGGCTTG 1276
Qy 361 CAAGACCTACCCGCGCTCTAAATTAATGAGCGCTGCTATCTGAGACGCCGACATCCTG 420
Db 1277 CAAGACCTACCCGCGCTCTAAATTAATGAGCGCTGCTATCTGAGACGCCGACATCCTG 1336
Qy 421 TGTCTAAGGAATGCAATAGTATAGATAGCTGATCTCCGGTCTCTTCAACACCTC 480
Db 1337 TGTCTAAGGAATGCAATAGTATAGATAGCTGATCTCCGGTCTCTTCAACACCTC 1396
Qy 481 CTGAGATPACCCCGGTGTCCTGTCGTCGTCCTTAAACAGTTCGCTGAGATGTG 540
Db 1397 CTGAGATPACCCCGGTGTCCTGTCGTCGTCCTTAAACAGTTCGCTGAGATGTG 1456
Qy 541 GCGGTGCGCAGGCTGTGGAATGTATGAGACTTGTAAAGCCTTGAGCCTGGCAACTTTGG 600
Db 1457 GCGGTGCGCAGGCTGTGGAATGTATGAGACTTGTAAAGCCTTGAGCCTGGCAACTTTGG 1516
Qy 601 ACTTGAAGCTGTAAACGCCCGCCATTAAGTGTAAACCTGTGATGGTGTGTTAA 660
Db 1517 ACTTGAAGCTGTAAACGCCCGCCATTAAGTGTAAACCTGTGATGGTGTGTTAA 1576
Qy 661 GCGCTTTGTTTGTGAATGATGATGATTAATTAAGGAGGATTAATGTTAACT 720
Db 1577 GCGCTTTGTTTGTGAATGATGATGATTAATTAAGGAGGATTAATGTTAACT 1636
Qy 721 TGCATGGGCTGTAAATGGGCGGGGCTTAAAGGATATATATGCGCGTGGCTAATCT 780
Db 1637 TGCATGGGCTGTAAATGGGCGGGGCTTAAAGGATATATATGCGCGTGGCTAATCT 1696
Qy 781 TGTGTTACATCTGACCTCATGAGAGCTTGGAGGTGTTGGAAGATTTTCTGCTGCTA 840
Db 1697 TGTGTTACATCTGACCTCATGAGAGCTTGGAGGTGTTGGAAGATTTTCTGCTGCTA 1756
Qy 841 ACTTGTGGAACAGAGCTCTTAAAGTACCTCTTGTGTTGAGGTTCTGCGGCTCAT 900
Db 1757 ACTTGTGGAACAGAGCTCTTAAAGTACCTCTTGTGTTGAGGTTCTGCGGCTCAT 1816
Qy 901 CCGAGGAAAGTTAGTGTGCAATTAAGAGATTAACAATGAGAAATTTGAAGACTTT 960
Db 1817 CCGAGGAAAGTTAGTGTGCAATTAAGAGATTAACAATGAGAAATTTGAAGACTTT 1876
Qy 961 TGAATCTGTGTGAGCTGTTGATTTTGAATCTGGTCAACAGGCTTTTCCAG 1020
Db 1877 TGAATCTGTGTGAGCTGTTGATTTTGAATCTGGTCAACAGGCTTTTCCAG 1936
Qy 1021 AGAAGTCTATCAAGACTTTGATTTTCCACAGCGGGCGGCTGCGGCTGCTGTGCTT 1080
Db 1937 AGAAGTCTATCAAGACTTTGATTTTCCACAGCGGGCGGCTGCGGCTGCTGTGCTT 1996
Qy 1081 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTAACTGTC 1140
Db 1997 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTAACTGTC 2056
Qy 1141 TGAATTTTCTGCGCATGATCTGTGAGAGCGGTTTGAACACAAGAAATGCTGTGAC 1200
Db 2057 TGAATTTTCTGCGCATGATCTGTGAGAGCGGTTTGAACACAAGAAATGCTGTGAC 2116
Qy 1201 TGTGTCTTCCGTCGCGCGCGGATTAATCCGACGAGAGCAGCAGAGCAGAGAGG 1260
Db 2117 TGTGTCTTCCGTCGCGCGCGGATTAATCCGACGAGAGCAGCAGAGCAGAGAGG 2176
Qy 1261 AAGCAGAGCGCGCGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGC 1320
Db 2177 AAGCAGAGCGCGCGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGC 2236
Qy 1321 GGAATGAATGTTGTACAGGTGCTGAACGTGTATCCAGAACTGAGACGCAATTTGACAT 1380

Db 3197 TTCCTTGATTTGGGTAAACAGAGAGGGGGTGTCTTACTTACCAATGCAATTTGATGCA 3256
Qy 2241 CACTTAAGATATTGCTTGAAGCCCGAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGGA 2400
Db 3257 CACTTAAGATATTGCTTGAAGCCCGAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGGA 3316
Qy 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGATGATGAGACCCGACACAGGTGACAGC 2460
Db 3317 CATGACCATGAAGATCTGGAAGGTGCTGAGGATGATGAGACCCGACACAGGTGACAGC 3376
Qy 2461 CTGCGAGTGTGGCGGTAAACAATATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGGA 2520
Db 3377 CTGCGAGTGTGGCGGTAAACAATATTAGGAACCAAGCTGTGATGCTGATGTGACCGAGGA 3436
Qy 2521 GCTGAGGCCCGATCATCTTGTGTGCTGCTGCAACCCGCGCTGATTTGGCTCTAGCGATGA 2580
Db 3437 GCTGAGGCCCGATCATCTTGTGTGCTGCTGCAACCCGCGCTGATTTGGCTCTAGCGATGA 3496
Qy 2581 AGATTACAGATTGAG 2594
Db 3497 AGATTACAGATTGAG 3510

RESULT 4

US-08-379-452-43
Sequence 43 Application US/08379452

Patent No. 6040174

GENERAL INFORMATION:

APPLICANT: IMLER, Jean-Luc

APPLICANT: MEHTALI, Majid

APPLICANT: PAVIRANI, Andrea

TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHEIS, L.L.P.

STREET: 1737 King Street, Suite 500

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22314-2756

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/379,452

FILING DATE: 26-JAN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR94/00624

FILING DATE: 27-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 93 06482

FILING DATE: 28-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Dadio, Susan M.

REGISTRATION NUMBER: 40,373

REFERENCE/DOCKET NUMBER: 029395-002

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 35935 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-379-452-43

Query Match 100.0%; Score 2594; DB 3; Length 35935;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATCTTACCTGCGACAGAGGCTGCTTTCACCCAGTGAACGAGATGAAGAGGT 60
Db 917 ATGATCTTACCTGCGACAGAGGCTGCTTTCACCCAGTGAACGAGATGAAGAGGT 976
Qy 61 GAGAGATTTGTGTAGATTATGTGAGCACCCCGGGACGGTTGACAGTCTTGTCAATTAT 120
Db 977 GAGAGATTTGTGTAGATTATGTGAGCACCCCGGGACGGTTGACAGTCTTGTCAATTAT 1036
Qy 121 CACCGAGGAATATGAGGGGACCCAGATATTATGTGTTCCGTTTGTCTATATAGAGACCTGT 180
Db 1037 CACCGAGGAATATGAGGGGACCCAGATATTATGTGTTCCGTTTGTCTATATAGAGACCTGT 1096
Qy 181 GGCATGTTTGTCTACAGTAAGTGAATATATGAGCAGTGGTGTATAGATGTGGGTTTG 240
Db 1097 GGCATGTTTGTCTACAGTAAGTGAATATATGAGCAGTGGTGTATAGATGTGGGTTTG 1156
Qy 241 GTGTGTAATTTTTTTTTTAATTTTACAGTTTGTGTGTTTAAAGAAATTTGTATTTGTA 300
Db 1157 GTGTGTAATTTTTTTTTTAATTTTACAGTTTGTGTGTTTAAAGAAATTTGTATTTGTA 1216
Qy 301 TTTTAAAAAGTCTGTGTCTGTAACCTGAGCCTGAGCCCGACGACCGAGACCTG 360
Db 1217 TTTTAAAAAGTCTGTGTCTGTAACCTGAGCCTGAGCCCGACGACCGAGACCTG 1276
Qy 361 CAAGACCTACCCGCGCTCTTAAATGAGCGCTGCTATCTGAGACGCCCGACATCACCTG 420
Db 1277 CAAGACCTACCCGCGCTCTTAAATGAGCGCTGCTATCTGAGACGCCCGACATCACCTG 1336
Qy 421 TGTCTAAGAAATGCAATATGATGATGAGATGCTGTGACTCCGTTCTTACACACCTC 480
Db 1337 TGTCTAAGAAATGCAATATGATGATGAGATGCTGTGACTCCGTTCTTACACACCTC 1396
Qy 481 CTGAGATACACCCGCGTCCCGCTGCGCCCATTAACCAAGTTCCGCTGAGATGTG 540
Db 1397 CTGAGATACACCCGCGTCCCGCTGCGCCCATTAACCAAGTTCCGCTGAGATGTG 1456
Qy 541 GGCCTCCGACGCTGTGGAATGTATCGAGACTTGCTTAAACGACCTGAGCAACTTTG 600
Db 1457 GGCCTCCGACGCTGTGGAATGTATCGAGACTTGCTTAAACGACCTGAGCAACTTTG 1516
Qy 601 ACTTGAGCTGTAAACGCCCGACGCGCATTAAGGTGTAACCTGTGATTCGCTGTGTTAA 660
Db 1517 ACTTGAGCTGTAAACGCCCGACGCGCATTAAGGTGTAACCTGTGATTCGCTGTGTTAA 1576
Qy 661 CGCCTTTGTTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 1577 CGCCTTTGTTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1636
Qy 721 TGCATGCGTGTAAATGAGGCGGGGCTTAAAGGATATATATGCGCGGTGATATCT 780
Db 1637 TGCATGCGTGTAAATGAGGCGGGGCTTAAAGGATATATATGCGCGGTGATATCT 1696
Qy 781 TGTGTAATCTGACCTGATGAGGCTTGGAGGTGTTGGAAGATTTTCTGCTGTGCTTA 840
Db 1697 TGTGTAATCTGACCTGATGAGGCTTGGAGGTGTTGGAAGATTTTCTGCTGTGCTTA 1756
Qy 841 ACTTGCTGGAACAGAGCTTAAACAGTACCTGCTTGGATTTGAGGTTCTGAGGCTCAT 900
Db 1757 ACTTGCTGGAACAGAGCTTAAACAGTACCTGCTTGGATTTGAGGTTCTGAGGCTCAT 1816
Qy 901 CCCAGCAAGTATGATGCTGACGAATTAAGAGATTAACAATGGAATTTGAAGACTTT 960
Db 1817 CCCAGCAAGTATGATGCTGACGAATTAAGAGATTAACAATGGAATTTGAAGACTTT 1876
Qy 961 TGAATCTGTGTGAGCTGTTGATTTGAAATCTGAGTACCAAGCGCTTTTCCAG 1020
Db 1877 TGAATCTGTGTGAGCTGTTGATTTGAAATCTGAGTACCAAGCGCTTTTCCAG 1936
Qy 1021 AGAAGTATCAAACTTTGATTTTCCACACCGGGGCGGCTGCGGCTGTGTGCTT 1080
Db 1937 AGAAGTATCAAACTTTGATTTTCCACACCGGGGCGGCTGCGGCTGTGTGCTT 1996
Qy 1081 TTTGAGTTTATTAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTACTGTC 1140

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-315-372-1

Query Match 100.0%; Score 2594; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCATCTTACCTGCGACGAGCGCTGGCTTTCCACCCAGTGA	CGAGAGATGAAGGGT	60
Db	917	ATGCATCTTACCTGCGACGAGCGCTGGCTTTCCACCCAGTGA	CGAGAGATGAAGGGT	976
Qy	61	GAGAGTTTGTGTTAGATTATGTGAGACACCCCGGGACG	GGTTGCAAGTCTTGTCAATTAT	120
Db	977	GAGAGTTTGTGTTAGATTATGTGAGACACCCCGGGACG	GGTTGCAAGTCTTGTCAATTAT	1036
Qy	121	CACCGAGGAATPACGGGGGACCCAGATATATATGTGCTT	GCTATATGAGACCTGT	180
Db	1037	CACCGAGGAATPACGGGGGACCCAGATATATATGTGCTT	GCTATATGAGACCTGT	1096
Qy	181	GGCATGTTTGTCTACAGTAAATTAATGAGGAGTGAATGA	GTGGGTTG	240
Db	1097	GGCATGTTTGTCTACAGTAAATTAATGAGGAGTGAATGA	GTGGGTTG	1156
Qy	241	GTGCGTAATTTTTTTTAAATTTTACAGTTTGTGGTTAA	GAATTTTGTATTTGA	300
Db	1157	GTGCGTAATTTTTTTTAAATTTTACAGTTTGTGGTTAA	GAATTTTGTATTTGA	1216
Qy	301	TTTTTTTAAAGTCTGTCTGACCTGAGCCGAGCCGAGCA	CCGAGCCGAGCTG	360
Db	1217	TTTTTTTAAAGTCTGTGTCTGACCTGAGCCGAGCCGAG	CAACCGAGCCG	1276
Qy	361	CAAGACTACCGCGCTCTTAAATGAGCGCTGTATCTTA	GAGCGCCGACATCACTG	420
Db	1277	CAAGACTACCGCGCTCTTAAATGAGCGCTGTATCTTA	GAGCGCCGACATCACTG	1336
Qy	421	TGCTAAGAAATGCAATAGTATGACGATCTCGGTCCTT	CTAACACACCTC	480
Db	1337	TGCTAAGAAATGCAATAGTATGACGATCTCGGTCCTT	CTAACACACCTC	1396
Qy	481	CTGAGATACACCCGGGTGCTCCGCTGACCCCAATTA	ACAGTTGCCGTGAGTTG	540
Db	1397	CTGAGATACACCCGGGTGCTCCGCTGACCCCAATTA	ACAGTTGCCGTGAGTTG	1456
Qy	541	GCGCTCGCAGGCTGTGAAATGTATGAGAACTTGCTT	TAACGAGCTGAGCAACTTTGG	600
Db	1457	GCGCTCGCAGGCTGTGAAATGTATGAGAACTTGCTT	TAACGAGCTGAGCAACTTTGG	1516
Qy	601	ACTGAGCTGTAACGCCCGACCATTAAGGTATACTGT	GAATTTGGGTGTGTTAA	660
Db	1517	ACTGAGCTGTAACGCCCGACCATTAAGGTATACTGT	GAATTTGGGTGTGTTAA	1576
Qy	661	CGCCTTTGTTGCTGATGATGATTAATTAAGGCTGA	TAAATGTTAACT	720
Db	1577	CGCCTTTGTTGCTGATGATGATTAATTAAGGCTGA	TAAATGTTAACT	1636
Qy	721	TGCATGCGGTGTTAAATGAGCGGGCTTAAAGGTA	TATAATGCGCGGTGCTAATCT	780
Db	1637	TGCATGCGGTGTTAAATGAGCGGGCTTAAAGGTA	TATAATGCGCGGTGCTAATCT	1696
Qy	781	TGCTTAACATCTGACCTCAATGAGGCTTGGAGTGT	TGGAAGATTTTCTGTGCGCTA	840
Db	1697	TGCTTAACATCTGACCTCAATGAGGCTTGGAGTGT	TGGAAGATTTTCTGTGCGCTA	1756
Qy	841	ACTGCTGGAACAGAGCTTAACAGTACTCTTGTTT	TGAGGTTCTGTGAGGCTCAT	900
Db	1757	ACTGCTGGAACAGAGCTTAACAGTACTCTTGTTT	TGAGGTTCTGTGAGGCTCAT	1816
Qy	901	CCCAAGCAAGTTAGTCTGACAGATTTAAAGAGATTA	CAAGTGGGAATTTGAAGGCTTT	960
Db	1817	CCCAAGCAAGTTAGTCTGACAGATTTAAAGAGATTA	CAAGTGGGAATTTGAAGGCTTT	1876

Qy	961	TGAATCTGTGAGGAGCTGTGTTGATTTCTTGAATCT	GGGCAACGAGCGCTTTCCAG	1020
Db	1877	TGAATCTGTGAGGAGCTGTGTTGATTTCTTGAATCT	GGGCAACGAGCGCTTTTCCAG	1936
Qy	1021	AGAGGTCATCAAGACTTTTGAATTTTTCACACCGGG	CGCGCTGCGCTGTGCTT	1080
Db	1937	AGAGGTCATCAAGACTTTTGAATTTTTCACACCGGG	CGCGCTGCGCTGTGCTT	1996
Qy	1081	TTTTGAAGTTTATTAAGATTAATGAGCGAAGAA	CCCATCTGAGCGGGGTTACTGC	1140
Db	1997	TTTTGAAGTTTATTAAGATTAATGAGCGAAGAA	CCCATCTGAGCGGGGTTACTGC	2056
Qy	1141	TGATTTTTCGGCCATCTGTGAGACCGGTGTGAGCA	CAAGATTCGCTGCTAC	1200
Db	2057	TGATTTTTCGGCCATCTGTGAGACCGGTGTGAGCA	CAAGATTCGCTGCTAC	2116
Qy	1201	TGTTGTCTTCGCTCCGCGCGCATTAATACCGA	CGAGAGCAGCAGCAGCAGGAG	1260
Db	2117	TGTTGTCTTCGCTCCGCGCGCATTAATACCGA	CGAGAGCAGCAGCAGCAGGAG	2176
Qy	1261	AAAGCGCGCGCGCGCGCAGAGCAGCCCATGGA	ACCGAGCGCGCTGCACTTC	1320
Db	2177	AAAGCGCGCGCGCGCGCAGAGCAGCCCATGGA	ACCGAGCGCGCTGCACTTC	2236
Qy	1321	GGGAATGAATGTTGTACAGGTGGCTGAACGTAT	CCAGAACTGAGACGCAATTTGA	1380
Db	2237	GGGAATGAATGTTGTACAGGTGGCTGAACGTAT	CCAGAACTGAGACGCAATTTGA	2296
Qy	1381	TACAGAGATGCGGAGGCGCTAAAGGGGTTAA	GAGGAGCGCGGCTGTGAGGCTAC	1440
Db	2297	TACAGAGATGCGGAGGCGCTAAAGGGGTTAA	GAGGAGCGCGGCTGTGAGGCTAC	2356
Qy	1441	AGAGAGGCTTAAGAAATCTAGCTTATTAATGA	CCAGACACCGCTCTGAGTATTA	1500
Db	2357	AGAGAGGCTTAAGAAATCTAGCTTATTAATGA	CCAGACACCGCTCTGAGTATTA	2416
Qy	1501	TTTTCAACAGATCAAGATTAATGCGCTTAAT	GAGCTTGCTGCGCAGAAATATTC	1560
Db	2417	TTTTCAACAGATCAAGATTAATGCGCTTAAT	GAGCTTGCTGCGCAGAAATATTC	2476
Qy	1561	CATAGAGAGCTGAACAATTACTGGCTGACAG	CCAGGGATGATTTTGAAGAGCTATTAG	1620
Db	2477	CATAGAGAGCTGAACAATTACTGGCTGACAG	CCAGGGATGATTTTGAAGAGCTATTAG	2536
Qy	1621	GATATATGCAAGGTGGCACTTAGCCAGATGCA	AGTACAAATCAGCAAACTTTGTTAA	1680
Db	2537	GATATATGCAAGGTGGCACTTAGCCAGATGCA	AGTACAAATCAGCAAACTTTGTTAA	2596
Qy	1681	TATCAGGAATTTGTTGCTACATTTCTGGGAA	CGGGCGAGGTGAGATAGATACGAGAGA	1740
Db	2597	TATCAGGAATTTGTTGCTACATTTCTGGGAA	CGGGCGAGGTGAGATAGATACGAGAGA	2656
Qy	1741	TAGGAGGCTTTAGATGATGATGATTAATAT	GTGCGCGGGGTGCTTGCGCATGAGCGG	1800
Db	2657	TAGGAGGCTTTAGATGATGATGATTAATAT	GTGCGCGGGGTGCTTGCGCATGAGCGG	2716
Qy	1801	GCTGCTTATTAATGATGATGATTTACTGGCC	CAATTTTAAGCGGTACGCTTTTCCGTGGC	1860
Db	2717	GCTGCTTATTAATGATGATGATTTACTGGCC	CAATTTTAAGCGGTACGCTTTTCCGTGGC	2776
Qy	1861	CAATACCAACCTTAATCCACACGCGTGA	AGCTTCTATGAGGTTTAACTGCTGTGGA	1920
Db	2777	CAATACCAACCTTAATCCACACGCGTGA	AGCTTCTATGAGGTTTAACTGCTGTGGA	2836
Qy	1921	AGCCTGGAACCGATGTAAGGTTGCGGGCTG	CTCTTTTACTGCTGCGAAAGGGGTTGT	1980
Db	2837	AGCCTGGAACCGATGTAAGGTTGCGGGCTG	CTCTTTTACTGCTGCGAAAGGGGTTGT	2896
Qy	1981	GTGTCGCCCAAAAGCAGGGCTTCAATTA	GAATGCTCTTTGAAAGTGTACCTTGGG	2040
Db	2897	GTGTCGCCCAAAAGCAGGGCTTCAATTA	GAATGCTCTTTGAAAGTGTACCTTGGG	2956

QY	2041	TATCTGCTGAGGGTA	CTCAAGGGTACGCA	CAATGTGGCTCC	CACTGTGGTGT	2100	
Db	2957	TATCTGCTGAGGGTA	CTCAAGGGTACGCA	CAATGTGGCTCC	CACTGTGGTGT	3016	
QY	2101	CATGCTAGTAAAAA	CGGTGGCTGTGATT	AAGCATTA	CACTGTATGTGGCA	CTGCGAGA	2168
Db	3017	CATGCTAGTAAAAA	CGGTGGCTGTGATT	AAGCATTA	CACTGTATGTGGCA	CTGCGAGA	3076
QY	2161	CAGGGCTCTCA	GATGCTGACCTGT	CGGACGGCA	CTGTCACTGTCTG	AAACATTTCA	2222
Db	3077	CAGGGCTCTCA	GATGCTGACCTGT	CGGACGGCA	CTGTCACTGTCTG	AAACATTTCA	3138
QY	2221	CGTAGCCAGCA	CTCTCGCAAGGCT	GTGGCCAGTGT	TGAGCATACAT	ACTGACCCGCTG	2280
Db	3137	CGTAGCCAGCA	CTCTCGCAAGGCT	GTGGCCAGTGT	TGAGCATACAT	ACTGACCCGCTG	3198
QY	2281	TTCTTTCGATT	TGGGTAA	CAGAGAGGGGGT	GTTCCTTACCTTA	CCAAATGCAATTTGAGTCA	2340
Db	3197	TTCTTTCGATT	TGGGTAA	CAGAGAGGGGGT	GTTCCTTACCTTA	CCAAATGCAATTTGAGTCA	3256
QY	2341	CACCTAAGAT	TATTTGCTTGAG	CCCCGAGACAT	GTCCAAAGGTAA	CTGAAACGGGGTGTGGA	2400
Db	3257	CACCTAAGAT	TATTTGCTTGAG	CCCCGAGACAT	GTCCAAAGGTAA	CTGAAACGGGGTGTGGA	3316
QY	2401	CATGACCATGA	AAAGCTGGAAGGT	GTCTGAGGTAA	GTAGACCCGCA	CCAGAGTGCAGAC	2466
Db	3317	CATGACCATGA	AAAGCTGGAAGGT	GTCTGAGGTAA	GTAGACCCGCA	CCAGAGTGCAGAC	3376
QY	2461	CTGCGAGTGT	GCGGTAA	CAATATTAGAA	CCAGCCTGTGAT	GTGATGACCGAGA	2520
Db	3377	CTGCGAGTGT	GCGGTAA	CAATATTAGAA	CCAGCCTGTGAT	GTGATGACCGAGA	3438
QY	2521	GCTAAGCCGAT	CACTTGGTGTCTG	GCCTGCACCCGCGCT	GATTTGGCTCTTA	GCGATGA	2580
Db	3437	GCTAAGCCGAT	CACTTGGTGTCTG	GCCTGCACCCGCGCT	GATTTGGCTCTTA	GCGATGA	3496
QY	2581	AGATACAGATT	GAG	2594			
Db	3497	AGATACAGATT	GAG	3510			
RESULT 6							
US-09-244-752-1							
Sequence 1, Application US/09244752							
Patent No. 6063622							
GENERAL INFORMATION:							
APPLICANT: Chamberlain, Jeffrey S.							
APPLICANT: Amalfitano, Andrea							
APPLICANT: Hauser, Michael A.							
APPLICANT: Kumar-Singh, Rajendra							
APPLICANT: Hartigan-O'Connor, Dennis J.							
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS							
NUMBER OF SEQUENCES: 15							
CORRESPONDENCE ADDRESS:							
ADDRESSEE: Medlen & Carroll, LLP							
STREET: 220 Montgomery Street, Suite 2200							
CITY: San Francisco							
STATE: California							
COUNTRY: United States Of America							
ZIP: 94104							
COMPUTER READABLE FORM:							
MEDIUM TYPE: Floppy disk							
COMPUTER: IBM PC compatible							
OPERATING SYSTEM: PC-DOS/MS-DOS							
SOFTWARE: PatentIn Release #1.0, Version #1.30							
CURRENT APPLICATION DATA:							
APPLICATION NUMBER: US/09/244,752							
FILING DATE:							
CLASSIFICATION:							
PRIOR APPLICATION DATA:							
APPLICATION NUMBER: 08/735,609							
FILING DATE:							
ATTORNEY/AGENT INFORMATION:							

Query Match	100.0%	Score 2594	DB 3	Length 35935
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2594	Conservative 0	Mismatches 0	Indels 0	Gaps 0
NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40, 027 REFERENCE/DOCKET NUMBER: UM-02484 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410 TELEFAX: (415) 397-8338 INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 35935 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA" US-09-244-752-1				
QY	1	ATCATCTTACCTGCGACGAGGCTGGCTTTCCACCAGTACGACGAGATGAAGAGGT	60	
DB	917	ATCATCTTACCTGCGACGAGGCTGGCTTTCCACCAGTACGACGAGATGAAGAGGT	976	
QY	61	GAGAGTTTGGTTAGATTATGTGGAGACCCCGGGGCAOAGTTGACGCTTGTCAATT	120	
DB	977	GAGAGTTTGGTTAGATTATGTGGAGACCCCGGGGCAOAGTTGACGCTTGTCAATT	103	
QY	121	CACCGSAGGATACGGGGGAGCCGAGATTTATGTGTTGCTTTCCTATATGAGACTGT	180	
DB	1037	CACCGSAGGATACGGGGGAGCCGAGATTTATGTGTTGCTTTCCTATATGAGACTGT	109	
QY	181	GGCATGTTTGTCTACAGTAACTGAAAATTATGGGACGTGGTATGAGTGTGGGTTTG	240	
DB	1097	GGCATGTTTGTCTACAGTAACTGAAAATTATGGGACGTGGTATGAGTGTGGGTTTG	115	
QY	241	GTGTGATTAATTTTTTTTAAATTTTAAACAGTTTGTGCTTTAAAGAAATTTGTATTGCA	300	
DB	1157	GTGTGATTAATTTTTTTTAAATTTTAAACAGTTTGTGCTTTAAAGAAATTTGTATTGCA	121	
QY	301	TTTTTTTAAAGAGCTCGTGTCTGAACTGAGCCGAGCCGAGCCAGAACCGAGCCCTG	360	
DB	1217	TTTTTTTAAAGAGCTCGTGTCTGAACTGAGCCGAGCCGAGCCAGAACCGAGCCCTG	127	
QY	361	CAGACCTACCCGCGCTCTTAAATGGCGCTGCTATCTGAGACGCCGACATCACCTG	420	
DB	1277	CAGACCTACCCGCGCTCTTAAATGGCGCTGCTATCTGAGACGCCGACATCACCTG	133	
QY	421	TGTCATGAAATGCAATGTATGTAACGATAGCTGTGACTCCGCTCTTCTAACACACTC	480	
DB	1337	TGTCATGAAATGCAATGTATGTAACGATAGCTGTGACTCCGCTCTTCTAACACACTC	139	
QY	481	CTGAGATPACACCGCGTGTCCCGCTGCGCCCATTTAAACGATGGCGGTGAGATTTGGT	540	
DB	1397	CTGAGATPACACCGCGTGTCCCGCTGCGCCCATTTAAACGATGGCGGTGAGATTTGGT	145	
QY	541	GGCGTCCGACGCTGTGGATGTATTCAGAGACTTGCTTAAACGAGCCTGGCAACTTTGG	600	
DB	1457	GGCGTCCGACGCTGTGGATGTATTCAGAGACTTGCTTAAACGAGCCTGGCAACTTTGG	151	
QY	601	ACTTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATTTGCGTGTGGTTAA	660	
DB	1517	ACTTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATTTGCGTGTGGTTAA	157	
QY	661	CGCCTTTTGTTCCTGATGATTTGATGTAACTTTAAATPAAAGGTGAGATTAATGTTAACT	720	
DB	1577	CGCCTTTTGTTCCTGATGATTTGATGTAACTTTAAATPAAAGGTGAGATTAATGTTAACT	163	
QY	721	TGCATGGCGTGTAAATGGGGCGGGGCTTAAAGGGTATATATCGCGCTGAGCTTAATCT	780	
DB	1637	TGCATGGCGTGTAAATGGGGCGGGGCTTAAAGGGTATATATCGCGCTGAGCTTAATCT	169	
QY	781	TGCTTAACTTGAACCTCATGAGGCTTGGGAGTGTGGAAGATTTTTTCTGCTGTGCTGA	840	

```

Db      1697 TGGTACATCTGACCTCTACGAGGCTTGGAGTGTGTTGGAAAGATTTTCTCTGTGGCTA 1756
Qy      841 ACTTGCTGGAACAGAGCTCTAAACAGTACCTCTGTGTTTGAAGSTTTCTGTGGGCTCAT 900
Db      1757 ACTTGCTGGAACAGAGCTCTAAACAGTACCTCTGTGTTTGAAGSTTTCTGTGGGCTCAT 1816
Qy      901 CCCAGGCAAACTTGTGCTGCAAGATTTAGGAGGATTAAGTGGGAAATTGAAGGCTTT 960
Db      1817 CCCAGGCAAACTTGTGCTGCAAGATTTAGGAGGATTAAGTGGGAAATTGAAGGCTTT 1876
Qy      961 TGAATCCTGTGTGAGCTGTTTGAATCTTGAATCTGTGTCACAGGCGCTTTTCCAAAG 1020
Db      1877 TGAATCCTGTGTGAGCTGTTTGAATCTTGAATCTGTGTCACAGGCGCTTTTCCAAAG 1936
Qy      1021 AGAAGGTCAATAGACTTTGATTTTTCACACCGGGGCGGCTGTGGCTGTGCTT 1080
Db      1937 AGAAGGTCAATAGACTTTGATTTTTCACACCGGGGCGGCTGTGGCTGTGCTT 1996
Qy      1081 TTTGAGTTTATTAAGGATTAATGAGAGCAAGAAACCATCTGAGCGGGGGTTACCTGC 1140
Db      1997 TTTGAGTTTATTAAGGATTAATGAGAGCAAGAAACCATCTGAGCGGGGGTTACCTGC 2056
Qy      1141 TGGATTTTCTGCGCATGTGATCTGTGAGAGCGGTTGTGAGACACAAAGATGCTGTAC 1200
Db      2057 TGGATTTTCTGCGCATGTGATCTGTGAGAGCGGTTGTGAGACACAAAGATGCTGTAC 2116
Qy      1201 TGTGTCTTCCGTCGCGCCCGGAGTAATACCGACGAGAGACAGACAGACAGAGAGG 1260
Db      2117 TGTGTCTTCCGTCGCGCCCGGAGTAATACCGACGAGAGACAGACAGACAGAGAGG 2176
Qy      1261 AAGCAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 1320
Db      2177 AAGCAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 2236
Qy      1321 GGGATGATGTTGTATCAGGTGTGTAACCTGTATCAGAACTGAGACGCAATTTTGAACAAT 1380
Db      2237 GGGATGATGTTGTATCAGGTGTGTAACCTGTATCAGAACTGAGACGCAATTTTGAACAAT 2296
Qy      1381 TACAGAGATGGGCGAGGGGCTTAAGAGGGGTTAAAGGGAGCGGGGGCTTGTGAGGCTAC 1440
Db      2297 TACAGAGATGGGCGAGGGGCTTAAGAGGGGTTAAAGGGAGCGGGGGCTTGTGAGGCTAC 2356
Qy      1441 AGAGAGGCTAGGATCTAGCTTTTAACTTATATGACAGACAGCGTCTGTGATTTAC 1500
Db      2357 AGAGAGGCTAGGATCTAGCTTTTAACTTATATGACAGACAGCGTCTGTGATTTAC 2416
Qy      1501 TTTTCAACAGATCAAGATTAATGGCTTAATGAGCTTATGAGCTTGTGCGCAGAAATATTC 1560
Db      2417 TTTTCAACAGATCAAGATTAATGGCTTAATGAGCTTATGAGCTTGTGCGCAGAAATATTC 2476
Qy      1561 CATAGAGAGCTGACCACTTACTGTGCTGACAGCCAGGGGATGATTTTGAAGGCTATTAG 1620
Db      2477 CATAGAGAGCTGACCACTTACTGTGCTGACAGCCAGGGGATGATTTTGAAGGCTATTAG 2536
Qy      1621 GGTATATCAAAAGGTGGCACTTAAAGCCAGATTTGCAAGATCAAGATCAAGCAATTTGTAAA 1680
Db      2537 GGTATATCAAAAGGTGGCACTTAAAGCCAGATTTGCAAGATCAAGATCAAGCAATTTGTAAA 2596
Qy      1681 TATCAGGAATTTGTGCTACATTTCTGGGAGCGGGGCGAGGTGAGATAGTACGGAAGA 1740
Db      2597 TATCAGGAATTTGTGCTACATTTCTGGGAGCGGGGCGAGGTGAGATAGTACGGAAGA 2656
Qy      1741 TAGGCTGCGCTTTAGATAGTACATGATTAATATGAGCGGGGGGCTTGGCATGAGACGG 1800
Db      2657 TAGGCTGCGCTTTAGATAGTACATGATTAATATGAGCGGGGGGCTTGGCATGAGACGG 2716
Qy      1801 GGTGTTATTAATGATTAAGGTTTACTGCGCCCAATTTTATGCGGTTACGTTTCTGCGC 1860
Db      2717 GGTGTTATTAATGATTAAGGTTTACTGCGCCCAATTTTATGCGGTTACGTTTCTGCGC 2776
Qy      1861 CAATACCAACCTTATCTTACACGAGTGAAGCTTCTATGAGGTTTAACAATACCTGTGGA 1920

```

```

Db      2777 CAATACCAACCTTATCTTACACGAGTGAAGCTTCTATGAGGTTTAAACATACCTGTGGA 2836
Qy      1921 AGCTGGAACGATGTAAGGTTGCGGGCTGTGCTTTTATCTGTCTGTGGAAGGGGGTGT 1980
Db      2837 AGCTGGAACGATGTAAGGTTGCGGGCTGTGCTTTTATCTGTCTGTGGAAGGGGGTGT 2896
Qy      1981 GTGTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGG 2040
Db      2897 GTGTGCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGG 2956
Qy      2041 TATCTGTCTGAAGGTAATCTTCAAGGTTGCGCCCAATGTGCGCTTCCGACTGTGTGCTT 2100
Db      2957 TATCTGTCTGAAGGTAATCTTCAAGGTTGCGCCCAATGTGCGCTTCCGACTGTGTGCTT 3016
Qy      2101 CATCTAGTGAAGGCTGTGCTGTGATTTAAGCATTAATGATATGTGGCACTGCGAGA 2160
Db      3017 CATCTAGTGAAGGCTGTGCTGTGATTTAAGCATTAATGATATGTGGCACTGCGAGA 3076
Qy      2161 CAGGCGCTCTCAGATGCTGACCTGTGAGAGCGGCACTGTCACTGTGAGAGACATTTCA 2220
Db      3077 CAGGCGCTCTCAGATGCTGACCTGTGAGAGCGGCACTGTCACTGTGAGAGACATTTCA 3136
Qy      2221 CGTAGCCAGCCACTCTGCAAGGCTGTGCGCAAGTTTGAAGCATTAATCTGACCCGCTG 2280
Db      3137 CGTAGCCAGCCACTCTGCAAGGCTGTGCGCAAGTTTGAAGCATTAATCTGACCCGCTG 3196
Qy      2281 TTCTTGTGATTTGGGTAAACAGAGAGGGGGTCTTCTACCTTAACAAATGCAATTTGAGTCA 2340
Db      3197 TTCTTGTGATTTGGGTAAACAGAGAGGGGGTCTTCTACCTTAACAAATGCAATTTGAGTCA 3256
Qy      2341 CACTAAGATATTTGCTTGAAGCCGAGAGCATGTCCAAAGTGAACCTGAAACGAGGAGTTTGA 2400
Db      3257 CACTAAGATATTTGCTTGAAGCCGAGAGCATGTCCAAAGTGAACCTGAAACGAGGAGTTTGA 3316
Qy      2401 CATGACCATGAAGATCTGAAGAGGTGTGAGGTAAGATGAGACCCGACAGGTGCAAGCC 2460
Db      3317 CATGACCATGAAGATCTGAAGAGGTGTGAGGTAAGATGAGACCCGACAGGTGCAAGCC 3376
Qy      2461 CTGCGAGTGTGCGGCTTAACATATTAAGAAACAGCCCTGTGATGCTGATGTGACCGAGA 2520
Db      3377 CTGCGAGTGTGCGGCTTAACATATTAAGAAACAGCCCTGTGATGCTGATGTGACCGAGA 3436
Qy      2521 GCTGAGCCCGCATCACTTGGGTGTGCGCTGTGACCCGCGCTGAGTTTGGCTTACGATGA 2580
Db      3437 GCTGAGCCCGCATCACTTGGGTGTGCGCTGTGACCCGCGCTGAGTTTGGCTTACGATGA 3496
Qy      2581 AGATACAGATTGAG 2594
Db      3497 AGATACAGATTGAG 3510

```

```

RESULT 7
US-09-245-497-1
; Sequence 1, Application US/09245497
; Patent No. 6083750
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Amalfitano, Andrea
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
; APPLICANT: Hartigan-O'Connor, Dennis J.
; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/245,497
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
APPLICATION NUMBER: FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-245-497-1

Query Match 100.0%; Score 2594; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATTCATCTTACTGCGCAGAGCGTGGCTTTCCACCCCATGACAGAGAGATGAAAGGCT 60
Db 917 ATTCATCTTACTGCGCAGAGCGTGGCTTTCCACCCCATGACAGAGAGATGAAAGGCT 976
Qy 61 GAGGAGTTTGTGTTAGATTATGTGAGACACCCCGGACGTTGAGGCTTGTCAATTAT 120
Db 977 GAGGAGTTTGTGTTAGATTATGTGAGACACCCCGGACGTTGAGGCTTGTCAATTAT 1036
Qy 121 CACCGAGAGAAATACGGGGAGACCCAGATATATATGTTGCTTTGCTATATAGAGACTGT 180
Db 1037 CACCGAGAGAAATACGGGGAGACCCAGATATATATGTTGCTTTGCTATATAGAGACTGT 1096
Qy 181 GGCATGTTTGTCTACAGTAAGTAAATTTATGCGAGTGGGTATGATGATGATGATG 240
Db 1097 GGCATGTTTGTCTACAGTAAGTAAATTTATGCGAGTGGGTATGATGATGATGATG 1156
Qy 241 GTGATGTAATTTTATTTTATTTTATTTTACAGTTTGTGTTTAAAGATTTTGTATTTGA 300
Db 1157 GTGATGTAATTTTATTTTATTTTATTTTACAGTTTGTGTTTAAAGATTTTGTATTTGA 1216
Qy 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCCGAGCCGAGACCGAGAGCTTG 360
Db 1217 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCCGAGCCGAGACCGAGAGCTTG 1276
Qy 361 CAAGACCTACCCCGCTCTTAAATGCGGCTGCTATCTTGAAGCCCGACATCACTG 420
Db 1277 CAAGACCTACCCCGCTCTTAAATGCGGCTGCTATCTTGAAGCCCGACATCACTG 1336
Qy 421 TGTCTAGAGATGCAATAGTAGTAGAGATGAGTAGTGTGATCTCGGCTCTTCAACACCTC 480
Db 1337 TGTCTAGAGATGCAATAGTAGTAGAGATGAGTAGTGTGATCTCGGCTCTTCAACACCTC 1396
Qy 481 CTGAGATACACCCGGTGTCTCCGCTGTGCCCATTTAAACAAGTTGCGTGTGAGAGTTG 540
Db 1397 CTGAGATACACCCGGTGTCTCCGCTGTGCCCATTTAAACAAGTTGCGTGTGAGAGTTG 1456
Qy 541 GCGCGTCGCAAGCTCTGGAATGTATCGAGAGACTTGAAGAGCTGGGCAACTTTGG 600
Db 1457 GCGCGTCGCAAGCTCTGGAATGTATCGAGAGACTTGAAGAGCTGGGCAACTTTGG 1516
Qy 601 ACTTGAGCTGTAAACGCCACAGGCCATTAAGGTGTAAACCTGTGATTTGGGTGTGTAA 660
Db 1517 ACTTGAGCTGTAAACGCCACAGGCCATTAAGGTGTAAACCTGTGATTTGGGTGTGTAA 1576

Qy 661 GCGCTTTGTTGCTGAATGAGTGTATGTAAGTTTAAAGAGGTGAGATTAATGTTAACT 720
Db 1577 GCGCTTTGTTGCTGAATGAGTGTATGTAAGTTTAAAGAGGTGAGATTAATGTTAACT 1636
Qy 721 TGCAATGGGTGTAAATGAGGCGGGGCTTAAAGGTAATATATGCGCGGTGGGCTAACT 780
Db 1637 TGCAATGGGTGTAAATGAGGCGGGGCTTAAAGGTAATATATGCGCGGTGGGCTAACT 1696
Qy 781 TGCTTACATCTGACCTCAGAGAGCTTGGAGTGTGGAAGATTTTCTGCTGCGCTA 840
Db 1697 TGCTTACATCTGACCTCAGAGAGCTTGGAGTGTGGAAGATTTTCTGCTGCGCTA 1756
Qy 841 ACTTGCTGGAACAGAGCTCTAACAGTACCTTTGTTGAGGTTTGTGGGCTCAT 900
Db 1757 ACTTGCTGGAACAGAGCTCTAACAGTACCTTTGTTGAGGTTTGTGGGCTCAT 1816
Qy 901 CCGAGGCAAGTTAGTCTGCAAGATTAAGAGATTAACAAGTGGGAATTTGAAGCTTT 960
Db 1817 CCGAGGCAAGTTAGTCTGCAAGATTAAGAGATTAACAAGTGGGAATTTGAAGCTTT 1876
Qy 961 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGAGTCAACAGGCGCTTTTCAAG 1020
Db 1877 TGAATCTGTGTGAGCTGTTGATTTCTTGAATCTGAGTCAACAGGCGCTTTTCAAG 1936
Qy 1021 AGAAGTCAATCAAGACTTTGGAATTTTCCACACCGGGGCGGCTGCGCTGTGCTT 1080
Db 1937 AGAAGTCAATCAAGACTTTGGAATTTTCCACACCGGGGCGGCTGCGCTGTGCTT 1996
Qy 1081 TTTTGAATTTATTAAGGATTAAGAGCGGAAGAACCACTGAGCGGGGGGTAACTGCG 1140
Db 1997 TTTTGAATTTATTAAGGATTAAGAGCGGAAGAACCACTGAGCGGGGGGTAACTGCG 2056
Qy 1141 TGATTTTCTGCGCATGATCTGTGAGAGCGGTTGTGAGACACAAGATGCTGTCTAC 1200
Db 2057 TGATTTTCTGCGCATGATCTGTGAGAGCGGTTGTGAGACACAAGATGCTGTCTAC 2116
Qy 1201 TGTGTCTTCCGTCGCGCGCGCATTAATCCAGAGAGACAGACAGACAGACAGAGG 1260
Db 2117 TGTGTCTTCCGTCGCGCGCGCATTAATCCAGAGAGACAGACAGACAGACAGAGG 2176
Qy 1261 AAGCAGCGCGCGCGAGAGAGAGCCCATGGAACCCGAGAGCGGCGCTGAGACCTC 1320
Db 2177 AAGCAGCGCGCGCGAGAGAGAGCCCATGGAACCCGAGAGCGGCGCTGAGACCTC 2236
Qy 1321 GGAATGATTTGTGTAAGTGTGCTGAACCTGTATCCAGACTGAGACGATTTTGACAT 1380
Db 2237 GGAATGATTTGTGTAAGTGTGCTGAACCTGTATCCAGACTGAGACGATTTTGACAT 2296
Qy 1381 TACAGAGATGGGCAAGGGGCTTAAAGGGGTAAAGAGGAGCGGGGGCTGTGAGGCTAC 1440
Db 2297 TACAGAGATGGGCAAGGGGCTTAAAGGGGTAAAGAGGAGCGGGGGCTGTGAGGCTAC 2356
Qy 1441 AGAGAGGCTTGAAGATCTAGCTTTTACCTTAATGACAGACACGCTGTGATGATTAAC 1500
Db 2357 AGAGAGGCTTGAAGATCTAGCTTTTACCTTAATGACAGACACGCTGTGATGATTAAC 2416
Qy 1501 TTTTCAACAGATCAAGATTAATTCGCTTAATGAGCTTGTGCGGCGAGAATATTC 1560
Db 2417 TTTTCAACAGATCAAGATTAATTCGCTTAATGAGCTTGTGCGGCGAGAATATTC 2476
Qy 1561 CATAGAGAGCTGACCACTTAAGCTGTGACGCGAGGGGATATTTTGGAGGCTAATTAG 1620
Db 2477 CATAGAGAGCTGACCACTTAAGCTGTGACGCGAGGGGATATTTTGGAGGCTAATTAG 2536
Qy 1621 GGTATATGCAAAAGGTGCACTTAGCCAGATTGCAAGTACCAAGTCCGAAACTTGTAA 1680
Db 2537 GGTATATGCAAAAGGTGCACTTAGCCAGATTGCAAGTACCAAGTCCGAAACTTGTAA 2596
Qy 1681 TATCAGGAATTTGTTGCTACATTTCTGGAACCGGGCCGAGGTGAGATGATACGAGGA 1740
Db 2597 TATCAGGAATTTGTTGCTACATTTCTGGAACCGGGCCGAGGTGAGATGATACGAGGA 2656

QY	1741	TAGGGTGGCCCTTTAGATGATACATGATATAATATGTGGCGGGGGGTGCTGGCAATGACG	1800
Db	2557	TAGGGTGGCCCTTTAGATGATACATGATATAATATGTGGCGGGGGGTGCTGGCAATGACG	2716
QY	1801	GGTGGTATATATGATGATGTAAGGTTTACTGTGCCCCCAATTTTATAGCGGTACGGTTTTCTTGCC	1860
Db	2717	GGTGGTATATATGATGATGTAAGGTTTACTGTGCCCCCAATTTTATAGCGGTACGGTTTTCTTGCC	2776
QY	1861	CAATACCAACCTTATCCACACGGGTATAGCTTATATGGGTTTAAACAATACCTGTGGGA	1920
Db	2777	CAATACCAACCTTATCCACACGGGTATAGCTTATATGGGTTTAAACAATACCTGTGTGGA	2836
QY	1921	AGCCTGGAACCGATGTAAAGGTTTCGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGGT	1980
Db	2837	AGCCTGGAACCGATGTAAAGGTTTCGGGCTGTGCTTTTACTGCTGTGGAAGGGGGTGGT	2896
QY	1981	GTGTGCGCCCAAAAGCAGGCGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGGG	2040
Db	2897	GTGTGCGCCCAAAAGCAGGCGCTTCAATTAAGAAATGCTCTTTGAAAGGTATACCTTGGG	2956
QY	2041	TATCCTGTCTGAGGGTAACTCAGGGGTGCGCAACAATGTGACTCCGACTGTGGTGGCTT	2100
Db	2957	TATCCTGTCTGAGGGTAACTCAGGGGTGCGCAACAATGTGACTCCGACTGTGGTGGCTT	3016
QY	2101	CATGCTAGTAAAAAGCGTGTGTGATTAAGCATATACATGTATGTGGCAACTCGCAGGA	2160
Db	3017	CATGCTAGTAAAAAGCGTGTGTGATTAAGCATATACATGTATGTGGCAACTCGCAGGA	3076
QY	2161	CAGGGGCTCTGAGATGCTGACCTGTGTGGGAAGGCAACTGTACCTGTGGAAGACATTTCA	2220
Db	3077	CAGGGGCTCTGAGATGCTGACCTGTGTGGGAAGGCAACTGTACCTGTGGAAGACATTTCA	3136
QY	2221	CGTACGACGACCACTCTGTGCAAGGCGCTGTGCAAGTGTGGAAGCATATACATGACCCGCTG	2280
Db	3137	CGTACGACGACCACTCTGTGCAAGGCGCTGTGCAAGTGTGGAAGCATATACATGACCCGCTG	3196
QY	2281	TTCTCTTGATTTTGGGGTAAACAGAGGGGGGTGTTCTTACCTTAACAATGCCATTTTGAATCA	2340
Db	3197	TTCTCTTGATTTTGGGGTAAACAGAGGGGGGTGTTCTTACCTTAACAATGCCATTTTGAATCA	3256
QY	2341	CACCTAAGATATTTGGTTTGAAGCCGAGAGCATGTCCAAGGTGAACCTGGAACGGGGTGTGTA	2400
Db	3257	CACCTAAGATATTTGGTTTGAAGCCGAGAGCATGTCCAAGGTGAACCTGGAACGGGGTGTGTA	3316
QY	2401	CATGACCATGAAGATCTGGAAGGTGTGAGGTATGATGACACCCGACACAGGTGACAC	2460
Db	3317	CATGACCATGAAGATCTGGAAGGTGTGAGGTATGATGACACCCGACACAGGTGACAC	3376
QY	2461	CTGCGAGGTGTGCGGGTAAACATATTTAGGAACAGCGTGTGATGTGCGATGTGAACGAGGA	2520
Db	3377	CTGCGAGGTGTGCGGGTAAACATATTTAGGAACAGCGTGTGATGTGCGATGTGAACGAGGA	3436
QY	2521	GCTGAGGCCCGATCACTTGTGTGCTGTGACCCGCGCTGAGTTTGGCTCTAGACGATGA	2580
Db	3437	GCTGAGGCCCGATCACTTGTGTGCTGTGACCCGCGCTGAGTTTGGCTCTAGACGATGA	3496
QY	2581	AGATACAGATTTGAG 2594	
Db	3497	AGATACAGATTTGAG 3510	
RESULT 8			
US-09-409-670-43			
Sequence 43, Application US/09409670			
Patent No. 6133028			
GENERAL INFORMATION:			
APPLICANT: IMLER, Jean-Luc			
APPLICANT: MEHTALI, Majid			
APPLICANT: PAVIRANI, Andrea			
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING			
TITLE OF INVENTION: COMPLEMENTATION LINES			
NUMBER OF SEQUENCES: 43			
CORRESPONDENCE ADDRESSES:			

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,670
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/379,452
FILING DATE: 26-JAN-1995
APPLICATION NUMBER: WO PCT/FR94/00624
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 029395-002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-409-670-43

Query Match	Similarity	Score	DB	Length
Match Local Similarity	100.0%	Pred. No. 0;		
Matches 2594;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	ATCGATCTTACCTGCGCACGAGGCTGCTTCCACCAGTAGCAGCAGATGAAGGGT	60	
Db	917	ATCGATCTTACCTGCGCACGAGGCTGCTTCCACCAGTAGCAGCAGATGAAGGGT	976	
Qy	61	GAGGAGTTTGTTAGATTATGTGGACACCCCGGACGAGTTGCAGTCTTGTCAATT	120	
Db	977	GAGGAGTTTGTTAGATTATGTGGACACCCCGGACGAGTTGCAGTCTTGTCAATT	1036	
Qy	121	CACCGGAGAAATACGGGGGACCCAGAAATTAATGTGTTGCTTATAGAGAACTGT	180	
Db	1037	CACCGGAGAAATACGGGGGACCCAGAAATTAATGTGTTGCTTATAGAGAACTGT	1096	
Qy	181	GGCATGTTTGTCTACAGTAAGTAAATTAATGGGCACTGGGTGATAGAGTGGGTTTG	240	
Db	1097	GGCATGTTTGTCTACAGTAAGTAAATTAATGGGCACTGGGTGATAGAGTGGGTTTG	1156	
Qy	241	GTGTGTAATTTTTTTTTTAATTTTACAGTTTGTGTAAAGAAATTTGTATTGTGA	300	
Db	1157	GTGTGTAATTTTTTTTTTAATTTTACAGTTTGTGTAAAGAAATTTGTATTGTGA	1216	
Qy	301	TTTTTTTTTAAAGGTCTGTGTCTGGAACCTGAGCTGAGCCGACCGAACCAGAGCTG	360	
Db	1217	TTTTTTTTTAAAGGTCTGTGTCTGGAACCTGAGCTGAGCCGACCGAACCAGAGCTG	1276	
Qy	361	CAAGACCTACCCGCGCTTAAATGGCGGCTGATCTGAGAGCGCCGACATCACTG	420	
Db	1277	CAAGACCTACCCGCGCTTAAATGGCGGCTGATCTGAGAGCGCCGACATCACTG	1336	
Qy	421	TGTTTAAGAAATGCAATAGTAGTACGATAGCTGTGACTCGGTCCTTCTTAACAACCTC	480	
Db	1337	TGTTTAAGAAATGCAATAGTAGTACGATAGCTGTGACTCGGTCCTTCTTAACAACCTC	1396	
Qy	481	CTGAGATACACCGGTGTCCTCGCTGTGCCCATTTAAACAGTTGCCGTGAGAGTTGGT	540	

Db 1397 CTGAGATACACCCGGTGGTCCCGCTGTGCCCATTTAAACCACTGCGCGTAAGTGGG 1456
Qy 541 GCGGTGCGCAGGCTGTGAAATGTATCGAGGACTTGTAAACGAGCTGGGCAACCTTTGG 600
Db 1457 GCGGTGCGCAGGCTGTGAAATGTATCGAGGACTTGTAAACGAGCTGGGCAACCTTTGG 1516
Qy 601 ACTTACGCTGTAAAGGCCCCAGGCCATTAAGGTGTAAACCTGTGATTTGGCTGTGTGTTAA 660
Db 1517 ACTTACGCTGTAAAGGCCCCAGGCCATTAAGGTGTAAACCTGTGATTTGGCTGTGTGTTAA 1576
Qy 661 CGCCTTTGTTTCTGAAATGATTTGATTTGATTTAAAGGGTGAAGATATGTTAACT 720
Db 1577 CGCCTTTGTTTCTGAAATGATTTGATTTGATTTAAAGGGTGAAGATATGTTAACT 1636
Qy 721 TGCATGCGGTGTAAATGGGCGGGGCTTAAAGGGTATATATGCGCGGTGGCTAACT 780
Db 1637 TGCATGCGGTGTAAATGGGCGGGGCTTAAAGGGTATATATGCGCGGTGGCTAACT 1696
Qy 781 TGGTTACATCTGACCTCATGAGGCTTGGGAGTGTGGAAGATTTTCTGTGTGCGTA 840
Db 1697 TGGTTACATCTGACCTCATGAGGCTTGGGAGTGTGGAAGATTTTCTGTGTGCGTA 1756
Qy 841 ACTTCTGGAACAGAGCTCTAACAGTACTCTTGGTTTGGAGTTTCTGTGTGGGCTCAT 900
Db 1757 ACTTCTGGAACAGAGCTCTAACAGTACTCTTGGTTTGGAGTTTCTGTGTGGGCTCAT 1816
Qy 901 CCCAGGCAAAAGTTAGTCTGCAAGATTTAAAGAGATTTAAAGTGGAAATTTGAAGAGCTTT 960
Db 1817 CCCAGGCAAAAGTTAGTCTGCAAGATTTAAAGAGATTTAAAGTGGAAATTTGAAGAGCTTT 1876
Qy 961 TGAATCTCTGTGTAGCTGTGTTGATTTCTTGAATCTGGGTCAACAAGGCGCTTTTCCAG 1020
Db 1877 TGAATCTCTGTGTAGCTGTGTTGATTTCTTGAATCTGGGTCAACAAGGCGCTTTTCCAG 1936
Qy 1021 AGAAGGTCATCAAGACTTTGATTTTTCACACGCGGGGCGGCTGGCTGTGTGCTT 1080
Db 1937 AGAAGGTCATCAAGACTTTGATTTTTCACACGCGGGGCGGCTGGCTGTGTGCTT 1996
Qy 1081 TTTTGAAGTTTATTAAGATTAATGAGAGCAAGAACCCATCTGAGCGGGGGTAACTGTC 1140
Db 1997 TTTTGAAGTTTATTAAGATTAATGAGAGCAAGAACCCATCTGAGCGGGGGTAACTGTC 2056
Qy 1141 TGGATTTTCTGGCCATGCTGTGTGAGAGCGGTTGTGAGACAAAGATGCGCTGTAC 1200
Db 2057 TGGATTTTCTGGCCATGCTGTGTGAGAGCGGTTGTGAGACAAAGATGCGCTGTAC 2116
Qy 1201 TGTGTCTTCCGTCGCGCCGCGGATTAACGAGCGGAGGAGCAGAGCAGAGCAGAGG 1260
Db 2117 TGTGTCTTCCGTCGCGCCGCGGATTAACGAGCGGAGGAGCAGAGCAGAGCAGAGG 2176
Qy 1261 AAGCCAGCGCGCGGAGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGACCTTC 1320
Db 2177 AAGCCAGCGCGCGGAGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGACCTTC 2236
Qy 1321 GGGAAATGATTTGTAACAGTGTGCTGAACTGTATCAAGACTGAGACCCATTTTGAACAT 1380
Db 2237 GGGAAATGATTTGTAACAGTGTGCTGAACTGTATCAAGACTGAGACCCATTTTGAACAT 2296
Qy 1381 TACAGAGATGGGCGGGGCTTAAAGGGGTAAAGGGAGCGGGGGGCTTGGAGGCTAC 1440
Db 2297 TACAGAGATGGGCGGGGCTTAAAGGGGTAAAGGGAGCGGGGGGCTTGGAGGCTAC 2356
Qy 1441 AGAGAGGCTAGGAATCTAGCTTTAGCTTAAATGACAGACCCGCTCTGATGTATTAAC 1500
Db 2357 AGAGAGGCTAGGAATCTAGCTTTAGCTTAAATGACAGACCCGCTCTGATGTATTAAC 2416
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTTAATGAGCTTGAATCTGCTGCGGCGAGAGTATTC 1560
Db 2417 TTTTCAACAGATCAAGATTAATGCGCTTAATGAGCTTGAATCTGCTGCGGCGAGAGTATTC 2476
Qy 1561 CATAGAGCAGCTGACCACTTAAGCTGAGCAGAGGAGTATTTTGAAGAGGCTATTAG 1620

Db 2477 CATAGAGCAGCTGACCACTTAAGCTGAGCAGAGGAGTATTTTGAAGAGGCTATTAG 2536
Qy 1621 GGTATATGCAAAAGGTGGCACTTAGGCCAGATTTGCAAGATCAAGATCAAGAACTTTGTA 1680
Db 2537 GGTATATGCAAAAGGTGGCACTTAGGCCAGATTTGCAAGATCAAGATCAAGAACTTTGTA 2596
Qy 1681 TATCAGAAATTTGCTATCAATTTCTGGGAGACGGGGCCGAGGTGAGATATGATACGAGGA 1740
Db 2597 TATCAGAAATTTGCTATCAATTTCTGGGAGACGGGGCCGAGGTGAGATATGATACGAGGA 2656
Qy 1741 TAGGGTGGCTTTAGATGTAGATGATATATATATGAGCGGGGGGCTTGGCATGAGAGG 1800
Db 2657 TAGGGTGGCTTTAGATGTAGATGATATATATATGAGCGGGGGGCTTGGCATGAGAGG 2716
Qy 1801 GGTGTATATTAATGATGTAGAGTTTACTGGCCCAATTTTAAAGCGGTATTCCTGGC 1860
Db 2717 GGTGTATATTAATGATGTAGAGTTTACTGGCCCAATTTTAAAGCGGTATTCCTGGC 2776
Qy 1861 CAATACCAACCTTATCTTACACGCTGTAGCTTATAGGTTTAAACAATACCTGTGTGA 1920
Db 2777 CAATACCAACCTTATCTTACACGCTGTAGCTTATAGGTTTAAACAATACCTGTGTGA 2836
Qy 1921 AGCTGAGCCGATGTAAAGGTTGCGGGGCTTGGCTTTTACTGTGCTGAGAGGGGCTGT 1980
Db 2837 AGCTGAGCCGATGTAAAGGTTGCGGGGCTTGGCTTTTACTGTGCTGAGAGGGGCTGT 2896
Qy 1981 GTGTGCCCCCAAAAGCAGGGGCTTCAATTAAGAAATGCCCTTTTGAAGGTGTACCTTGGG 2040
Db 2897 GTGTGCCCCCAAAAGCAGGGGCTTCAATTAAGAAATGCCCTTTTGAAGGTGTACCTTGGG 2956
Qy 2041 TATCTGTCTAGAGGTAACTCAAGGTGCGGCAATGTGCTTCCATCTGTGTGCTT 2100
Db 2957 TATCTGTCTAGAGGTAACTCAAGGTGCGGCAATGTGCTTCCATCTGTGTGCTT 3016
Qy 2101 CATGTAGTGAAGGCGGTGCTGTATTAAGCATTAACATGATATGTGCAATCTGAGAGA 2160
Db 3017 CATGTAGTGAAGGCGGTGCTGTATTAAGCATTAACATGATATGTGCAATCTGAGAGA 3076
Qy 2161 CAGGGGCTCTGAGATGCTGACCTGTGAGCGGCACTGTCACTGTGAGAACCATTTCA 2220
Db 3077 CAGGGGCTCTGAGATGCTGACCTGTGAGCGGCACTGTCACTGTGAGAACCATTTCA 3136
Qy 2221 CGTAGCCAGCCACTCTGCGCAAGGCTGTGCGAGGTGTTGAGATTAACATCTGACCCGCTG 2280
Db 3137 CGTAGCCAGCCACTCTGCGCAAGGCTGTGCGAGGTGTTGAGATTAACATCTGACCCGCTG 3196
Qy 2281 TTCCTGTATTTGGGTAAACAGAGAGGGGGGTGTTCTTACCTTAACCAATGCAATTTGAGTCA 2340
Db 3197 TTCCTGTATTTGGGTAAACAGAGAGGGGGGTGTTCTTACCTTAACCAATGCAATTTGAGTCA 3256
Qy 2341 CACTAAGATATTTGCTTGAAGCCGAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGGA 2400
Db 3257 CACTAAGATATTTGCTTGAAGCCGAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGGA 3316
Qy 2401 CATACCATTAAGATCTGGAAGGTGCTGAGGTATGATGAGACCCGCAACAGGTGACAGCC 2460
Db 3317 CATACCATTAAGATCTGGAAGGTGCTGAGGTATGATGAGACCCGCAACAGGTGACAGCC 3376
Qy 2461 CTGCGAGTGTGGGGGTAAACATATTAGGAACCACTGTGATGTGATGTCGAGCCGAGGA 2520
Db 3377 CTGCGAGTGTGGGGGTAAACATATTAGGAACCACTGTGATGTGATGTCGAGTCGAGGA 3436
Qy 2521 GCTGAGGCCCGATCACTTGTGCTGAGCTGTGACCCGCGCTGAGTTTGGCTTACGATGA 2580
Db 3437 GCTGAGGCCCGATCACTTGTGCTGAGCTGTGACCCGCGCTGAGTTTGGCTTACGATGA 3496
Qy 2581 AGATACAGATTGAG 2594
Db 3497 AGATACAGATTGAG 3510

RESULT 9
US-09-562-919-1

Sequence 1, Application US/09562919
Patent No. 6451596
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
Amalitano, Andrea
Hauser, Michael A.
Kumar-Singh, Rajendra
Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/562,919
FILING DATE: 02-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-562-919-1
Query Match 100.0%; Score 2594; DB 3; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCATCTTACTCGCAGAGGCTGGCTTTCCACCCCATGACGAGAGATGAAAGGCT 60
DB 917 ATCGATCTTACTCGCAGAGGCTGGCTTTCCACCCCATGACGAGAGATGAAAGGCT 976
QY 61 GAGAGATTGTTGATGATTATGAGACACCCCGGACAGGTTGACGGCTTGTCAATTAT 120
DB 977 GAGAGATTGTTGATGATTATGAGACACCCCGGACAGGTTGACGGCTTGTCAATTAT 1036
QY 121 CACCGAGAGATACCGGGGACCCAGATATTATGTTGCTTGTCTATATAGAGACTGT 180
DB 1037 CACCGAGAGATACCGGGGACCCAGATATTATGTTGCTTGTCTATATAGAGACTGT 1096
QY 181 GGCATGTTTGTCTAAGTAAGTAAATTATAGGAGAGTGGTGAATGAGTGGCTTGG 240
DB 1097 GGCATGTTTGTCTAAGTAAGTAAATTATAGGAGAGTGGTGAATGAGTGGCTTGG 1156
QY 241 GTGTGTAATTTTTTTTAAATTTTAAAGTTTGTGTTAAAGATTTTGTATTTGA 300
DB 1157 GTGTGTAATTTTTTTTAAATTTTAAAGTTTGTGTTAAAGATTTTGTATTTGA 1216
QY 301 TTTTAAAAAGTCTGTGTGAACCTGAGCTGAGCCCGAGCCGAGAACCGAGCCTG 360

DB 1217 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCCGAGCCAGAACCGAGCCTG 1276
QY 361 CAAGACTTACCCCGCCGCTTAAATGCGGCTGTATCTGAGAGCGCCGACATCACCTG 420
DB 1277 CAAGACTTACCCCGCCGCTTAAATGCGGCTGTATCTGAGAGCGCCGACATCACCTG 1336
QY 421 TGCTAGAGATGCAATAGTATGATGAGATAGCTGTGACTCGCGCTCTTCAACACACTC 480
DB 1337 TGCTAGAGATGCAATAGTATGATGAGATAGCTGTGACTCGCGCTCTTCAACACACTC 1396
QY 481 CTGAGATPACACCCGGTGTCCCGCTGTGCCCATTTAAACAATTGCCGTGAGAGTTGG 540
DB 1397 CTGAGATPACACCCGGTGTCCCGCTGTGCCCATTTAAACAAGTCCGTGAGAGTTGG 1456
QY 541 GCGCTGCCAGGCTGTGGAATGTATGAGAGCTTGCTTACGAGCCGCGCAACTTTGG 600
DB 1457 GCGCTGCCAGGCTGTGGAATGTATGAGAGCTTGCTTACGAGCCGCGCAACTTTGG 1516
QY 601 ACTTGAAGCTGTAAACGCCAGGCCATAGGTGTAAACCTGTGATTGCGTGTGTTAA 660
DB 1517 ACTTGAAGCTGTAAACGCCAGGCCATAGGTGTAAACCTGTGATTGCGTGTGTTAA 1576
QY 661 CGCCTTGTGTTGCTGAATGATGATGATTAATTAAGGCTGAGATTAATTTAACT 720
DB 1577 CGCCTTGTGTTGCTGAATGATGATGATTAATTAAGGCTGAGATTAATTTAACT 1636
QY 721 TGCAATGCGGTGTTAAATGCGGCGGCTTAAAGGGTATTAATGCGCGGTAACT 780
DB 1637 TGCAATGCGGTGTTAAATGCGGCGGCTTAAAGGGTATTAATGCGCGGTAACT 1696
QY 781 TGCTTACATCTGACCTGATGAGAGCTTGGAGTGTGTTGAAAGATTTTCTGCTGCGTA 840
DB 1697 TGCTTACATCTGACCTGATGAGAGCTTGGAGTGTGTTGAAAGATTTTCTGCTGCGTA 1756
QY 841 ACTTGTGGAACAGAGCTCTPACATGTAACCTTGTGTTGAGGTTTCTGTGGGCTCAT 900
DB 1757 ACTTGTGGAACAGAGCTCTPACATGTAACCTTGTGTTGAGGTTTCTGTGGGCTCAT 1816
QY 901 CCCAGGCAAGTTAGTGTGAGATTAAGAGATTAACAAGGGAATTTGAAGAGCTTT 960
DB 1817 CCCAGGCAAGTTAGTGTGAGATTAAGAGATTAACAAGGGAATTTGAAGAGCTTT 1876
QY 961 TGAATCTGTGTGAGCTGTTGATCTTGAATCTGGGTACACAGCGCTTTTCCAAG 1020
DB 1877 TGAATCTGTGTGAGCTGTTGATCTTGAATCTGGGTACACAGCGCTTTTCCAAG 1936
QY 1021 AGAAGTCAATCAGACTTTGATTTTCCACACCGGGCGCGCTGCGCTGTGCTT 1080
DB 1937 AGAAGTCAATCAGACTTTGATTTTCCACACCGGGCGCGCTGCGCTGTGCTT 1996
QY 1081 TTTTGAAGTTTATPAAGATPAATGAGCGAAGAACCAATCTGAGCGGGGGTAACTGC 1140
DB 1997 TTTTGAAGTTTATPAAGATPAATGAGCGAAGAACCAATCTGAGCGGGGGTAACTGC 2056
QY 1141 TGAATTTTCCGCAATCATCTGTGAGAGAGGTTGTGAGACACAGAAATGCGCTGTAC 1200
DB 2057 TGAATTTTCCGCAATCATCTGTGAGAGAGGTTGTGAGACACAGAAATGCGCTGTAC 2116
QY 1201 TGTGTCTTCCGTCCGCCCGCCATTAATCCGAGGAGAGACACAGACAGAGAGG 1260
DB 2117 TGTGTCTTCCGTCCGCCCGCCATTAATCCGAGGAGAGACACAGACAGAGAGG 2176
QY 1261 AAGCCAGGCGGCGGAGAGAGAGAGCCCATGAAACCGAGAGCGGCGCTGAGACCTC 1320
DB 2177 AAGCCAGGCGGCGGAGAGAGAGAGCCCATGAAACCGAGAGCGGCGCTGAGACCTC 2236
QY 1321 GGAATGAATGTTGTATACAGGTGCTGAACCTGTATCCAGAACTGAGACGATTTTGAAT 1380
DB 2237 GGAATGAATGTTGTATACAGGTGCTGAACCTGTATCCAGAACTGAGACGATTTTGAAT 2236
QY 1381 TACAGAGATGCGGAGGCTTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 1440
DB 2297 TACAGAGATGCGGAGGCTTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 2356

1441 AAGAGAGCTAGGAATCTAGCTTTAGCTTAAATGACAGACACCGTCTGAGTATATAC 1500
2357 AAGAGAGCTAGGAATCTAGCTTTAGCTTAAATGACAGACACCGTCTGAGTATATAC 2416
1501 TTTTCAAGAGATCAAGGATATATGAGCTTAAATGAGCTTATCTGAGGAGGAGATATC 1560
2417 TTTTCAAGAGATCAAGGATATATGAGCTTAAATGAGCTTATCTGAGGAGGAGATATC 2476
1561 CATAGAGAGCTGACCACTTACTGCTGACAGGAGGAGATATTTTGAAGAGCTATTTAG 1620
2477 CATAGAGAGCTGACCACTTACTGCTGACAGGAGGAGATATTTTGAAGAGCTATTTAG 2536
1621 GGTATATGCAAAAGGTGGCACTTAAAGCCAGATTGCAAGTCAAGATCAGCAAACTTGTA 1680
2537 GGTATATGCAAAAGGTGGCACTTAAAGCCAGATTGCAAGTCAAGATCAGCAAACTTGTA 2596
1681 TATCAGGAATGTGCTACTTCTGAGGAAAGGAGGAGGAGATATGATACGAGAGA 1740
2597 TATCAGGAATGTGCTACTTCTGAGGAAAGGAGGAGGAGATATGATACGAGAGA 2656
1741 TAGGAGTGGCTTTAGATGATGATGATATATATATGAGCCGAGGAGTCTTGCAATGACG 1800
2657 TAGGAGTGGCTTTAGATGATGATGATATATATATGAGCCGAGGAGTCTTGCAATGACG 2716
1801 GGTGTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
2717 GGTGTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2776
1861 CAATACCAACCTTATCTCAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1920
2777 CAATACCAACCTTATCTCAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 2836
1921 AGCCTGAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
2837 AGCCTGAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2896
1981 GGTGTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
2897 GGTGTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2956
2041 TATCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
2957 TATCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3016
2101 CATGCTAGTGAAGAAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2160
3017 CATGCTAGTGAAGAAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 3076
2161 CAGGAGCTCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
3077 CAGGAGCTCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3136
2221 GGTAGCCAGCACTCTCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2280
3137 GGTAGCCAGCACTCTCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3196
2281 TTTCTTGAATTTGGGTTAAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
3197 TTTCTTGAATTTGGGTTAAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3256
2341 CATTAAGATATTTGCTTGAAGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2400
3257 CACTTAAGATATTTGCTTGAAGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3316
2401 CATGACCAATGAAGATCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2460
3317 CATGACCAATGAAGATCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3376
2461 CTGCGAGTGTGGCGGTTAAACATATTTAGAACAGGCTGATGATGATGATGATGATGAT 2520
3377 CTGCGAGTGTGGCGGTTAAACATATTTAGAACAGGCTGATGATGATGATGATGATGAT 3436

2521 GGTAGAGCCCGATCACTTGTGCTGCTGACACCCGCTGAGATTGGCTTACGAGTGA 2580
3437 GGTAGAGCCCGATCACTTGTGCTGCTGACACCCGCTGAGATTGGCTTACGAGTGA 3496
2581 AGTACAGATTGAG 2594
3497 AGATACAGATTGAG 3510

RESULT 10
US-09-956-335-1
; Sequence 1, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly
; APPLICANT: KUPPASWAMI, Mohan
; APPLICANT: DORONIN, Konstantin
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
; TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
; FILE REFERENCE: 16153-8394
; CURRENT APPLICATION NUMBER: US/09/956,335
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 35978
; TYPE: DNA
; ORGANISM: Adenovirus
US-09-956-335-1

Query Match 100.0%; Score 2594; DB 4; Length 35978;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATCCATCTTACCTGCGACAGAGGCTGCTTCCACCCATGACAGAGATGAAGAGGT 60
917 ATCCATCTTACCTGCGACAGAGGCTGCTTCCACCCATGACAGAGATGAAGAGGT 976
61 GAGGAGTTTGTGTTAGATTATGATGAGAGCAGCCGAGGACAGGTTGCAAGTCTTGTCAATTAT 120
977 GAGGAGTTTGTGTTAGATTATGATGAGAGCAGCCGAGGACAGGTTGCAAGTCTTGTCAATTAT 1036
121 CACCGAGAAATACGAGGAGGAGCCAGATATATGATGATGATGATGATGATGATGATGATG 180
1037 CACCGAGAAATACGAGGAGGAGCCAGATATATGATGATGATGATGATGATGATGATGATG 1096
181 GGCATGTTTGTCTACAGTAAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
1097 GGCATGTTTGTCTACAGTAAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1156
241 GTGAGTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 300
1157 GTGAGTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1216
301 TTTTATTTTAAAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
1217 TTTTATTTTAAAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1276
361 CAAAGACCTACCCGCTGCTTAAATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
1277 CAAAGACCTACCCGCTGCTTAAATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1336
421 TGTCTAGAGATGCAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
1337 TGTCTAGAGATGCAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1396
481 CTGAGATACACCCGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
1397 CTGAGATACACCCGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1456
541 GGCCTGCGCAGGCTGTGGAATGATATGAGAGGCTTGAACAGACCTGGGCAACCTTTGG 600

Db 1457 GACGTCGACGAGCTGTGGATGTATCGAGGACTTGTCTTAACGAGCTGGCAACCTTTGG 1516
Qy 601 ACTTGAGCTGTAAACGCCCCAGGCCATTAAGGTAAACCTGTGATTTGGTGTGTGTTAA 660
Db 1517 ACTTGAGCTGTAAACGCCCCAGGCCATTAAGGTAAACCTGTGATTTGGTGTGTGTTAA 1576
Qy 661 GCGCTTTGTTGCTGAATGAGTGTGAATTAATTAAGGGGTGAGTAAATGTTTAACT 720
Db 1577 GCGCTTTGTTGCTGAATGAGTGTGAATTAATTAAGGGGTGAGTAAATGTTTAACT 1636
Qy 721 TGCATGGCTGTAAATGGGCGGGGCTTAAAGGTAATATATGCGCGGTGCTAATCT 780
Db 1637 TGCATGGGCTGTAAATGGGCGGGGCTTAAAGGTAATATATGCGCGGTGCTAATCT 1696
Qy 781 TGGTACATCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGAGCTA 840
Db 1697 TGGTACATCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGAGCTA 1756
Qy 841 ACTTGCTGAAACAGAGCTCTAACAGTACCTTGTGTTTGGAGGTTTCTGTGTGGCTCAT 900
Db 1757 ACTTGCTGAAACAGAGCTCTAACAGTACCTTGTGTTTGGAGGTTTCTGTGTGGCTCAT 1816
Qy 901 CCCAGGCAAGTGTATCTGCAAGATTAAGAGGATTAACAATGGGAAATTTGAAGCTTT 960
Db 1817 CCCAGGCAAGTGTATCTGCAAGATTAAGAGGATTAACAAGTGGGAATTTGAAGGCTTT 1876
Qy 961 TGAATTCCTGTGTGAGCTGTGATTTGATCTTGAATCTGGGTCAACAGGCGCTTTCCAG 1020
Db 1877 TGAATTCCTGTGTGAGCTGTGATTTGATCTTGAATCTGGGTCAACAGGCGCTTTCCAG 1936
Qy 1021 AGAAGTCATCAAGACTTTGGAATTTTTCACAACCGGGGCGGCTGCGCTGTGTGCTT 1080
Db 1937 AGAAGTCATCAAGACTTTGGAATTTTTCACAACCGGGGCGGCTGCGCTGTGTGCTT 1996
Qy 1081 TTTTGAAGTTTATTAAGATTAATGAGCGAAAGAAACCATCTGTGCGGGGGTATCTGTC 1140
Db 1997 TTTTGAAGTTTATTAAGATTAATGAGCGAAAGAAACCATCTGTGCGGGGGTATCTGTC 2056
Qy 1141 TGGATTTTCTGAGCCATGTCATCTGTGAGAGCGGTTGTGAGACAACAAGATGCGCTGTAC 1200
Db 2057 TGGATTTTCTGAGCCATGTCATCTGTGAGAGCGGTTGTGAGACAACAAGATGCGCTGTAC 2116
Qy 1201 TGTGTCTTCCGTCGCGCCGCGGATTAATACCGACGGAAGAGAGCAGCAGCAGAGAG 1260
Db 2117 TGTGTCTTCCGTCGCGCCGCGGATTAATACCGACGGAAGAGAGCAGCAGCAGAGAG 2176
Qy 1261 AAGCAGGCGCGCGGAGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGAGACCTTC 1320
Db 2177 AAGCAGGCGCGCGGAGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGAGACCTTC 2236
Qy 1321 GGGAAATGAATGTTGTACAGTGTGCTGAATCTGTATCCAGAACTGAGACCTTTGACAAAT 1380
Db 2237 GGGAAATGAATGTTGTACAGTGTGCTGAATCTGTATCCAGAACTGAGACCTTTGACAAAT 2296
Qy 1381 TACAGAGATGGGCGAGGGGCTTAAAGGGGCTTAAAGGAGCGGGGGGCTTGTGAGGCTAC 1440
Db 2297 TACAGAGATGGGCGAGGGGCTTAAAGGGGCTTAAAGGAGCGGGGGGCTTGTGAGGCTAC 2356
Qy 1441 AGAGAGGCTGAGAAATCTAGCTTTTAACTTAAATGACAGACCCGTCTGTAGTGTATAC 1500
Db 2357 AGAGAGGCTGAGAAATCTAGCTTTTAACTTAAATGACAGACCCGTCTGTAGTGTATAC 2416
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTATCTGTGCGGCGAGAAATATTC 1560
Db 2417 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTATCTGTGCGGCGAGAAATATTC 2476
Qy 1561 CATAGAGAGCTGACCACTTAATGCTGACAGCAGGGGATGATTTTGAAGAGGCTATTTAG 1620
Db 2477 CATAGAGAGCTGACCACTTAATGCTGACAGCAGGGGATGATTTTGAAGAGGCTATTTAG 2536
Qy 1621 GGTATATGCAAAAGGTGCACTTAAAGCCAGATTGCAAGTACAGCAAACTTGTAAA 1680
Db 2537 GGTATATGCAAAAGGTGCACTTAAAGCCAGATTGCAAGTACAGCAAACTTGTAAA 2596

Qy 1681 TATCAGGAATTTGTTGTTACATTTCTGGGAAACGAGGCGGAGGTGAGATAGATACGAGGA 1740
Db 2597 TATCAGGAATTTGTTGTTACATTTCTGGGAAACGAGGCGGAGGTGAGATAGATACGAGGA 2656
Qy 1741 TAGGGTGGCTTTAGATGATGATGATTAATATGTGACCGGAGGCTGTGCAATGAGACGG 1800
Db 2657 TAGGGTGGCTTTAGATGATGATGATTAATATGTGACCGGAGGCTGTGCAATGAGACGG 2716
Qy 1801 GGTGGTATTTATGATATGATGATTTACTGGGCCCAATTTTAAAGCGGTACGTTTCTGTC 1860
Db 2717 GGTGGTATTTATGATATGATGATTTACTGGGCCCAATTTTAAAGCGGTACGTTTCTGTC 2776
Qy 1861 CAATACCAACCTTATCTTACACGAGGTGATGCTTATGAGGTTTAAACAATACCTGTGTGA 1920
Db 2777 CAATACCAACCTTATCTTACACGAGGTGATGCTTATGAGGTTTAAACAATACCTGTGTGA 2836
Qy 1921 AGCTGGAACCGATGTAAGGTTGCGGGCTGTGCTTTTAACTGTCTGTGAAGGGGGTGT 1980
Db 2837 AGCTGGAACCGATGTAAGGTTGCGGGCTGTGCTTTTAACTGTCTGTGAAGGGGGTGT 2896
Qy 1981 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGGG 2040
Db 2897 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTACTTGGG 2956
Qy 2041 TATCTGTCTGAGGGTAACTTCAAGGCTGCGCAACAATGTGAGCTCCGACTGTGGTGTCTT 2100
Db 2957 TATCTGTCTGAGGGTAACTTCAAGGCTGCGCAACAATGTGAGCTCCGACTGTGGTGTCTT 3016
Qy 2101 CATCTATGTGAAGAGCTGTGTGATTAAGCATTAACATGATATGTGCAACTCGAGGA 2160
Db 3017 CATCTATGTGAAGAGCTGTGTGATTAAGCATTAACATGATATGTGCAACTCGAGGA 3076
Qy 2161 CAGGCGCTCTCAAGATGCTGACCTGTGAGCGGAACCTGTCACTGTGAAAGACATTTCA 2220
Db 3077 CAGGCGCTCTCAAGATGCTGACCTGTGAGCGGAACCTGTCACTGTGAAAGACATTTCA 3136
Qy 2221 CGTAGCAGCACTCTGCAAGGCTGTGAGGCTTTGAGCATTAACATGACCCGCTG 2280
Db 3137 CGTAGCAGCACTCTGCAAGGCTGTGAGGCTTTGAGCATTAACATGACCCGCTG 3196
Qy 2281 TTCTTGCATTTTGGGTAAACAGAGAGGGGGTGTCTTACTTACCAATGCAATTTGAGTCA 2340
Db 3197 TTCTTGCATTTTGGGTAAACAGAGAGGGGGTGTCTTACTTACCAATGCAATTTGAGTCA 3256
Qy 2341 CACTAAGATATTTGTTAGGCCGAGACATGTCCAAGGTGAACCTGAACCGGGGTGTTGA 2400
Db 3257 CACTAAGATATTTGTTAGGCCGAGACATGTCCAAGGTGAACCTGAACCGGGGTGTTGA 3316
Qy 2401 CATGACCATGAAGATCTGGAAGGTGTGAGGTGATGAGTGAACCCGCAACAGGTGCAAGC 2460
Db 3317 CATGACCATGAAGATCTGGAAGGTGTGAGGTGATGAGTGAACCCGCAACAGGTGCAAGC 3376
Qy 2461 CTGCAAGTGTGCGGTAAACATATTAAGAACCAAGCTGTGTGATGTTGATGTCAGAGGA 2520
Db 3377 CTGCAAGTGTGCGGTAAACATATTAAGAACCAAGCTGTGTGATGTTGATGTCAGAGGA 3436
Qy 2521 GCTGAGGCCGATCACTTGTGTGCTGTGCAACCGGCGTGAAGTTTGGCTTACGATGA 2580
Db 3437 GCTGAGGCCGATCACTTGTGTGCTGTGCAACCGGCGTGAAGTTTGGCTTACGATGA 3496
Qy 2581 AGATACAGATTTAG 2594
Db 3497 AGATACAGATTTAG 3510

RESULT 11
US-09-956-335-2
; Sequence No. Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly

APPLICANT: KUPPASWAMI, Mohan
APPLICANT: DORONIN, Konstantin
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
FILE REFERENCE: 16153-8394
CURRENT APPLICATION NUMBER: US/09/956,335
CURRENT FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 35871
TYPE: DNA
ORGANISM: Adenovirus
US-09-956-335-2

Query Match 99.5%; Score 2582; DB 4; Length 35871;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 2582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

13 TGGCAGGAGCTGGCTTTCCACCCAGTACGACGAGATGAAAGAGGTGAGAGTTTGTG 72
824 TGGCAGGAGCTGGCTTTCCACCCAGTACGACGAGATGAAAGAGGTGAGAGTTTGTG 883
73 TTAAGTTATGTGAGACACCCGGGGACCGTTGAGAGTCTTGTCAATTATCACCGAGAGAT 132
884 TTAAGTTATGTGAGACACCCGGGGACCGTTGAGAGTCTTGTCAATTATCACCGAGAGAT 943
133 ACGGGGAGCCAGATATTATGTGTGCTTTGCTATATGAGAGACCTGTGAGATGTTTGTG 192
944 ACGGGGAGCCAGATATTATGTGTGCTTTGCTATATGAGAGACCTGTGAGATGTTTGTG 1003
193 TACAGTATGTAATAATTATGAGCAATGAGTGTGAGTGTGTTGTGTGTAATTT 252
1004 TACAGTATGTAATAATTATGAGCAATGAGTGTGAGTGTGTTGTGTGTAATTT 1063
253 TTTTATTAATTTTAAAGTTTGTGTTTAAAGATTTTGTATGTGATTTTAAAG 312
1064 TTTTATTAATTTTAAAGTTTGTGTTTAAAGATTTTGTATGTGATTTTAAAG 1123
313 GTCTGTGTCTGAACCTGAGCCTGAGCCGAGCCGAGACCGAGAGCTGCAAGACTTACC 372
1124 GTCTGTGTCTGAACCTGAGCCTGAGCCGAGCCGAGACCGAGAGCTGCAAGACTTACC 1183
373 GCGGTCTTAAATGAGCGCTGTCTATCTGAGACGCGCCGACATCACTGTGTCTAGAGAT 432
1184 GCGGTCTTAAATGAGCGCTGTCTATCTGAGACGCGCCGACATCACTGTGTCTAGAGAT 1243
433 GCAATAGTATGAGGATGAGTGTGACCTGCGGTCTTAAAGACCTCTGAGATACACC 492
1244 GCAATAGTATGAGGATGAGTGTGACCTGCGGTCTTAAAGACCTCTGAGATACACC 1303
493 CGGTGTCTCCGCTGTGCCCCATTAACCAAGTTGCGTGAAGATTGTGGGGCTGCCAGG 552
1304 CGGTGTCTCCGCTGTGCCCCATTAACCAAGTTGCGTGAAGATTGTGGGGCTGCCAGG 1363
553 CTGTGAGATGTATGAGGACCTTGTCTTAACGAGCCTGGGCAACTTTGAGCTTGAAGCTTA 612
1364 CTGTGAGATGTATGAGGACCTTGTCTTAACGAGCCTGGGCAACTTTGAGCTTGAAGCTTA 1423
613 AACGCCCAAGGCAATAGGATTAACCTGTATGCGGTGTGAGTTAAAGCTTTGTTTG 672
1424 AACGCCCAAGGCAATAGGATTAACCTGTATGCGGTGTGAGTTAAAGCTTTGTTTG 1483
673 CTGAATGAGTGTATGATTAATTAAGGATGAGATTAATGATTAATGATGAGCGGTGT 732
1484 CTGAATGAGTGTATGATTAATTAAGGATGAGATTAATGATTAATGATGAGCGGTGT 1543
733 TAAATGAGGCGGGCTTAAAGGATTAATTAAGCGCGGTGAGCTTAATCTTGTGTACATCTG 792
1544 TAAATGAGGCGGGCTTAAAGGATTAATTAAGCGCGGTGAGCTTAATCTTGTGTACATCTG 1603
793 ACCTCATGAGAGCTTGGAGTGTGTGAAAGATTTTCTGTGTGCTGAACCTTGTGAGAC 852

1604 ACCTCATGAGAGCTTGGAGTGTGTGAAAGATTTTCTGTGTGCTGAACCTTGTGAGAC 1663
853 AGAGCTTAACAGTAACTCTTGTGTTTGAAGTTTCTGTGGGCTCATCCAGGCAAGT 912
1664 AGAGCTTAACAGTAACTCTTGTGTTTGAAGTTTCTGTGGGCTCATCCAGGCAAGT 1723
913 TAGTCTGAGAAATTAAGAGATTAACAAGTGGAAATTTGAAGAGCTTTGAATCTCTGTG 972
1724 TAGTCTGAGAAATTAAGAGATTAACAAGTGGAAATTTGAAGAGCTTTGAATCTCTGTG 1783
973 GTGAGCTGTGTTGATTTCTTGAATCTGGGTGACCAAGGCGCTTTCCAGAGAGGATCA 1032
1784 GTGAGCTGTGTTGATTTCTTGAATCTGGGTGACCAAGGCGCTTTCCAGAGAGGATCA 1843
1033 AGACTTGTGATTTTCCACACCGGGGCGCGTGGCGCTGTGCTTGTCTTTTGAATTTTA 1092
1844 AGACTTGTGATTTTCCACACCGGGGCGCGTGGCGCTGTGCTTGTCTTTTGAATTTTA 1903
1093 TAAAGATTAATGAGAGGAAACCACTTGAACCGGGGGTACTGCTGATTTTCTTG 1152
1904 TAAAGATTAATGAGAGGAAACCACTTGAACCGGGGGTACTGCTGATTTTCTTG 1963
1153 CCATGATCTGTGAGAGCGGTGTGAGACCAAGAAATGCGCTGACTGTGCTTTCG 1212
1964 CCATGATCTGTGAGAGCGGTGTGAGACCAAGAAATGCGCTGACTGTGCTTTCG 2023
1213 TCCGCCCCGAGTAATACCGACGAGAGACAGACAGACAGAGAGAACCAAGCGCG 1272
2024 TCCGCCCCGAGTAATACCGACGAGAGACAGACAGACAGAGAGAACCAAGCGCG 2083
1273 GCGCGCAGAGACAGACCCATGAGAACCGAGAGCGCGCTGTGACCTTGGGAAATGAT 1332
2084 GCGCGCAGAGACAGACCCATGAGAACCGAGAGCGCGCTGTGACCTTGGGAAATGAT 2143
1333 TGTAAGGTGTGATCTGTATCCAGAACTGAGACGATTTTGAATTAAGAGAGATG 1392
2144 TGTAAGGTGTGATCTGTATCCAGAACTGAGACGATTTTGAATTAAGAGAGATG 2203
1393 GCAGGGGCTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGCTACAGAGAGGCTAG 1452
2204 GCAGGGGCTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGCTACAGAGAGGCTAG 2263
1453 GAATCTAGCTTTTATGCTTAATGACCAAGACCGCTCTGAGTGTATTAATTTCAACAGAT 1512
2264 GAATCTAGCTTTTATGCTTAATGACCAAGACCGCTCTGAGTGTATTAATTTCAACAGAT 2323
1513 CAAGGATTAATGAGCTATGAGCTTGAATCTGCGGCGCAGAGATTTCCATAGAGCAGCT 1572
2324 CAAGGATTAATGAGCTATGAGCTTGAATCTGCGGCGCAGAGATTTCCATAGAGCAGCT 2383
1573 GACCACTTACGTGCTGAGCGAGGAGATTAATTTGAGAGGCTATTAAGGATATGCAAA 1632
2384 GACCACTTACGTGCTGAGCGAGGAGATTAATTTGAGAGGCTATTAAGGATATGCAAA 2443
1633 GGTGGCACTTAAGGCAATGAGTGAAGTACAGAACTTTGAATATCAGAAATTTG 1692
2444 GGTGGCACTTAAGGCAATGAGTGAAGTACAGAACTTTGAATATCAGAAATTTG 2503
1693 TTGCTACATTTCTGGGAAACGGGGCCGAGGTGAGATGATGATGAGGATAGGGGTGCTT 1752
2504 TTGCTACATTTCTGGGAAACGGGGCCGAGGTGAGATGATGATGAGGATAGGGGTGCTT 2563
1753 TAGATGATGAGATTAATTAATGAGTGGCGGGGGTGTCTTGGACAGGAGCGGGGTGATTAAT 1812
2564 TAGATGATGAGATTAATTAATGAGTGGCGGGGGTGTCTTGGACAGGAGCGGGGTGATTAAT 2563
1813 GAATGTAAGGTTTACGCGCCCAATTTTACCGGTATCGGTCTTGTGCAATACCAACT 1872
2624 GAATGTAAGGTTTACGCGCCCAATTTTACCGGTATCGGTCTTGTGCAATACCAACT 2683
1873 TATCTTACAGGCTGTGATCTTATGAGGTTTAAATTAATTAATTAATTAATTAATTAAT 1932
2684 TATCTTACAGGCTGTGATCTTATGAGGTTTAAATTAATTAATTAATTAATTAATTAAT 2743

US-08-735-609-4

Query Match 83.3%; Score 2161; DB 2; Length 34303;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	434	CAATAGTAGTACGATAGCTGACTCCGGTCTCTTCAACACACCTCTGAGATACACC	493
Db	2853	CAATAGTAGTACGATAGCTGACTCCGGTCTCTTCAACACACCTCTGAGATACACC	2912
Qy	494	GGTGGTCCCGCTGTGGCCCATTTAAACCAAGTTCGGTGAAGATTGGTGGCCCTCCGACGGC	553
Db	2213	GGTGGTCCCGCTGTGGCCCATTTAAACCAAGTTCGGTGAAGATTGGTGGCCCTCCGACGGC	2972
Qy	554	TGTGGAATGTATGAGAGACTGTGCTTAAAGACCTGGGACCTTTGACTGAGCTGA	613
Db	2973	TGTGGAATGTATGAGAGACTGTGCTTAAAGACCTGGGACCTTTGACTGAGCTGA	3032
Qy	614	ACGCCCCAGGCCATTAAGGTGTAAACCTGTGATTGGTGTGTTAACGCCCTTGTGTTGC	673
Db	3033	ACGCCCCAGGCCATTAAGGTGTAAACCTGTGATTGGTGTGTTAACGCCCTTGTGTTGC	3092
Qy	674	TGAATGAGTATGATGATTAATTAAGGGTGAATATGTTTAACTTGCATGGCGTGT	733
Db	3093	TGAATGAGTATGATGATTAATTAAGGGTGAATATGTTTAACTTGCATGGCGTGT	3152
Qy	734	AAATGGGGCGGGGCTTAAAGGGTATATATAGCGCGTGGGCTAATCTTGATACATCGA	793
Db	3153	AAATGGGGCGGGGCTTAAAGGGTATATATAGCGCGTGGGCTAATCTTGATACATCGA	3212
Qy	794	CCTCATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGCTTAACTTGCTGGAACA	853
Db	3213	CCTCATGAGGCTTGGAGTGTGGAAGATTTTCTGCTGTGCTTAACTTGCTGGAACA	3272
Qy	854	GAGCTTAAACATACCTCTTGGTTTGGAGTTTCTGTGGGGCTCATCCGACCAAGTT	913
Db	3273	GAGCTTAAACATACCTCTTGGTTTGGAGTTTCTGTGGGGCTCATCCGACCAAGTT	3332
Qy	914	AGTGTGAGATTTAAGAGGATTAACAAGTGGAAATTTGAAGCTTTGAAATCCTGGG	973
Db	3333	AGTGTGAGATTTAAGAGGATTAACAAGTGGAAATTTGAAGCTTTGAAATCCTGGG	3392
Qy	974	TGAGCTGTTTGAATCTTGAATCTGGGTCAACAGGCGCTTTTCCAAGAAAGTCATCAA	1033
Db	3393	TGAGCTGTTTGAATCTTGAATCTGGGTCAACAGGCGCTTTTCCAAGAAAGTCATCAA	3452
Qy	1034	GACTTTGATTTTTCACACCGGGGGCGGCTGGCGTCTGTGCTTTTGAAGTTTAT	1093
Db	3453	GACTTTGATTTTTCACACCGGGGGCGGCTGGCGTCTGTGCTTTTGAAGTTTAT	3512
Qy	1094	AAAGGATTAATGAGCGGAAGAAACCATCTGAGCGGGGGGTACCTGCTGAATTTTCTGGC	1153
Db	3513	AAAGGATTAATGAGCGGAAGAAACCATCTGAGCGGGGGGTACCTGCTGAATTTTCTGGC	3572
Qy	1154	CATGATCTGTGAGAGCGGTTGTGAGACACAAGATCGCTGCTAATGTTTCTTCCGT	1213
Db	3573	CATGATCTGTGAGAGCGGTTGTGAGACACAAGATCGCTGCTAATGTTTCTTCCGT	3632
Qy	1214	CCGCCCGGCGATTAATACCGAGGAGAGACAGACAGACAGAGAGAAAGCCAGCGCG	1273
Db	3633	CCGCCCGGCGATTAATACCGAGGAGAGACAGACAGACAGAGAGAAAGCCAGCGCG	3692
Qy	1274	GGGCGAGGAGAGAGCCCATGGAACCCGAGAGCGGGCGCTGAGCCCTGGGGAATGAAATGT	1333
Db	3693	GGGCGAGGAGAGAGCCCATGGAACCCGAGAGCGGGCGCTGAGCCCTGGGGAATGAAATGT	3752
Qy	1334	GTAACAGGTGCTGAACCTGATCCAGAACTGAGACGATTTTGAACAATTAAGAGATGGG	1393
Db	3753	GTAACAGGTGCTGAACCTGATCCAGAACTGAGACGATTTTGAACAATTAAGAGATGGG	3812
Qy	1394	CAGGGGCTTAAAGGGGGTAAAGAGGGAGCGGGGGCTTTGTGAGGCTTACAGAGAGGCTAGG	1453
Db	3813	CAGGGGCTTAAAGGGGGTAAAGAGGGAGCGGGGGCTTTGTGAGGCTTACAGAGAGGCTAGG	3872

Qy	1454	AATCTAGCTTTAGCTTAATGACACAGACCGTCTGAGTATTAATTTTCAACAGATC	1513
Db	3873	AATCTAGCTTTAGCTTAATGACACAGACCGTCTGAGTATTAATTTTCAACAGATC	3932
Qy	1514	AAGGATTAATGCGCTTAATGACTTGATCTGTGGCGGAGAAATTCATAGACAGCTG	1573
Db	3933	AAGGATTAATGCGCTTAATGACTTGATCTGTGGCGGAGAAATTCATAGACAGCTG	3992
Qy	1574	ACCACTTAATGCGCTGACGCCAGGGATGATTTTGAAGAGCTAATGAGTATAGCAAG	1633
Db	3993	ACCACTTAATGCGCTGACGCCAGGGATGATTTTGAAGAGCTAATGAGTATAGCAAG	4052
Qy	1634	GTGGCACTTAAGGCCAGATTCAGATCAAGATCAGCAAACTTGTAATATCAGGAATGT	1693
Db	4053	GTGGCACTTAAGGCCAGATTCAGATCAAGATCAGCAAACTTGTAATATCAGGAATGT	4112
Qy	1694	TGCTAATTTCTGGGAACGGGGCCGAGGTGAGATTAAGATACGAGAGATAGGCTGCTT	1753
Db	4113	TGCTAATTTCTGGGAACGGGGCCGAGGTGAGATTAAGATACGAGAGATAGGCTGCTT	4172
Qy	1754	AGATGATGATGATTAATTAATGAGCGGGGCTGTGGCAATGAGCGGGTGGTATTAATG	1813
Db	4173	AGATGATGATGATTAATTAATGAGCGGGGCTGTGGCAATGAGCGGGTGGTATTAATG	4232
Qy	1814	AATGTAAGTTTACTGGCCCAATTTTACGGGTACGGTTCCTGGCCAAATACCAACTT	1873
Db	4233	AATGTAAGTTTACTGGCCCAATTTTACGGGTACGGTTCCTGGCCAAATACCAACTT	4292
Qy	1874	ATCTTAACAGCGTGTAACTTCTATAGGTTTAAACAATCTGTGTGAACCTTGACCGAT	1933
Db	4293	ATCTTAACAGCGTGTAACTTCTATAGGTTTAAACAATCTGTGTGAACCTTGACCGAT	4352
Qy	1934	GTAAGGTTTGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGGTGTGTGCGCCCAA	1993
Db	4353	GTAAGGTTTGGGGCTGTGCTTTTACTGCTGTGGAAGGGGGGTGTGTGCGCCCAA	4412
Qy	1994	AGCAGGCTTCAATTAAGAAATGCTCTTGAAGGTATCCTTGAGGATCTGTCTGAG	2053
Db	4413	AGCAGGCTTCAATTAAGAAATGCTCTTGAAGGTATCCTTGAGGATCTGTCTGAG	4472
Qy	2054	GTTAATCTCAAGGGTGGCCCAATGTGGCTCCGACTGTGGTCTTCACTAGTGA	2113
Db	4473	GTTAATCTCAAGGGTGGCCCAATGTGGCTCCGACTGTGGTCTTCACTAGTGA	4532
Qy	2114	AGCGTGTGTGATTAAGCATTAATGATATGTGGCAATGCGAGGACAGGGGCTCTAG	2173
Db	4533	AGCGTGTGTGATTAAGCATTAATGATATGTGGCAATGCGAGGACAGGGGCTCTAG	4592
Qy	2174	ATGCTGACCTGTGCGAGCGGCACTGTCACTGCTGAAGACATTCAGTACGACGAC	2233
Db	4593	ATGCTGACCTGTGCGAGCGGCACTGTCACTGCTGAAGACATTCAGTACGACGAC	4652
Qy	2234	TCTGCAAGGCTTGGCCAGATGTTTGAACATTAACATTAAGTCTTCTTGACATTTG	2293
Db	4653	TCTGCAAGGCTTGGCCAGATGTTTGAACATTAACATTAAGTCTTCTTGACATTTG	4712
Qy	2294	GTTAACAAGAGGGGGGTCTCTAATCAATGCAATTTGAATCACTAAGAATTTG	2353
Db	4713	GTTAACAAGAGGGGGGTCTCTAATCAATGCAATTTGAATCACTAAGAATTTG	4772
Qy	2354	CTTGAGCCCGAGACATGTCCAAAGTGAACCTGAAACGGGGTGTGACATGACATGAAG	2413
Db	4773	CTTGAGCCCGAGACATGTCCAAAGTGAACCTGAAACGGGGTGTGACATGACATGAAG	4832
Qy	2414	ATCTGAAAGTGTGAGGTACATGAGACCCGACACAGGTGCAACCTCTGAGGTGGC	2473
Db	4833	ATCTGAAAGTGTGAGGTACATGAGACCCGACACAGGTGCAACCTCTGAGGTGGC	4892
Qy	2474	GTTAACAATTAATTAAGAACCGAGCTGTGATGTGATGACCGAGGAGCTGAGGCTGAT	2533
Db	4893	GTTAACAATTAATTAAGAACCGAGCTGTGATGTGATGACCGAGGAGCTGAGGCTGAT	4952

Db 4113 TGTCAATTTTGGGAAAGGGGCGAGGTGAGATAGATACGAGAGATAGGGTGGCTTT 4172
Qy 1754 AGATGATACATGATTAATATATGTGCGGGGGTCTTGGCATGAGCGGGGTGTTATATG 1813
Db 4173 AGATGATACATGATTAATATATGTGCGGGGGTCTTGGCATGAGCGGGGTGTTATATG 4232
Qy 1814 AATGTAAGTTTAACTGGGCGCAATTTTAAAGGGTACGGTTTCCCTGGGCAATACCACTT 1873
Db 4233 AATGTAAGTTTAACTGGGCGCAATTTTAAAGGGTACGGTTTCCCTGGGCAATACCACTT 4292
Qy 1874 ATCTCAACGGTGTATAGCTTATAGGTTTAAACATATCTGTGTGAAAGCTTGACCGAT 1933
Db 4293 ATCTCAACGGTGTATAGCTTATAGGTTTAAACATATCTGTGTGAAAGCTTGACCGAT 4352
Qy 1934 GTAAAGGTTCCGGGCTGTGCTTTTAACTGCTGCTGTGAAAGGGGGTGTGTGCCCCAA 1993
Db 4353 GTAAAGGTTCCGGGCTGTGCTTTTAACTGCTGCTGTGAAAGGGGGTGTGTGCCCCAA 4412
Qy 1994 AGCAGGGCTTCAATTAAGAAATGCTCTTGAAGGTTACCTTGGGTTATCTGTGTAG 2053
Db 4413 AGCAGGGCTTCAATTAAGAAATGCTCTTGAAGGTTATCTTGGGTTATCTGTGTAG 4472
Qy 2054 GGTAACTTCAGGGTGCAGCAATGTGCTCTCCGACTGTGTTGCTTCACTAGTAA 2113
Db 4473 GGTAACTTCAGGGTGCAGCAATGTGCTCTCCGACTGTGTTGCTTCACTAGTAA 4532
Qy 2114 AGCTGCTGTGTATTAAGCATTAATGTATGTGCAACTGTGAGAGACAGGGCTCTAG 2173
Db 4533 AGCTGCTGTGTATTAAGCATTAATGTATGTGCAACTGTGAGAGACAGGGCTCTAG 4592
Qy 2174 ATGCTGACTGTGTGAGAGCACTGTACCTGTGTGAGAGACCATTCAGTAAAGCAGCAG 2233
Db 4593 ATGCTGACTGTGTGAGAGCACTGTACCTGTGTGAGAGACCATTCAGTAAAGCAGCAG 4652
Qy 2234 TCTGCAAGGCTGTGCAAGTGTGTGAGCATTAACATATGACCCGCTGTCTTGCATTG 2293
Db 4653 TCTGCAAGGCTGTGCAAGTGTGTGAGCATTAACATATGACCCGCTGTCTTGCATTG 4712
Qy 2294 GGTAAACAGGAGGGGGTGTCTTCACTTAACATGCAATTTGAGTCAACATTAATATG 2353
Db 4713 GGTAAACAGGAGGGGGTGTCTTCACTTAACATGCAATTTGAGTCAACATTAATATG 4772
Qy 2354 CTTGAGCCCGAGAGCATGTCCAAAGTGAACCTGAACGGGGTGTGTAATGACCATGAAG 2413
Db 4773 CTTGAGCCCGAGAGCATGTCCAAAGTGAACCTGAACGGGGTGTGTAATGACCATGAAG 4832
Qy 2414 ATCTGGAAGGTGCTGAGTACGATGAGACCCGACACAGGTGAGACCTTGCGAGTGTGC 2473
Db 4833 ATCTGGAAGGTGCTGAGTACGATGAGACCCGACACAGGTGAGACCTTGCGAGTGTGC 4892
Qy 2474 GGTAAACATTAATTAAGAACCAAGCTGTGTATGCTGTGATGTGACCGAGAGACTGAGGCCAT 2533
Db 4893 GGTAAACATTAATTAAGAACCAAGCTGTGTATGCTGTGATGTGACCGAGAGACTGAGGCCAT 4952
Qy 2534 CACTTGATGTGAGCTTGACCCGCGCTGAGTTTGTGCTTAAAGGATGAAGATACAGATTGA 2593
Db 4953 CACTTGATGTGAGCTTGACCCGCGCTGAGTTTGTGCTTAAAGGATGAAGATACAGATTGA 5012
Qy 2594 G 2594
Db 5013 G 5013

RESULT 15
US-09-244-752-4
; Sequence 4, Application US/09244752
; Patent No. 6063622
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Amalitano, Andrea
; APPLICANT: Hauber, Michael A.
; APPLICANT: Kumar-Singh, Rajendra

APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,752
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane R.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
STRAND: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-244-752-4
Query Match 83.3%; Score 2161; DB 3; Length 34303;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 434 CAATAGTAGTACGAGTACGTGTGACTCCGGTCTTCTTAACACACCTCTGAGATACACC 493
Db 2853 CAATAGTAGTACGAGTACGTGTGACTCCGGTCTTCTTAACACACCTCTGAGATACACC 2912
Qy 494 GGTGTCCTCCGTGTGCCCATTAACCAAGTTGCCGTGAGAGTTGTGGCGTCCGACAGC 553
Db 2913 GGTGTCCTCCGTGTGCCCATTAACCAAGTTGCCGTGAGAGTTGTGGCGTCCGACAGC 2972
Qy 554 TGTGGAATGTATCGAGACTTGTCTTAACGAGCCCTGGGCAACCTTTGACTGATGA 613
Db 2973 TGTGGAATGTATCGAGACTTGTCTTAACGAGCCCTGGGCAACCTTTGACTGATGA 3032
Qy 614 ACGCCCCAGGCATTAAGGTGAACCTGTGATTCGTGTGTGTTAAAGCCTTTGTGTC 673
Db 3033 ACGCCCCAGGCATTAAGGTGAACCTGTGATTCGTGTGTGTTAAAGCCTTTGTGTC 3092
Qy 674 TGAATGAGTTGATGTAAGTTTAATTAAGGTGAGATATGTTTAACTTGATGAGCGTGT 733
Db 3093 TGAATGAGTTGATGTAAGTTTAATTAAGGTGAGATATGTTTAACTTGATGAGCGTGT 3152
Qy 734 AAATGGGGCGGGGCTTAAAGGTATATTAATGCGCGCGGTAACTTTGTTAATCTGA 793
Db 3153 AAATGGGGCGGGGCTTAAAGGTATATTAATGCGCGCGGTAACTTTGTTAATCTGA 3212
Qy 794 CCTCATGAGGCTTGGAGAGTGTGGAAGATTTTCTGCTGTGCTAATCTTGAGAAC 853
Db 3213 CCTCATGAGGCTTGGAGAGTGTGGAAGATTTTCTGCTGTGCTAATCTTGAGAAC 3272
Qy 854 GAGCTTAACAGTACCTTGTGTTTGAAGGTTTCTGTGGGCTCATCCAGGCAAGTT 913

Db 3273 GAGCTCAACAGTACCTTGGTTTGGAGGTTTCTGTGGGCTCATCCAGCAAGTT 3332
Qy 914 AGCTGCAGAAATTAGAGGATTACAAGTGGGAATTTGAAGACTTTTGAATCTGTGG 973
Db 3333 AGTCTGCAGAAATTAGAGGATTACAAGTGGGAATTTGAAGACTTTTGAATCTGTGG 3392
Qy 974 TGAGCTGTTTGAATCTTGGATTCTGGGGTCAACAGGCGCTTTTCCAGAGAAAGTCAACA 1033
Db 3393 TGAGCTGTTTGAATCTTGGATTCTGGGGTCAACAGGCGCTTTTCCAGAGAAAGTCAACA 3452
Qy 1034 GACTTTGGAATTTTCCACAGCGGGCGGCTGCGGCTGCTGTTGCTTTTGAATTTAT 1093
Db 3453 GACTTTGGAATTTTCCACAGCGGGCGGCTGCGGCTGCTGTTGCTTTTGAATTTAT 3512
Qy 1094 AAAGGATTAATGAGACGGAAGAAACCATCTGAGCGGGGGTAACTCTGAGATTTTCTGGC 1153
Db 3513 AAAGGATTAATGAGACGGAAGAAACCATCTGAGCGGGGGTAACTCTGAGATTTTCTGGC 3572
Qy 1154 CATGATCTGTGAGAGGGGTTGTGAGACAGAGAAATGGCCCTGCTACTGTTGTCTTCCGT 1213
Db 3573 CATGATCTGTGAGAGGGGTTGTGAGACAGAGAAATGGCCCTGCTACTGTTGTCTTCCGT 3632
Qy 1214 CCGGCGCGGCGATTAATACCGAGCGAGAGACAGACAGACAGAGAGAGAGAGAGAGAGAGAG 1273
Db 3633 CCGGCGCGGCGATTAATACCGAGCGAGAGACAGACAGACAGAGAGAGAGAGAGAGAGAGAG 3692
Qy 1274 GCGGAG 1333
Db 3693 GCGGAG 3752
Qy 1334 GTACAGGGGCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAAGATTTCAAGAGATGGG 1393
Db 3753 GTACAGGGGCTGAACCTGTATCCAGAACTGAGACGCAATTTTGAAGATTTCAAGAGATGGG 3812
Qy 1394 CAGGGGCTAAAGGGGGTAAAG 1453
Db 3813 CAGGGGCTAAAGGGGGTAAAG 3872
Qy 1454 AATCTAGCTTTTAACTTAATGACAGACACCGTCTGAGTGAATTAATTTTCAACAGATC 1513
Db 3873 AATCTAGCTTTTAACTTAATGACAGACACCGTCTGAGTGAATTAATTTTCAACAGATC 3932
Qy 1514 AAGGATTAATGCGGCTAAATGAGCTTGAATCTGTGGGGGAGAGATTTCCATAGAGAGAGCTG 1573
Db 3933 AAGGATTAATGCGGCTAAATGAGCTTGAATCTGTGGGGGAGAGATTTCCATAGAGAGAGCTG 3992
Qy 1574 ACCACTTAATGCGGCTGAG 1633
Db 3993 ACCACTTAATGCGGCTGAG 4052
Qy 1634 GTGGCACTTAAGGCGGAGATTGCAAGATCAGCAAACTTTGTAATATCAGAGATTTGT 1693
Db 4053 GTGGCACTTAAGGCGGAGATTGCAAGATCAGCAAACTTTGTAATATCAGAGATTTGT 4112
Qy 1694 TGCTAACATTTTCTGGGAAAGGGGGCGAGAGTGAAGATAGATAAGAGAGATAGAGGCTGCTTT 1753
Db 4113 TGCTAACATTTTCTGGGAAAGGGGGCGAGAGTGAAGATAGATAAGAGAGATAGAGGCTGCTTT 4172
Qy 1754 AGATGTAGATGATTAATATATATGAGCGGGGGTGTGTCATGAGAGAGAGAGAGAGAGAGAG 1813
Db 4173 AGATGTAGATGATTAATATATATGAGCGGGGGTGTGTCATGAGAGAGAGAGAGAGAGAGAG 4232
Qy 1814 AATGTAAAGTTTACTGGCCCAATTTTAAAGCGGTAAAGGTTTTCTGGCCAATACCAACTT 1873
Db 4233 AATGTAAAGTTTACTGGCCCAATTTTAAAGCGGTAAAGGTTTTCTGGCCAATACCAACTT 4292
Qy 1874 ATCTTAACAGGATTAATGATTAATGAGGTTTAAACAATCTGTGAGAGAGAGAGAGAGAGAG 1933
Db 4293 ATCTTAACAGGATTAATGATTAATGAGGTTTAAACAATCTGTGAGAGAGAGAGAGAGAGAG 4352
Qy 1934 GTAAGGGTTCCGGGCTGTGCTTTTAACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1993
Db 4353 GTAAGGGTTCCGGGCTGTGCTTTTAACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4412

Qy 1994 AGCAGGGCTTCAATTAAGAAATGCTCTTTTGAAGAGTGAACCTTGAGTATCTGTCTGAG 2053
Db 4413 AGCAGGGCTTCAATTAAGAAATGCTCTTTTGAAGAGTGAACCTTGAGTATCTGTCTGAG 4472
Qy 2054 GGTAACTTCAGAGGGGCGGCAAAATGAGGCGGCAAGTGTGAGTGTGTTGCTTGAATCTGAGTGA 2113
Db 4473 GGTAACTTCAGAGGGGCGGCAAAATGAGGCGGCAAGTGTGAGTGTGTTGCTTGAATCTGAGTGA 4532
Qy 2114 AGCGTGTCTGTATTAAGCATTAATGATGATGAGCACTGCGAGAGAGAGAGAGAGAGAGAG 2173
Db 4533 AGCGTGTGTATTAAGCATTAATGATGATGAGCACTGCGAGAGAGAGAGAGAGAGAGAGAGAG 4592
Qy 2174 ATGCTGATCTGTGAG 2233
Db 4593 ATGCTGATCTGTGAG 4652
Qy 2234 TCTGCAAGGGCTGGCCAGTGTGAGATTAACATGACATCCGCTGTTCTTGATTTG 2293
Db 4653 TCTGCAAGGGCTGGCCAGTGTGAGATTAACATGACATCCGCTGTTCTTGATTTG 4712
Qy 2294 GGTAAACAGAGAGGGGGTGTCTTCTTACCTTAACATGCAATTTGAGTCACTTAAGATATTG 2353
Db 4713 GGTAAACAGAGAGGGGGTGTCTTCTTACCTTAACATGCAATTTGAGTCACTTAAGATATTG 4772
Qy 2354 CTTAGAGCCGAGAGATGTCCAAGGTGAACCTGAAACGGGGTGTGATGATGATGATGATGATG 2413
Db 4773 CTTAGAGCCGAGAGATGTCCAAGGTGAACCTGAAACGGGGTGTGATGATGATGATGATGATG 4832
Qy 2414 ATCTGAAAGGTGTGAGGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2473
Db 4833 ATCTGAAAGGTGTGAGGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4892
Qy 2474 GGTAAACATTAATTAAGAAACAGAGCTGTGATGCTGATGATGATGATGATGATGATGATGAT 2533
Db 4893 GGTAAACATTAATTAAGAAACAGAGCTGTGATGCTGATGATGATGATGATGATGATGATGAT 4952
Qy 2534 CACTTGTGTGCTGCTGCTGCAACCGGCGCTGAGATTTGCTTGAAGATGAAGATGAAGATTTGA 2593
Db 4953 CACTTGTGTGCTGCTGCTGCAACCGGCGCTGAGATTTGCTTGAAGATGAAGATGAAGATTTGA 5012
Qy 2594 G 2594
Db 5013 G 5013

Search completed: October 31, 2005, 01:17:04
Job time : 438 secs

This Page Blank (uspio)

Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	ATGCATCTTACTGCGCACGAGGCTGGCTTTTCCACCCAGTGACGACGAGATGAAAGGGT	60	
Db	459	ATGCATCTTACTGCGCACGAGGCTGGCTTTTCCACCCAGTGACGACGAGATGAAAGGGT	518	
Qy	61	GAGAGTTTGTTAGATTATGTGGAGCACCCGGGACGGTTGCGAGGCTTGTCAATAT	120	
Db	519	GAGAGTTTGTTAGATTATGTGGAGCACCCGGGACGGTTGCGAGGCTTGTCAATAT	578	
Qy	121	CACCGAGAAATACGGGGGACCCAGATATATGTGTTCCTTTGCTATATAGACCTGT	180	
Db	579	CACCGAGAAATACGGGGGACCCAGATATATGTGTTCCTTTGCTATATAGACCTGT	638	
Qy	181	GGCAGTTTGTCTACAGTAAGTGAATAATTATGGGAGTGGGTATAGTGTGGGTTTG	240	
Db	639	GGCAGTTTGTCTACAGTAAGTGAATAATTATGGGAGTGGGTATAGTGTGGGTTTG	698	
Qy	241	GTGAGTAAATTTTTTTTAAATTTTAACTGTTTGTGTTTAAAGAAATTTGTATGTGA	300	
Db	699	GTGAGTAAATTTTTTTTAAATTTTAACTGTTTGTGTTTAAAGAAATTTGTATGTGA	758	
Qy	301	TTTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCGAGCCAGAACCGAGCTTG	360	
Db	759	TTTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCGAGCCAGAACCGAGCTTG	818	
Qy	361	CAAGACCTACCCGCGCTCTAAATATGGGCGCTGCTATCTGAGACGCCGACATCACTTG	420	
Db	819	CAAGACCTACCCGCGCTCTAAATATGGGCGCTGCTATCTGAGACGCCGACATCACTTG	878	
Qy	421	TGTCTAGAGAAATGCAATAGTATAGTACGATAGCTGTGACTCCGCTCTTCTAACAACCTC	480	
Db	879	TGTCTAGAGAAATGCAATAGTATAGTACGATAGCTGTGACTCCGCTCTTCTAACAACCTC	938	
Qy	481	CTGAGATACACCCGGTGTCCGCTGTGCCCATTTAAACAAGTCCGTGAGAGTTGTG	540	
Db	939	CTGAGATACACCCGGTGTCCGCTGTGCCCATTTAAACAAGTCCGTGAGAGTTGTG	998	
Qy	541	GGCGTCGCAAGCTGTGAAATGTAATCGAGGACTTGCTTAAAGAGCTGGGACCTTTTG	600	
Db	999	GGCGTCGCAAGCTGTGAAATGTAATCGAGGACTTGCTTAAAGAGCTGGGACCTTTTG	1058	
Qy	601	ACTTGAGCTGTAAACGCCACGAGCCATTAAGGTGTAAACCTGTGATTCGTGTGTGTTAA	660	
Db	1059	ACTTGAGCTGTAAACGCCACGAGCCATTAAGGTGTAAACCTGTGATTCGTGTGTGTTAA	1118	
Qy	661	CGCTTTGTTGCTGAATGAGTTGATGTAAATTAATAAGGTGAGATTAATGTTAACT	720	
Db	1119	CGCTTTGTTGCTGAATGAGTTGATGTAAATTAATAAGGTGAGATTAATGTTAACT	1178	
Qy	721	TGCATGGCGTGTAAATGGGCGGGGCTTAAAGGTAATATATGCGCGTGGCTAATCT	780	
Db	1179	TGCATGGCGTGTAAATGGGCGGGGCTTAAAGGTAATATATGCGCGTGGCTAATCT	1238	
Qy	781	TGTTTACATCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCTGA	840	
Db	1239	TGTTTACATCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCTGA	1298	
Qy	841	ACTTGCTGAAACAGAGCTCTAAACAGTACCTCTGTGTTTGAAGTTCGTGTGGGCTCAT	900	
Db	1299	ACTTGCTGAAACAGAGCTCTAAACAGTACCTCTGTGTTTGAAGTTCGTGTGGGCTCAT	1358	
Qy	901	CCCGAGGAAAGTATGTGCGAAGATTAGAGGATTAAGAAGGGAATTTGAAGGCTTT	960	
Db	1359	CCCGAGGAAAGTATGTGCGAAGATTAGAGGATTAAGAAGGGAATTTGAAGGCTTT	1418	
Qy	961	TGAATCCTGTGTAGCTGTGTTGATCTTTGAATCTGGGTCAACGAGCGCTTTTCCAG	1020	
Db	1419	TGAATCCTGTGTAGCTGTGTTGATCTTTGAATCTGGGTCAACGAGCGCTTTTCCAG	1478	
Qy	1021	AGAAAGTCATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGTGCTT	1080	
Db	1479	AGAAAGTCATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGTGCTT	1538	

Qy	1081	TTTTGAGTTTTTAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTAACTTGC	1140	
Db	1539	TTTTGAGTTTTTAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTAACTTGC	1598	
Qy	1141	TGAAATTTTCGCCCATCTGTGTGAGAGCGGTTGTGAACAAGAATTCCTGTCTAC	1200	
Db	1599	TGAAATTTTCGCCCATCTGTGTGAGAGCGGTTGTGAACAAGAATTCCTGTCTAC	1658	
Qy	1201	TGTTGTCTTCGCTCCGCTCCGCGCATATACCAGAGAGAGACACAGACAGAGAGG	1260	
Db	1659	TGTTGTCTTCGCTCCGCTCCGCGCATATACCAGAGAGAGACACAGACAGAGAGG	1718	
Qy	1261	AAGCCAGCGCGCGGCGCAGAGCAGAGCCCATGGAACCCGAGAGCGGCTTGACCTTC	1320	
Db	1719	AAGCCAGCGCGCGGCGCAGAGCAGAGCCCATGGAACCCGAGAGCGGCTTGACCTTC	1778	
Qy	1321	GGGAATGAATGTTGTACAGGTGTGCTGTAATCTGTATCCAGAACTGAGACGCAATTTGACAT	1380	
Db	1779	GGGAATGAATGTTGTGTACAGGTGTGCTGTAATCTGTATCCAGAACTGAGACGCAATTTGACAT	1838	
Qy	1381	TACAGAGATGGCGAGGGGCTTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGCTAC	1440	
Db	1839	TACAGAGATGGCGAGGGGCTTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGCTAC	1898	
Qy	1441	AGAGAGGCTAGGAATCTAGCTTTTACCTTAAATGACACAGACACCGTCTGAGTGAATTAC	1500	
Db	1899	AGAGAGGCTAGGAATCTAGCTTTTACCTTAAATGACACAGACACCGTCTGAGTGAATTAC	1958	
Qy	1501	TTTTCAACAGATCAAGATTAATTCGCTAATGAGCTTGAATCTGTGCGCAGAAATATTC	1560	
Db	1959	TTTTCAACAGATCAAGATTAATTCGCTAATGAGCTTGAATCTGTGCGCAGAAATATTC	2018	
Qy	1561	CATGAGACGCTGACCACTTATCTGCTGACGCCAGGGGATGATTTTGAAGAGCTAATTAG	1620	
Db	2019	CATGAGACGCTGACCACTTATCTGCTGACGCCAGGGGATGATTTTGAAGAGCTAATTAG	2078	
Qy	1621	GGTATATGCAAAAGGTGACACTTAGGCGAGATTGCAAGTACCAAGTACCAAACTTGTAAA	1680	
Db	2079	GGTATATGCAAAAGGTGACACTTAGGCGAGATTGCAAGTACCAAGTACCAAACTTGTAAA	2138	
Qy	1681	TATCAGGAATTTGTTGCTACATTTCTGGGAAACGGGGCGGAGTGGAGATGATACGAGGA	1740	
Db	2139	TATCAGGAATTTGTTGCTACATTTCTGGGAAACGGGGCGGAGTGGAGATGATACGAGGA	2198	
Qy	1741	TAGGCTGGCTTTAGATGATGATGATTAATATGTGCGCGGGGCTGTTGGCATGAGACGG	1800	
Db	2199	TAGGCTGGCTTTAGATGATGATGATTAATATGTGCGCGGGGCTGTTGGCATGAGACGG	2258	
Qy	1801	GGTGGTATTAATGAATGTAAGGTTTAACTGGGCCCAATTTTATGCGGTACGGTTTCTGTC	1860	
Db	2259	GGTGGTATTAATGAATGTAAGGTTTAACTGGGCCCAATTTTATGCGGTACGGTTTCTGTC	2318	
Qy	1861	CAATACCAACCTTATCTTACACGGGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGTGA	1920	
Db	2319	CAATACCAACCTTATCTTACACGGGTGTAAGCTTCTATGGGTTTAAACAATACCTGTGTGA	2378	
Qy	1921	AGCTTGACCGATATAGGCTTGGGGCTGTGCTTTTATCTGCTGTGCGAAGGGGGTGGT	1980	
Db	2379	AGCTTGACCGATATAGGCTTGGGGCTGTGCTTTTATCTGCTGTGCGAAGGGGGTGGT	2438	
Qy	1981	GTGTGCGCCCAAAAGCAGAGGCTTCAATTAAGAATATGCTCTTTGAAAGGTATACCTTGGG	2040	
Db	2439	GTGTGCGCCCAAAAGCAGAGGCTTCAATTAAGAATATGCTCTTTGAAAGGTATACCTTGGG	2498	
Qy	2041	TATCTGTCTGAGGGTAACTTCAGAGGTGCGCCACAATGTGCGCTCCGACTGTGTGCTT	2100	
Db	2499	TATCTGTCTGAGGGTAACTTCAGAGGTGCGCCACAATGTGCGCTCCGACTGTGTGCTT	2558	
Qy	2101	CATGCTATGAAAAGCGTGTGCTGTGATTAAGCAATTAAGTATGTGGCACTGCGAAGA	2160	
Db	2559	CATGCTATGAAAAGCGTGTGCTGTGATTAAGCAATTAAGTATGTGGCACTGCGAAGA	2618	

QY	2161	CAGGGCCCTTCAGATGCTGACCTGCTGGACGGCACTGTACCTGCTGAAAGACATTCA	2220
Db	2619	CAGGGCCCTTCAGATGCTGACCTGCTGGACGGCACTGTACCTGCTGAAAGACATTCA	2678
QY	2221	CGTAGCCAGCACACTCTGCGAAGGCTGGCCAGTGTTTGAGCATAAACATCTGAACCCCTTG	2280
Db	2679	CGTAGCCAGCACACTCTGCGAAGGCTGGCCAGTGTTTGAGCATAAACATCTGAACCCGCTG	2738
QY	2281	TTCCCTTGCAATTTGGGTAAACAGAGGGGGGTCTCTACCTTACCAATGCAATTTGAATCA	2340
Db	2739	TTCCCTTGCAATTTGGGTAAACAGAGGGGGGTCTCTACCTTACCAATGCAATTTGAATCA	2798
QY	2341	CACATAAGATATTGCTTGAGCCCGAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTTTGA	2400
Db	2799	CACATAAGATATTGCTTGAGCCCGAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTTTGA	2858
QY	2401	CATACCATGTAAGATCTGGAAAGTGTCTGAGGTACGATGACAGCCCGCACCAAGTGTCAAGCC	2460
Db	2859	CATACCATGTAAGATCTGGAAAGTGTCTGAGGTACGATGACAGCCCGCACCAAGTGTCAAGCC	2918
QY	2461	CTGCGAGTGTGCGCGGTAAACATATTAGGAACAGAGCTGTGATGCTGATGTGAAACGAGGA	2520
Db	2919	CTGCGAGTGTGCGCGGTAAACATATTAGGAACAGAGCTGTGATGCTGATGTGAAACGAGGA	2978
QY	2521	GCTGAGGCCCGCATCACTTGTGTGCTGGACCTGCAACCGCGCTGATGTTTGGCTCTACGATGA	2580
Db	2979	GCTGAGGCCCGCATCACTTGTGTGCTGGACCTGCAACCGCGCTGATGTTTGGCTCTACGATGA	3038
QY	2581	AGATACAGATTTGAG 2594	
Db	3039	AGATACAGATTTGAG 3052	

```

RESULT 2
US-09-847-101B-34
/ Sequence 34, Application US/09847101B
/ Publication No. US20020193327A1
/ GENERAL INFORMATION:
/ APPLICANT: VON SEGGERN, DANIEL
/ APPLICANT: NEMEROW, GLEN R.
/ APPLICANT: FRIEDLANDER, MARTIN
/ TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
/ FILE REFERENCE: 23908-1226B
/ CURRENT APPLICATION NUMBER: US/09/847,101B
/ CURRENT FILING DATE: 2001-05-01
/ PRIOR APPLICATION NUMBER: 09/562,934
/ PRIOR FILING DATE: 2000-05-01
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 34
/ LENGTH: 7607
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: plasmid GRES-El-SV40-Hygro
/ US-09-847-101B-34

```

Query Match	100.0%	Score 2594	DB 9	Length 7607
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2594	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ATCGATCTTACCTTCCACGAGGCTGGCTTTCCACCCAGTAGCGACGAGATGAAGAGGT	60	
Db	1334	ATCGATCTTACCTTCCACGAGGCTGGCTTTCCACCCAGTAGCGACGAGATGAAGAGGT	1393	
QY	61	GAGGAGTTTGTTAGATTATGTGAGACACCCGGGACAGGTTGACAGTCTTGCATTAT	120	
Db	1394	GAGGAGTTTGTTAGATTATGTGAGACACCCGGGACAGGTTGACAGTCTTGCATTAT	1453	
QY	121	CACCGGAGGAATACGGGGGACCCAGATTATATGTGTTGCTTCTATATGAGACCTGT	180	
Db	1454	CACCGGAGGAATACGGGGGACCCAGATTATATGTGTTGCTTCTATATGAGACCTGT	1513	

QY	181	GGCATGTTTGTCTACAGTAAGTAAATTTATGGCACTGGGTGATTAAGTGTGGGTTTG	240
Db	1514	GGCATGTTTGTCTACAGTAAGTAAATTTATGGCACTGGGTGATTAAGTGTGGGTTTG	1573
QY	241	GTGATGATAATTTTTTTTTTAATTTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATGTGA	300
Db	1574	GTGATGATAATTTTTTTTTTAATTTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATGTGA	1633
QY	301	TTTTTTTTAAAGGTCCTGTGTCTGAACCTGAGCTGAGCCCGAGCCGAACCCGAGCCTG	360
Db	1634	TTTTTTTTAAAGGTCCTGTGTCTGAACCTGAGCTGAGCCCGAGCCGAACCCGAGCCTG	1693
QY	361	CAAGACCTACCCCGCGCTCTAAATTTGGCGCTGCTATCTGAGACGCCCGACATCACTGT	420
Db	1694	CAAGACCTACCCCGCGCTCTAAATTTGGCGCTGCTATCTGAGACGCCCGACATCACTGT	1753
QY	421	TGTCATAGGAATGCAATAGTATGTAAGTACGTGATCTCCGGCTCTTCAACACACTC	480
Db	1754	TGTCATAGGAATGCAATAGTATGTAAGTACGTGATCTCCGGCTCTTCAACACACTC	1813
QY	481	CTGAGATACACCCGGTGGTCCCGCTGTGCCCATTAACGAGTCCGATGAGATTGGTG	540
Db	1814	CTGAGATACACCCGGTGGTCCCGCTGTGCCCATTAACGAGTCCGATGAGATTGGTG	1873
QY	541	GGCGTCCGACAGGCTGTGGAATGTATCGAGACTTGTCTTAACAGCCTGGGCAACTTTGG	600
Db	1874	GGCGTCCGACAGGCTGTGGAATGTATCGAGACTTGTCTTAACAGCCTGGGCAACTTTGG	1933
QY	601	ACTTACGCTGTAACGGCCCAAGGCTATTAAGGTGTAACCTGTGATTCGGTGTGGTTAA	660
Db	1934	ACTTACGCTGTAACGGCCCAAGGCTATTAAGGTGTAACCTGTGATTCGGTGTGGTTAA	1993
QY	661	CGCCTTGTGTTGCTGAATGAGTTGATGTAAATTAAATAAAGGCTGAGATATGTTTAAT	720
Db	1994	CGCCTTGTGTTGCTGAATGAGTTGATGTAAATTAAATAAAGGCTGAGATATGTTTAAT	2053
QY	721	TGCATGCGGTGTAAATGCGGCGGGGCTTAAAGGGTATATATGCGCGCTGGGCTAATCT	780
Db	2054	TGCATGCGGTGTAAATGCGGCGGGGCTTAAAGGGTATATATGCGCGCTGGGCTAATCT	2113
QY	781	TGCTTACATCTGACCTCATAGGAGCTTGGAGTGTTTGGAAATTTTCTGCTGTGGTA	840
Db	2114	TGCTTACATCTGACCTCATAGGAGCTTGGAGTGTTTGGAAATTTTCTGCTGTGGTA	2173
QY	841	ACTTGTGGAACAGAGCTCTAACGTACCTCTTGTGTTGGAAGTTTCTGTGGGGCTCAT	900
Db	2174	ACTTGTGGAACAGAGCTCTAACGTACCTCTTGTGTTGGAAGTTTCTGTGGGGCTCAT	2233
QY	901	CCGAGCAAGTATGTCGAGATTAAGAGATTAACAATGGGAATTTGAAGAGCTTT	960
Db	2234	CCGAGCAAGTATGTCGAGATTAAGAGAGATTAACAATGGGAATTTGAAGAGCTTT	2293
QY	961	TGAAATCTGTGTGTGAGCTGTTTGATCTTTGAAATCTGGGTCAACAGCGCTTTCCAG	1020
Db	2294	TGAAATCTGTGTGTGAGCTGTTTGATCTTTGAAATCTGGGTCAACAGCGCTTTCCAG	2353
QY	1021	AGAGGTTCATCAACACTTTGGATTTTTTCCACACCGGGGCGGCTGCGGCTGTGCTT	1080
Db	2354	AGAGGTTCATCAACACTTTGGATTTTTTCCACACCGGGGCGGCTGCGGCTGTGCTT	2413
QY	1081	TTTTGAGTTTTATTAAGATTAATGAGCGAGAAACCACTTGAGCGGGGGATCACTGC	1140
Db	2414	TTTTGAGTTTTATTAAGATTAATGAGCGAGAAACCACTTGAGCGGGGGATCACTGC	2473
QY	1141	TGGAATTTTCTGGCCATGCAATCTGTGGAGACGGGTGTGAAACACAAATTCGCTGTAC	1200
Db	2474	TGGAATTTTCTGGCCATGCAATCTGTGGAGACGGGTGTGAAACACAAATTCGCTGTAC	2533
QY	1201	TGTTGTCTTCCGTCGCGCCGAGCAATATTAACGACGAGAGACAGCAGCAGCAGGAGG	1260
Db	2534	TGTTGTCTTCCGTCGCGCCGAGCAATATTAACGACGAGAGACAGCAGCAGCAGGAGG	2593
QY	1261	AAGCAGGCGGCGGACAGAGCAGGCCATGGAACCCGAGAGCGGCGCTGAGCCCTC	1320

Db	2594	AAGCAGCGCGCGCGGAGAGCAGAGCCATGGAACCCAGAGCGGCTTGACCTTC	2653
Qy	1321	GGGAATGAATGTTGTACAGGTGGCTGAACTGTATTCAGAACTGAGACGATTTTGACAT	1380
Db	2654	GGGAATGAATGTTGTACAGGTGGCTGAACTGTATTCAGAACTGAGACGATTTTGACAT	2713
Qy	1381	TACAGAGATGGGACGGGCTTAAAGGGGTAAAGGGAGGGGGGGCTTTGAGGGCTAC	1440
Db	2714	TACAGAGATGGGACGGGCTTAAAGGGGTAAAGGGAGGGGGGGCTTTGAGGGCTAC	2773
Qy	1441	AGAGAGGCTAGGAATCTAGCTTTTATGATGACAGACACGCTCTGATGATTAAC	1500
Db	2774	AGAGAGGCTAGGAATCTAGCTTTTATGATGACAGACACGCTCTGATGATTAAC	2833
Qy	1501	TTTTCAACAGATCAAGATTAATTGGCTTAATGAGCTTGTCTGGCGCAGAAATATTC	1560
Db	2834	TTTTCAACAGATCAAGATTAATTGGCTTAATGAGCTTGTCTGGCGCAGAAATATTC	2893
Qy	1561	CATAGAGAGCTGACCACTTACTGGCTGACCGAGGGAGATATTTTGAGGAGCTATTAG	1620
Db	2894	CATAGAGAGCTGACCACTTACTGGCTGACCGAGGGAGATATTTTGAGGAGCTATTAG	2953
Qy	1621	GGTATATGCAAAAGGTGGCACTTAGGCGAGATTGCAAGTACAGCAAACTTGTA	1680
Db	2954	GGTATATGCAAAAGGTGGCACTTAGGCGAGATTGCAAGTACAGCAAACTTGTA	3013
Qy	1681	TATCAGAAATGTTGCTACATTTCTGGGACCGGGCCGAGGTGAGATATACCGAGGA	1740
Db	3014	TATCAGAAATGTTGCTACATTTCTGGGACCGGGCCGAGGTGAGATATACCGAGGA	3073
Qy	1741	TAGGCTGCGCTTTGATGATGATGATTAATATGAGCGGGGGGCTTGGCATGGAACG	1800
Db	3074	TAGGCTGCGCTTTGATGATGATGATTAATATGAGCGGGGGGCTTGGCATGGAACG	3133
Qy	1801	GGTGGTATTAATGATGATGATGATTAATATGAGCGGGGGGCTTGGCATGGAACG	1860
Db	3134	GGTGGTATTAATGATGATGATGATTAATATGAGCGGGGGGCTTGGCATGGAACG	3193
Qy	1861	CAATATCCAACTTATCTTACACGCGTGAAGCTTCTATGAGGTTTAACTACCTGTGGA	1920
Db	3194	CAATATCCAACTTATCTTACACGCGTGAAGCTTCTATGAGGTTTAACTACCTGTGGA	3253
Qy	1921	AGCGTGGACCGATGTAAGGTTCCGGGGCTGCTTACTGCTGCTGGAAGGGGGTGT	1980
Db	3254	AGCGTGGACCGATGTAAGGTTCCGGGGCTGCTTACTGCTGCTGGAAGGGGGTGT	3313
Qy	1981	GTGTCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGACCTTGG	2040
Db	3314	GTGTCGCCCAAAAGCAGGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGACCTTGG	3373
Qy	2041	TATCTGTCTGAGGTAATCTCAAGGCTGCGCAATGTGGCTTCCGACTGTGTGCTT	2100
Db	3374	TATCTGTCTGAGGTAATCTCAAGGCTGCGCAATGTGGCTTCCGACTGTGTGCTT	3433
Qy	2101	CATGCTATGAAAAGCGTGGCTGTAATTAAGCATTAACGTGATGTCGCACTGGAAGA	2160
Db	3434	CATGCTATGAAAAGCGTGGCTGTAATTAAGCATTAACGTGATGTCGCACTGGAAGA	3493
Qy	2161	CAGGCGCTCTCAGATGTCGACCTGCTGCAAGGCAATGTCACTCTGGAAGCACTTCA	2220
Db	3494	CAGGCGCTCTCAGATGTCGACCTGCTGCAAGGCAATGTCACTCTGGAAGCACTTCA	3553
Qy	2221	CGTAGCCAGCCACTTCCGAAAGGCTGGCCAGTGTGTTGACATAACATACGACCGCTG	2280
Db	3554	CGTAGCCAGCCACTTCCGAAAGGCTGGCCAGTGTGTTGACATAACATACGACCGCTG	3613
Qy	2281	TTCCCTGATTTGGGTAAACAGGAGGGGGGTGTTCTACCTTAACCAATTAATTTGATCA	2340
Db	3614	TTCCCTGATTTGGGTAAACAGGAGGGGGGTGTTCTACCTTAACCAATTAATTTGATCA	3673
Qy	2341	CACATAAGATATTTGCTGAGCCGAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTGA	2400

Db	3674	CACATAAGATATTTGCTTGAGCCCGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGGA	3723
Qy	2401	CATGACCATGAAGATCTTGAAAGGTGCTGAGTACGATGAGAACCCCGCACAGGTGCAAGC	2460
Db	3734	CATGACCATGAAGATCTTGAAAGGTGCTGAGTACGATGAGAACCCCGCACAGGTGCAAGC	3793
Qy	2461	CTGCGAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGTGATGACCGAGGA	2520
Db	3794	CTGCGAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGTGATGACCGAGGA	3853
Qy	2521	GCTGAGCCCGATCACTTGTGTCTGCTGCTGCAACCCGCGCTGAGTTTGGCTTACGATGA	2580
Db	3854	GCTGAGCCCGATCACTTGTGTCTGCTGCTGCAACCCGCGCTGAGTTTGGCTTACGATGA	3913
Qy	2581	AGATACGATTTGAG	2594
Db	3914	AGATACGATTTGAG	3927
RESULT 3			
US-09-482-682-48			
Sequence 48, Application US/09482682			
Publication No. US20030157688A1			
GENERAL INFORMATION:			
APPLICANT: VON SEGGERN, DANIEL			
APPLICANT: NEMEROW, GLEN R.			
APPLICANT: HALLENBECK, PAUL			
APPLICANT: STEVENSON, SUSAN			
TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,			
FILE REFERENCE: 1294, 0010001			
CURRENT APPLICATION NUMBER: US/09/482,682			
NUMBER OF INVENTION: AND METHODS FOR PREPARATION AND USE			
CURRENT FILING DATE: 2000-01-14			
NUMBER OF SEQ ID NOS: 76			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 48			
LENGTH: 7607			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Description of Artificial Sequence: plasmid			
US-09-482-682-48			
Query Match 100.0%; Score 2594; DB 10; Length 7607;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	ATCGATCTTACCTGCAAGAGGCTGCTTCCACCCAGTGAAGAGATGAAGAGGT	60
Db	1334	ATCGATCTTACCTGCAAGAGGCTGCTTCCACCCAGTGAAGAGATGAAGAGGT	1393
Qy	61	GAGGAGTTTGTGTTAGATTAATGTGAGACACCCCGGGACGGTTCAAGTCTTGTCAATTAT	120
Db	1394	GAGGAGTTTGTGTTAGATTAATGTGAGACACCCCGGGACGGTTCAAGTCTTGTCAATTAT	1453
Qy	121	CACCGAGGAATTAAGGGGAGCCGAGATTAATGCTTGGCTTGTATATGAGACCTGT	180
Db	1454	CACCGAGGAATTAAGGGGAGCCGAGATTAATGCTTGGCTTGTATATGAGACCTGT	1513
Qy	181	GGCATGTTTGTCTACATTAAGTGAATAATGAGCAGTGGGTGATAGAGTGGGTTTG	240
Db	1514	GGCATGTTTGTCTACATTAAGTGAATAATGAGCAGTGGGTGATAGAGTGGGTTTG	1573
Qy	241	GTGTGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	300
Db	1574	GTGTGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	1633
Qy	301	TTTTTTTAAAGGTCGTGCTGAACCTGAGCCTGAGCCCGAGACCGAAGCGGAGCTG	360
Db	1634	TTTTTTTAAAGGTCGTGCTGAACCTGAGCCTGAGCCCGAGACCGAAGCGGAGCTG	1693
Qy	361	CAGACCTACCCGCGTCTTAAATGCGCCTGCTATCTGAGACGCCGACATCACTTG	420

Db 1694 CAAAGCTAACCCGCGCTCTTAAATAGCGCCCTGCTATCTGAGAGCCCGACATCACTG 1753
Qy 421 TGTCTAGAGAAATGCAATATAGTATGAGTACGATAGCTGAGCTCCGCTCTTCTAACAACCTC 480
Db 1754 TGTCTAGAGAAATGCAATATAGTATGAGTACGATAGCTGAGCTCCGCTCTTCTAACAACCTC 1813
Qy 481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCATTTAAACCAAGTTGCCGTGAGAGTTGGTG 540
Db 1814 CTGAGATACACCCGGTGGTCCCGCTGTGCCCATTTAAACCAAGTTGCCGTGAGAGTTGGTG 1873
Qy 541 GGCCTCGCAGAGCTGTGAAATGTATCGAGACTTGTCTTAAAGAGCCGTGAGCAACTTTGG 600
Db 1874 GGCCTCGCAGAGCTGTGAAATGTATCGAGACTTGTCTTAAAGAGCCGTGAGCAACTTTGG 1933
Qy 601 ACTTGAAGCTGTAAAGCCCGCAGGCCATTAAGGTGTAAACCTGTGATTCGTGTGTGTAA 660
Db 1934 ACTTGAAGCTGTAAAGCCCGCAGGCCATTAAGGTGTAAACCTGTGATTCGTGTGTGTAA 1993
Qy 661 GCGCTTGT 720
Db 1994 GCGCTTGT 2053
Qy 721 TGCATGAGGCTGTAAATAGGAGGCGGCTTAAAGGGTATATATGCGCGGTGCTAATCT 780
Db 2054 TGCATGAGGCTGTAAATAGGAGGCGGCTTAAAGGGTATATATGCGCGGTGCTAATCT 2113
Qy 781 TGTGTATCATCTGACCTCATGAGAGGCTTGTGAGAGATTTTCTGTGTGTGTGTGTGTGT 840
Db 2114 TGTGTATCATCTGACCTCATGAGAGGCTTGTGAGAGATTTTCTGTGTGTGTGTGTGTGT 2173
Qy 841 ACTTGTCTGAAACAGAGCTCTTAACAGTACTCTGTGTTTGTGAGAGTTTCTGTGTGTGTGT 900
Db 2174 ACTTGTCTGAAACAGAGCTCTTAACAGTACTCTGTGTTTGTGAGAGTTTCTGTGTGTGTGT 2233
Qy 901 CCGAGGCAAAAGTTAGTGTGAGAAATTAAGAGAAATTAAGAGAAATTAAGAGAAATTAAGAG 960
Db 2234 CCGAGGCAAAAGTTAGTGTGAGAAATTAAGAGAAATTAAGAGAAATTAAGAGAAATTAAGAG 2293
Qy 961 TGAATCTGTGTGAGAGCTGTGTTGATCTTGTGAATCTGTGTGTGTGTGTGTGTGTGTGTGT 1020
Db 2294 TGAATCTGTGTGAGAGCTGTGTTGATCTTGTGAATCTGTGTGTGTGTGTGTGTGTGTGTGT 2353
Qy 1021 AGAAGCTCATAGACTTTTGTGATTTTTCACACCGGAGCGGCTGTGCTGTGTGTGTGTGT 1080
Db 2354 AGAAGCTCATAGACTTTTGTGATTTTTCACACCGGAGCGGCTGTGCTGTGTGTGTGTGT 2413
Qy 1081 TTTTGAAGTTTATTAAGGATTAATGAGAGCAAGAAACCATCTGAGCGGAGGAGTAACTGAC 1140
Db 2414 TTTTGAAGTTTATTAAGGATTAATGAGAGCAAGAAACCATCTGAGCGGAGGAGTAACTGAC 2473
Qy 1141 TGAATTTTCTGCGCATGATCTGTGAGAGAGGCTTGTGAGACACAGAAATGCGCTGTATC 1200
Db 2474 TGAATTTTCTGCGCATGATCTGTGAGAGAGGCTTGTGAGACACAGAAATGCGCTGTATC 2533
Qy 1201 TGTGTCTTCCGCTCCGCGCGCATATATACCGAGCGAGAGCAACAGACAGACAGAGAGAG 1260
Db 2534 TGTGTCTTCCGCTCCGCGCGCATATATACCGAGCGAGAGCAACAGACAGACAGAGAGAG 2593
Qy 1261 AAGCAGAGCGGCGGAG 1320
Db 2594 AAGCAGAGCGGCGGAG 2653
Qy 1321 GGAATATATGTTTATACAGTGTGTGTATCTGTATCTGAGAACTGAGAGCAATTTTGAACAT 1380
Db 2654 GGAATATATGTTTATACAGTGTGTGTATCTGTATCTGAGAACTGAGAGCAATTTTGAACAT 2713
Qy 1381 TACAGAGATGAGGCAAGGAGCTTAAAGGGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 2714 TACAGAGATGAGGCAAGGAGCTTAAAGGGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 2773
Qy 1441 AGAGAGAGCTGAGATCTAGCTTTTATAGCTTAATGACAGACAGAGTCTGTAGATTAATAC 1500

Db 2774 AGAGAGAGCTGAGATCTAGCTTTTATAGCTTAATGACAGACAGAGTCTGTAGATTAATAC 2833
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTATGTGTGTGTGTGTGTGTGTGTGTGT 1560
Db 2834 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTATGTGTGTGTGTGTGTGTGTGTGTGT 2893
Qy 1561 CATAGAGAGCTGACCACTTACTGCTGACAGCGAGATGATTTTGTAGAGAGCTATTAG 1620
Db 2894 CATAGAGAGCTGACCACTTACTGCTGACAGCGAGATGATTTTGTAGAGAGCTATTAG 2953
Qy 1621 GGTATATGCAAAAGGTGACCTTAAAGCCAGATTGCAAGTACAGCAACTTGTAA 1680
Db 2954 GGTATATGCAAAAGGTGACCTTAAAGCCAGATTGCAAGTACAGCAACTTGTAA 3013
Qy 1681 TATCAGAAATTTGTGTACATTTCTGTGAGAGCGGAGCCAGAGTGAATAGTACGAGAGA 1740
Db 3014 TATCAGAAATTTGTGTACATTTCTGTGAGAGCGGAGCCAGAGTGAATAGTACGAGAGA 3073
Qy 1741 TAGGCTGACCTTTAGATGTAGATGATTAATATGTGCGCGGAGTCTTGTGATGTACAG 1800
Db 3074 TAGGCTGACCTTTAGATGTAGATGATTAATATGTGCGCGGAGTCTTGTGATGTACAG 3133
Qy 1801 GATGATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
Db 3134 GATGATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3193
Qy 1861 CAATACCAACCTTATCTTACACGAGTGTAGAGCTTCTATGAGTTTAAACATACCTGTGTGA 1920
Db 3194 CAATACCAACCTTATCTTACACGAGTGTAGAGCTTCTATGAGTTTAAACATACCTGTGTGA 3253
Qy 1921 AGCTTGACCGATGTAAAGGTTGCGGAGCTGTGCTTTTACTGTCTGTGAAAGGGAGTGT 1980
Db 3254 AGCTTGACCGATGTAAAGGTTGCGGAGCTGTGCTTTTACTGTCTGTGAAAGGGAGTGT 3313
Qy 1981 GTGTGCGCCCAAAAGCAAGGCTTCAATTAAGAAATGCTCTTAAAGGTGTACCTTGG 2040
Db 3314 GTGTGCGCCCAAAAGCAAGGCTTCAATTAAGAAATGCTCTTAAAGGTGTGTACCTTGG 3373
Qy 2041 TATCTGTCTGAGAGGTAACTTCAAGGAGTGTGCGCAATGTGTGCTTCCGATCTGTGTGTGT 2100
Db 3374 TATCTGTCTGAGAGGTAACTTCAAGGAGTGTGCGCAATGTGTGCTTCCGATCTGTGTGTGT 3433
Qy 2101 CATCTAGTGAAGGCGT 2160
Db 3434 CATCTAGTGAAGGCGT 3493
Qy 2161 CAGGAGCTCTGAGATGTGACCTGTGCGAGCGCAACGTGTACCTGTGAAGACCATTTCA 2220
Db 3494 CAGGAGCTCTGAGATGTGACCTGTGCGAGCGCAACGTGTACCTGTGAAGACCATTTCA 3553
Qy 2221 CGTAGCAGGCACTCTGCAAGGCTGTGCGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2280
Db 3554 CGTAGCAGGCACTCTGCAAGGCTGTGCGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3613
Qy 2281 TTCTTGTGATTTGGGTAAACAGAGAGGAGGAGTGTCTTACCTTAACTGAATTTGAGTCA 2340
Db 3614 TTCTTGTGATTTGGGTAAACAGAGAGGAGGAGTGTCTTACCTTAACTGAATTTGAGTCA 3673
Qy 2341 CACTTAAGATATGCTTGAAGCCGAGAGCATGTCCAAAGTGAACCTGAACGGGAGGTTTGA 2400
Db 3674 CACTTAAGATATGCTTGAAGCCGAGAGCATGTCCAAAGTGAACCTGAACGGGAGGTTTGA 3733
Qy 2401 CATGACCATGAAAGTCTGGAAGGAGTGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
Db 3734 CATGACCATGAAAGTCTGGAAGGAGTGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3793
Qy 2461 CTGAGATGTGTGCGGTAAACATATTAGAAACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGT 2520
Db 3794 CTGAGATGTGTGCGGTAAACATATTAGAAACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGT 3853
Qy 2521 GCTGAGGCGCGATCATCTTGT 2580
Db 3854 GCTGAGGCGCGATCATCTTGT 3913

Qy	1521	GGTATATGCAAAAGGTGGCACTTAGCCGAGATTGGCAAGTACAAAGTACGAAACCTTGTAAA	1680
Dp	2954	GGTATATGCAAAAGGTGGCACTTAGCCGAGATTGGCAAGTACAAAGTACGAAACCTTGTAAA	3013
Qy	1681	TATCAGGAATATGTTGCTCACTTTCGGGAAACGGGGCCAGGTGGAGATAGATACGAGAGA	1740
Dp	3014	TATCAGGAATATGTTGCTCACTTTCGGGAAACGGGGCCAGGTGGAGATAGATACGAGAGA	3073
Qy	1741	TAGGGTGGCCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATAGACGG	1800
Dp	3074	TAGGGTGGCCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATAGACGG	3133
Qy	1801	GGTGGTTATATATGATATGTAAGGTTTACTAGGCCCAATTTTACGGGTACGGTTTCTGGCC	1860
Dp	3134	GGTGGTTATATATGATATGTAAGGTTTACTAGGCCCAATTTTACGGGTACGGTTTCTGGCC	3193
Qy	1861	CAATACCAACCTTATCTTACACAGGTGAAGCTTCTATGGGTTTAAACATACTGTGTGGA	1920
Dp	3194	CAATACCAACCTTATCTTACACAGGTGAAGCTTCTATGGGTTTAAACATACTGTGTGGA	3253
Qy	1921	AGCTTGAACCGATGTAAAGGTTTCGGGGCTGTGCTTTATCTGTGTGTGGAAGGGGGTGT	1980
Dp	3254	AGCTTGAACCGATGTAAAGGTTTCGGGGCTGTGCTTTATCTGTGTGTGGAAGGGGGTGT	3313
Qy	1981	GTTGTGCCCCCAAAAGCAGGGGCTTCAATTAAAGAAATGCTCTTTGAAAGGTACCTTGGG	2040
Dp	3314	GTTGTGCCCCCAAAAGCAGGGGCTTCAATTAAAGAAATGCTCTTTGAAAGGTACCTTGGG	3373
Qy	2041	TATCTGTGTCTGAGGGTAACTTCAGGGTGTGGCCACAAATGTGGCTTCCGACTGTGGTGTCTT	2100
Dp	3374	TATCTGTGTCTGAGGGTAACTTCAGGGTGTGGCCACAAATGTGGCTTCCGACTGTGGTGTCTT	3433
Qy	2101	CATCTGTATGTAAAGCCGTGGCTGTGATTAACATTAACAATGTATGTGGCACTGTGGAGA	2160
Dp	3434	CATCTGTATGTAAAGCCGTGGCTGTGATTAACATTAACAATGTATGTGGCACTGTGGAGA	3493
Qy	2161	CAGGGCCTCTCAGATGTCTGACCTGTCCGAGCGGCACTGTCACTGTGCGAAGACCATTC	2220
Dp	3494	CAGGGCCTCTCAGATGTCTGACCTGTCCGAGCGGCACTGTCACTGTGCGAAGACCATTC	3553
Qy	2221	CGTAGCCACCACTCTCGCAGACGCGCTGGCCAGTGTTTGAGCATTAATATCTGACCCGCTG	2280
Dp	3554	CGTAGCCACCACTCTCGCAGACGCGCTGGCCAGTGTTTGAGCATTAATATCTGACCCGCTG	3613
Qy	2281	TTCTCTTCAATTTGGGTAAACAGAGAGGGGGGTCTCTCTCAACAAATGCAATTTGAGTCA	2340
Dp	3614	TTCTCTTCAATTTGGGTAAACAGAGAGGGGGGTCTCTCTCAACAAATGCAATTTGAGTCA	3673
Qy	2341	CACCTAAGATATTCCTTGAAGCCCGAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTTGA	2400
Dp	3674	CACCTAAGATATTCCTTGAAGCCCGAGAGCATGTCCAAAGGTGAACCTGAAACGGGGTGTTGA	3733
Qy	2401	CATGACCATGAAGATCTGGAAGGTGTCTGAGGTACGATGACACCCGACCAAGGTGCAAC	2460
Dp	3734	CATGACCATGAAGATCTGGAAGGTGTCTGAGGTACGATGACACCCGACCAAGGTGCAAC	3793
Qy	2461	CTGGGAGGTGGCGGTAAACATATTTAGGAACACAGCTGTGATGTGCTGGAATGTGAACGAGA	2520
Dp	3794	CTGGGAGGTGGCGGTAAACATATTTAGGAACACAGCTGTGATGTGCTGGAATGTGAACGAGA	3853
Qy	2521	GCTGAGGCCCGCATCACTTGTGTGTGTGACCTGTGACCCGCGCTGAGTTGGCTTACGATGA	2580
Dp	3854	GCTGAGGCCCGCATCACTTGTGTGTGTGACCTGTGACCCGCGCTGAGTTGGCTTACGATGA	3913
Qy	2581	AGATACAGATTGAG 2594	
Dp	3914	AGATACAGATTGAG 3927	

RESULT 5
US-10-351-890-41
; Sequence 41, Application US/10351890

Query Match	Similarity	Score	DB	Length	7607
Best Local Similarity	100.0%	Pred. No. 0			
Matches 2594	Conservative	0	Mismatches	0	Gaps 0
US-10-351-890-41					
GENERAL INFORMATION:					
Publication No. US20040002060A1					
APPLICANT: Stevenson, Susan C.					
APPLICANT: Kaleko, Michael					
APPLICANT: Smith, Theodore					
APPLICANT: Nemerow, Glen R.					
TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting					
FILE REFERENCE: 22908-1236					
CURRENT APPLICATION NUMBER: US/10/351,890					
CURRENT FILING DATE: 2003-01-28					
PRIOR APPLICATION NUMBER: 60/350,388					
PRIOR FILING DATE: 2002-01-24					
PRIOR APPLICATION NUMBER: 60/391,967					
PRIOR FILING DATE: 2002-06-26					
NUMBER OF SEQ ID NOS: 72					
SOFTWARE: PatentIn version 3.0					
SEQ ID NO 41					
LENGTH: 7607					
TYPE: DNA					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Plasmid GRES-EI-SV40-Hygro					
US-10-351-890-41					
Query Match	100.0%	Score 2594	DB 18	Length 7607	
Best Local Similarity	100.0%	Pred. No. 0			
Matches 2594	Conservative	0	Mismatches	0	Gaps 0
US-10-351-890-41					
GENERAL INFORMATION:					
Publication No. US20040002060A1					
APPLICANT: Stevenson, Susan C.					
APPLICANT: Kaleko, Michael					
APPLICANT: Smith, Theodore					
APPLICANT: Nemerow, Glen R.					
TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting					
FILE REFERENCE: 22908-1236					
CURRENT APPLICATION NUMBER: US/10/351,890					
CURRENT FILING DATE: 2003-01-28					
PRIOR APPLICATION NUMBER: 60/350,388					
PRIOR FILING DATE: 2002-01-24					
PRIOR APPLICATION NUMBER: 60/391,967					
PRIOR FILING DATE: 2002-06-26					
NUMBER OF SEQ ID NOS: 72					
SOFTWARE: PatentIn version 3.0					
SEQ ID NO 41					
LENGTH: 7607					
TYPE: DNA					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Plasmid GRES-EI-SV40-Hygro					
US-10-351-890-41					
Query Match	100.0%	Score 2594	DB 18	Length 7607	
Best Local Similarity	100.0%	Pred. No. 0			
Matches 2594	Conservative	0	Mismatches	0	Gaps 0
US-10-351-890-41					
GENERAL INFORMATION:					
Publication No. US20040002060A1					
APPLICANT: Stevenson, Susan C.					
APPLICANT: Kaleko, Michael					
APPLICANT: Smith, Theodore					
APPLICANT: Nemerow, Glen R.					
TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting					
FILE REFERENCE: 22908-1236					
CURRENT APPLICATION NUMBER: US/10/351,890					
CURRENT FILING DATE: 2003-01-28					
PRIOR APPLICATION NUMBER: 60/350,388					
PRIOR FILING DATE: 2002-01-24					
PRIOR APPLICATION NUMBER: 60/391,967					
PRIOR FILING DATE: 2002-06-26					
NUMBER OF SEQ ID NOS: 72					
SOFTWARE: PatentIn version 3.0					
SEQ ID NO 41					
LENGTH: 7607					
TYPE: DNA					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Plasmid GRES-EI-SV40-Hygro					
US-10-351-890-41					
Query Match	100.0%				

Db 1994 CGCCTTTGTTGCTGAGTGAATGATGATTAATAAGGCTGAGATTAATGTTAACT 2053
Qy 721 TGCATGCGCTTTAAATGCGCGCGGCTTAAAGGATATATATGCGCGCTAACTCT 780
Db 2054 TGCATGCGCTTTAAATGCGCGCGGCTTAAAGGATATATATGCGCGCTAACTCT 2113
Qy 781 TGCATGCGCTTTAAATGCGCGCGGCTTAAAGGATATATATGCGCGCTAACTCT 840
Db 2114 TGCATGCGCTTTAAATGCGCGCGGCTTAAAGGATATATATGCGCGCTAACTCT 2173
Qy 841 ACTGCTGGAACAGAGCTCTTAACAGTACCTCTTGTTTGGAGGTTTCTGCGGCTCAT 900
Db 2174 ACTGCTGGAACAGAGCTCTTAACAGTACCTCTTGTTTGGAGGTTTCTGCGGCTCAT 2233
Qy 901 CCCAGGCGAAAGTGTGCTGCAAGATTAAGAGGATTAACAAGGGAATTTGAAGAGCTTT 960
Db 2234 CCCAGGCGAAAGTGTGCTGCAAGATTAAGAGGATTAACAAGGGAATTTGAAGAGCTTT 2293
Qy 961 TGAATCCGTGAGCTGTTGATCTTTGAATCTGGATCACAGGCGCTTTTCCAG 1020
Db 2294 TGAATCCGTGAGCTGTTGATCTTTGAATCTGGATCACAGGCGCTTTTCCAG 2353
Qy 1021 AGAAGTCATCAAGACTTTGGATTTTTCACACCGGCGCGCTGCGGCTGTTGCTT 1080
Db 2354 AGAAGTCATCAAGACTTTGGATTTTTCACACCGGCGCGCTGCGGCTGTTGCTT 2413
Qy 1081 TTTTGAAGTTTAAAGATTAATGAGAGCGAAGAACCCATCTGAGCGGCGGATACCTGC 1140
Db 2414 TTTTGAAGTTTAAAGATTAATGAGAGCGAAGAACCCATCTGAGCGGCGGATACCTGC 2473
Qy 1141 TGAATTTTCTGCGCATCTGAGAGAGCGGTTGTGAGACACAAAGATGCGCTGTAC 1200
Db 2474 TGAATTTTCTGCGCATCTGAGAGAGCGGTTGTGAGAGACAAAGATGCGCTGTAC 2533
Qy 1201 TGTGTCTTCCGTCGCGCGCGGATTAATACCGAGAGAGCAGGAGCAGGAGAGG 1260
Db 2534 TGTGTCTTCCGTCGCGCGCGGATTAATACCGAGAGAGCAGGAGCAGGAGAGG 2593
Qy 1261 AAGCAGCGCGCGCGGAGAGAGAGCCATGGAACCCGAGAGCGGCGCTGTGACCTTC 1320
Db 2594 AAGCAGCGCGCGCGGAGAGAGAGCCATGGAACCCGAGAGCGGCGCTGTGACCTTC 2653
Qy 1321 GGAATGATTTGTTGACAGTGTGCTGAATCTGATCAGAACCTGAGAGCTTTGACAT 1380
Db 2654 GGAATGATTTGTTGACAGTGTGCTGAATCTGATCAGAACCTGAGAGCTTTGACAT 2713
Qy 1381 TACAGAGATGGGAGGCGGCTAAAGGGGTAAAGGAGCGGCGGCGCTTGTGAGCTAC 1440
Db 2714 TACAGAGATGGGAGGCGGCTAAAGGGGTAAAGGAGCGGCGGCGCTTGTGAGCTAC 2773
Qy 1441 AGAGAGGCTTGAATCTGAGTGTGCTGAATCTGATCAGAACCTGAGAGCTTTGACAT 1500
Db 2774 AGAGAGGCTTGAATCTGAGTGTGCTGAATCTGATCAGAACCTGAGAGCTTTGACAT 2833
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTGCGGCGAGAGTATTC 1560
Db 2834 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGTGCGGCGAGAGTATTC 2893
Qy 1561 CATAGAGAGCTGACCACTTAAGCTGAGCGAGCGGAGATGATTTTGAAGAGCTATTAG 1620
Db 2894 CATAGAGAGCTGACCACTTAAGCTGAGCGAGCGGAGATGATTTTGAAGAGCTATTAG 2953
Qy 1621 GGTATATTCAGAAAGGTGCACTTAAGCGCAGATTTGCAAGTACAGCAACTTTGTAA 1680
Db 2954 GGTATATTCAGAAAGGTGCACTTAAGCGCAGATTTGCAAGTACAGCAACTTTGTAA 3013
Qy 1681 TATCAGAAATTTGCTACATTTTCTGAGGAGCGGCGGAGGTGAGATGATGAGAGGA 1740
Db 3014 TATCAGAAATTTGCTACATTTTCTGAGGAGCGGCGGAGGTGAGATGATGAGAGGA 3073
Qy 1741 TAGGCTGCGCTTTAGATGTAGCATGATTAATATGTGCGCGGCGGCTTGTGACATGACGG 1800

Db 3074 TAGGCTGCGCTTTAGATGTAGCATGATTAATATGTGCGCGGCGGCTTGTGACATGACGG 3133
Qy 1801 GGTGTTATTAATGAATGAATGTTTACTGCGCCCAATTTTAAGCGGTACGTTTCTGCGC 1860
Db 3134 GGTGTTATTAATGAATGAATGTTTACTGCGCCCAATTTTAAGCGGTACGTTTCTGCGC 3193
Qy 1861 CAATACCAACCTTATCTTACACGAGTGAATCTTATGAGTTTAAATACCTGTGAGA 1920
Db 3194 CAATACCAACCTTATCTTACACGAGTGAATCTTATGAGTTTAAATACCTGTGAGA 3253
Qy 1921 AGCTGAGCGAGTGAAGGTTGCGGCGCTGCTTTTACTGCTGCTGGAAGGCGGTGCT 1980
Db 3254 AGCTGAGCGAGTGAAGGTTGCGGCGCTGCTTTTACTGCTGCTGGAAGGCGGTGCT 3313
Qy 1981 GTGTGCGCCCAAGAGCGGCTTCAATTAAGAAATGCTCTTGAAGGTGTACTTGGG 2040
Db 3314 GTGTGCGCCCAAGAGCGGCTTCAATTAAGAAATGCTCTTGAAGGTGTACTTGGG 3373
Qy 2041 TATCTGTGAGAGGTAACTTCAAGGCTGCGCACAAATGTGCGCTCCGACTGTGTTGCTT 2100
Db 3374 TATCTGTGAGAGGTAACTTCAAGGCTGCGCACAAATGTGCGCTCCGACTGTGTTGCTT 3433
Qy 2101 CATGCTAGTGAAGAGCTGCTGTGATTAAGCATTAACATGTATGTGCAACTCGAGGA 2160
Db 3434 CATGCTAGTGAAGAGCTGCTGTGATTAAGCATTAACATGTATGTGCAACTCGAGGA 3493
Qy 2161 CAGGCGCTCTCAGATGCTGACCTGCTGGAAGGCACTGTACCTGTCGAGACATTTCA 2220
Db 3494 CAGGCGCTCTCAGATGCTGACCTGCTGGAAGGCACTGTACCTGTCGAGACATTTCA 3553
Qy 2221 CGTAGCCAGCACTCTGCAAGGCGCTGCGCAAGTGTGAGCATTAACATGACCCGCTG 2280
Db 3554 CGTAGCCAGCACTCTGCAAGGCGCTGCGCAAGTGTGAGCATTAACATGACCCGCTG 3613
Qy 2281 TTCTTGTGATTTGGGTAAACAGAGGCGGCTGTTCTTACCTTAACATGCAATTTGAGTCA 2340
Db 3614 TTCTTGTGATTTGGGTAAACAGAGGCGGCTGTTCTTACCTTAACATGCAATTTGAGTCA 3673
Qy 2341 CACTTAAGATTTGTTGAGCCGAGACATGTCCAAAGTGAACCTGAACCGGCGGTTTGA 2400
Db 3674 CACTTAAGATTTGTTGAGCCGAGACATGTCCAAAGTGAACCTGAACCGGCGGTTTGA 3733
Qy 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTAGATGAGACCCGACCAAGTGCAGACC 2460
Db 3734 CATGACCATGAAGATCTGGAAGGTGCTGAGGTAGATGAGACCCGACCAAGTGCAGACC 3793
Qy 2461 CTGCGAGTGTGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGAGCCGAGGA 2520
Db 3794 CTGCGAGTGTGCGGTAAACATATTAGGAACCAAGCTGTGATGCTGATGAGCCGAGGA 3853
Qy 2521 GCTGAGGCGCGATCACTTGTGCTGCGCTGCAACCGGCGTGAATTTGCTTGAAGATGA 2580
Db 3854 GCTGAGGCGCGATCACTTGTGCTGCGCTGCAACCGGCGTGAATTTGCTTGAAGATGA 3913
Qy 2581 AGATACAGATTGAG 2594
Db 3914 AGATACAGATTGAG 3927

RESULT 6
US-10-731-961-3
; Sequence 3, Application US/10731961
; Publication No. US20050130306A1
; GENERAL INFORMATION:
; APPLICANT: Voelklmy, Richard W.
; TITLE OF INVENTION: VIRAL VECTORS WHOSE REPLICATION AND, OPTIONALLY, PASSENGER GENE
; TITLE OF INVENTION: ARE CONTROLLED BY A GENE SWITCH ACTIVATED BY HEAT IN THE PRESENCE
; FILE REFERENCE: Replicating virus
; CURRENT APPLICATION NUMBER: US/10/731,961
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 09/939,161
; PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: 60/191,580
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent version 3.3
SEQ ID NO: 3
LENGTH: 9905
TYPE: DNA
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: pxc1 plasmid
US-10-731-961-3

Query Match 100.0%; Score 2594; DB 24; Length 9905;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCATCTTACCTGCGACGAGGCTGCTTTCCACCCAGTGAAGAGATGAGAGGCT 60
DB 916 ATGCATCTTACCTGCGACGAGGCTGCTTTCCACCCAGTGAAGAGATGAGAGGCT 975
QY 61 GAGAGATTGTTAGATTATGATGAGACACCCCGGACCGGTTGAGGCTTGTCTATT 120
DB 976 GAGAGATTGTTAGATTATGATGAGACACCCCGGACCGGTTGAGGCTTGTCTATT 1035
QY 121 CACCGAGGATACGGGGGACCCAGATATATATGTTGCTTTGCTATATGAGACCTGT 180
DB 1036 CACCGAGGATACGGGGGACCCAGATATATATGTTGCTTTGCTATATGAGACCTGT 1095
QY 181 GGCATGTTTGTCTACAGTAAGTGAATAATTATGGGAGTGGGATAGAGTGGGTTTG 240
DB 1096 GGCATGTTTGTCTACAGTAAGTGAATAATTATGGGAGTGGGATAGAGTGGGTTTG 1155
QY 241 GTGGTAAATTTTTTTTAAATTTTACAGTTTGTGGTTTAAAGATTTTGTATTTGA 300
DB 1156 GTGGTAAATTTTTTTTAAATTTTACAGTTTGTGGTTTAAAGATTTTGTATTTGA 1215
QY 301 TTTTTTAAAGGTCCTGTCTGAACCTGAGCCCTGAGCCCGACGACGACCTG 360
DB 1216 TTTTTTAAAGGTCCTGTGTCTGAACCTGAGCCCTGAGCCCGACGACGACCTG 1275
QY 361 CAAGACCTACCCGCGCTCTAAATATGAGGCTGCTATCTTGAAGAGCCGACATCACTG 420
DB 1276 CAAGACCTACCCGCGCTCTAAATATGAGGCTGCTATCTTGAAGAGCCGACATCACTG 1335
QY 421 TGTCTAAGAAATGCAATATGATAGTACGATGCTGATCTCCGGTCTTCTAACAACCTC 480
DB 1336 TGTCTAAGAAATGCAATATGATAGTACGATGCTGATCTCCGGTCTTCTAACAACCTC 1395
QY 481 CTGAGATACACCCGCTGCTCCCGCTGTGCCCATTTAAACCACTTGCCTGAGAGTTG 540
DB 1396 CTGAGATACACCCGCTGCTCCCGCTGTGCCCATTTAAACCACTTGCCTGAGAGTTG 1455
QY 541 GGCCTGCGCAGGCTGTGATATGATGAGAGCTTGCTTAAAGAGCTGGGCAACCTTTG 600
DB 1456 GGCCTGCGCAGGCTGTGATATGATGAGAGCTTGCTTAAAGAGCTGGGCAACCTTTG 1515
QY 601 ACTTGAAGCTGTAAACGCCCCAGGCTATAGGTGTAAACCTGTGATTTGCTGTGTAA 660
DB 1516 ACTTGAAGCTGTAAACGCCCCAGGCTATAGGTGTAAACCTGTGATTTGCTGTGTAA 1575
QY 661 CGCCTTTGTTTGTGATATGATATGATTTTAAAGGATGATTAATGTTTAACT 720
DB 1576 CGCCTTTGTTTGTGATATGATATGATTTTAAAGGATGATTAATGTTTAACT 1635
QY 721 TGCATGCGTGTAAATATGAGGCTTAAAGGATATATATGAGGCTGGCTAATCT 780
DB 1636 TGCATGCGTGTAAATATGAGGCTTAAAGGATATATATGAGGCTGGCTAATCT 1695
QY 781 TGTATCAATCTGACCTCAATGAGGCTTGGAGGTGTTTGAAGATTTTCTGCTGTGCTA 840
DB 1696 TGTATCAATCTGACCTCAATGAGGCTTGGAGGTGTTTGAAGATTTTCTGCTGTGCTA 1755
QY 841 ACTTGTGGAACAGAGCTTAAACATGATCTTGTGTTTGAAGGTTTCTGTGGGCTCAT 900

DB 1756 ACTTGTGGAACAGAGCTTAAACATGATCTTGTGTTTGAAGGTTTCTGTGGGCTCAT 1815
QY 901 CCCAGGCAAGTTAGTCTGACAGATTAAGAGATTACAATGGGAATTTGAAGGCTTT 960
DB 1816 CCCAGGCAAGTTAGTCTGACAGATTAAGAGATTACAATGGGAATTTGAAGGCTTT 1875
QY 961 TGAATCTGTGTGAGCTGTTTGAATCTTGAATCTGGGTACCAAGGCGCTTTTCAAG 1020
DB 1876 TGAATCTGTGTGAGCTGTTTGAATCTTGAATCTGGGTACCAAGGCGCTTTTCAAG 1935
QY 1021 AGAAGCTATCAACCTTTGATTTTCCACACCGGGCGGCTGCGGCTCTGTGCTT 1080
DB 1936 AGAAGCTATCAACCTTTGATTTTCCACACCGGGCGGCTGCGGCTCTGTGCTT 1995
QY 1081 TTTTGAAGTTTATTAAGATTAATGAGCGGAACCACTGAGCGGAGGATACCTGC 1140
DB 1996 TTTTGAAGTTTATTAAGATTAATGAGCGGAACCACTGAGCGGAGGATACCTGC 2055
QY 1141 TGAATTTTCTGCGCATGATCTGTGAGAGCGGTTGTGAGACACAAGATCGCTCTAC 1200
DB 2056 TGAATTTTCTGCGCATGATCTGTGAGAGCGGTTGTGAGACACAAGATCGCTCTAC 2115
QY 1201 TGTGTCTTCCGTCCGCGCGGATTAATCCGAGGAGACACAGACGAGAGAG 1260
DB 2116 TGTGTCTTCCGTCCGCGCGGATTAATCCGAGGAGACACAGACGAGAGAG 2175
QY 1261 AAGCAGGCGGCGGCGGACGAGACAGAGCCATGGAACCCGAGAGCCGCTGACCTC 1320
DB 2176 AAGCAGGCGGCGGCGGACGAGACAGAGCCATGGAACCCGAGAGCCGCTGACCTC 2235
QY 1321 GGAATGATTTGTATACAGTGTGCTGAACTGTATCCAGAACTGAGACGATTTTGAAT 1380
DB 2236 GGAATGATTTGTATACAGTGTGCTGAACTGTATCCAGAACTGAGACGATTTTGAAT 2295
QY 1381 TACAGAGATGAGGAGGCGCTAAAGGGGCTAAAGAGGAGCGGGGCTTGTGAGGCTAC 1440
DB 2296 TACAGAGATGAGGAGGCGCTAAAGGGGCTAAAGAGGAGCGGGGCTTGTGAGGCTAC 2355
QY 1441 AGAGAGGCTAGAGATCTAGCTTTTACCTTATAGCAGACACCGCTCTGAGTATTTAC 1500
DB 2356 AGAGAGGCTAGAGATCTAGCTTTTACCTTATAGCAGACACCGCTCTGAGTATTTAC 2415
QY 1501 TTTTCAACAGATCAAGATTAATTCGCTAATGAGCTTGAATCTGTGCGCAGAAATTC 1560
DB 2416 TTTTCAACAGATCAAGATTAATTCGCTAATGAGCTTGAATCTGTGCGCAGAAATTC 2475
QY 1561 CATAGACAGCTGACCACTTAATGCTGCGACGCCAGGAGATATTTTGAAGAGCTATTAG 1620
DB 2476 CATAGACAGCTGACCACTTAATGCTGCGACGCCAGGAGATATTTTGAAGAGCTATTAG 2535
QY 1621 GGTATATGCAAAAGGTGACCTTAGAGCCAGATTTGCAAGTACAGAACTTGTAA 1680
DB 2536 GGTATATGCAAAAGGTGACCTTAGAGCCAGATTTGCAAGTACAGAACTTGTAA 2595
QY 1681 TATCAGAAATTTGTTGCTACATTTCTGGAACGAGGCTGAGATGATACGAGGA 1740
DB 2596 TATCAGAAATTTGTTGCTACATTTCTGGAACGAGGCTGAGATGATACGAGGA 2655
QY 1741 TAGGGTGGCCTTTAGATGATGATTAATATGATGAGGCTGCTGCGCAGAGAG 1800
DB 2656 TAGGGTGGCCTTTAGATGATGATTAATATGATGAGGCTGCTGCGCAGAGAG 2715
QY 1801 GGTGTATTATGATGATTAAGGTTTACCTGAGCCCAATTTTACGCTGCTTCTGTC 1860
DB 2716 GGTGTATTATGATGATTAAGGTTTACCTGAGCCCAATTTTACGCTGCTTCTGTC 2775
QY 1861 CAATACCAACCTTATCTTACACGCTGATGATGAGGTTTAAACAATCTGTGTGA 1920
DB 2776 CAATACCAACCTTATCTTACACGCTGATGATGAGGTTTAAACAATCTGTGTGA 2835
QY 1921 AGCCTGAGCCGAGTATAGGAGTGGGCTGCTTTTACCTGCTGAGAGGAGGCTGCT 1980

Db 2836 AGCTGAGCCGATGTAAGGGTTGCGGGCTGTGCTTTTACTGTGTGTAAGAGGGGTGT 2895
Qy 1981 GTGTGCGCCCAAAAGCAGGGGTTTCAATTAAAGAAATGCTCTTTTAAAGTGTACTTGGG 2040
Db 2896 GTGTGCGCCCAAAAGCAGGGGTTTCAATTAAAGAAATGCTCTTTTAAAGTGTACTTGGG 2955
Qy 2041 TATCTGTCTGAGGGTAACTCAAGGGTCCGCCAATGTGACCTCCGACTGTGGTGTCTT 2100
Db 2956 TATCTGTCTGAGGGTAACTCAAGGGTCCGCCAATGTGACCTCCGACTGTGGTGTCTT 3015
Qy 2101 CATGCTAGTAAAGCGTGTGTGTATTAAGCATTAACATGATGTGGCAACTCGAGAGA 2160
Db 3016 CATGCTAGTAAAGCGTGTGTATTAAGCATTAACATGATGTGGCAACTCGAGAGA 3075
Qy 2161 CAGGGCCCTCTAGATGCTGACCTGTGCGAAGGCACTGTCACTGTGCTGAAGACATTCA 2220
Db 3076 CAGGGCCCTCTAGATGCTGACCTGTGCGAAGGCACTGTCACTGTGCTGAAGACATTCA 3135
Qy 2221 CGTAGCCAGCACTCTCGCAAGGCTGTGCGACAGTGTGAGCATTAACATCTGACCCGCTG 2280
Db 3136 CGTAGCCAGCACTCTCGCAAGGCTGTGCGACAGTGTGAGCATTAACATCTGACCCGCTG 3195
Qy 2281 TTCTTGATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCA 2340
Db 3196 TTCTTGATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTACCAATGCAATTTGAGTCA 3255
Qy 2341 CACTAAGATATTGTGTCGAGCCCGAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGA 2400
Db 3256 CACTAAGATATTGTGTCGAGCCCGAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGA 3315
Qy 2401 CATGACCATGAAGATCTGGAAGTGTCTGAGGTACGATGAGACCCGACCAAGTGCAGACC 2460
Db 3316 CATGACCATGAAGATCTGGAAGTGTCTGAGGTACGATGAGACCCGACCAAGTGCAGACC 3375
Qy 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGTGATGTGACCGAGGA 2520
Db 3376 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGATGTGATGTGACCGAGGA 3435
Qy 2521 GCTAGAGCCGATGATCTGTGAGTGTGCTGTGACCCGCGCTGAGTTGGCTGTAGCGATGA 2580
Db 3436 GCTAGAGCCGATGATCTGTGAGTGTGCTGTGACCCGCGCTGAGTTGGCTGTAGCGATGA 3495
Qy 2581 AGATACAGATTGAG 2594
Db 3496 AGATACAGATTGAG 3509

RESULT 7
US-09-847-101B-12
; Sequence 12, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847.101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 11152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-847-101B-12

Query Match 100.0%; Score 2594; DB 9; Length 11152;
; Best Local Similarity 100.0%; Pred. No. 0;

Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATCATCTTACCTGCCACGAGGCTGTGCTTCCACCCAGTGAACGACGAGATGAAGAGGT 60
Db 1825 ATCATCTTACCTGCCACGAGGCTGTGCTTCCACCCAGTGAACGACGAGATGAAGAGGT 1884
Qy 61 GAGGAGTTTGTGTTAGATTATGTTGAGACACCCCGGGACAGGTTTCAAGTCTTGTCAATTAT 120
Db 1885 GAGGAGTTTGTGTTAGATTATGTTGAGACACCCCGGGACAGGTTTCAAGTCTTGTCAATTAT 1944
Qy 121 CACCGAGGAATACGGGGGACCCAGATATTATGTTCCTTGGCTATATGAGGACCTGT 180
Db 1945 CACCGAGGAATACGGGGGACCCAGATATTATGTTCCTTGGCTATATGAGGACCTGT 2004
Qy 181 GGCATTTTGTGTACATTAAGTAAATTTATGCGCACTGGGTGATTAAGTGTGGTTTG 240
Db 2005 GGCATTTTGTGTACATTAAGTAAATTTATGCGCACTGGGTGATTAAGTGTGGTTTG 2064
Qy 241 GTGTGTAATTTTATTTTAAATTTTACAGTTTGTGGTTTAAAGAAATTTTGTATTGTGA 300
Db 2065 GTGTGTAATTTTATTTTAAATTTTACAGTTTGTGGTTTAAAGAAATTTTGTATTGTGA 2124
Qy 301 TTTTAAAGGCTGTGTGTCTGAACCTGAGCCTGAGCCCGACGACGACCGAGCCTG 360
Db 2125 TTTTAAAGGCTGTGTGTCTGAACCTGAGCCTGAGCCCGACGACGACCGAGCCTG 2184
Qy 361 CAAGACCTACCCCGGCTTAAATTTGAGGCTGTATCTGAGAGCGCCGACATCACCTG 420
Db 2185 CAAGACCTACCCCGGCTTAAATTTGAGGCTGTATCTGAGAGCGCCGACATCACCTG 2244
Qy 421 TGTCTAGAGATGCAATAGTATGATGAGATAGCTGTGACTCGGTCTCTTAAACACACTC 480
Db 2245 TGTCTAGAGATGCAATAGTATGATGAGATAGCTGTGACTCGGTCTCTTAAACACACTC 2304
Qy 481 CTGAGATACACCCGGTGTCTGAGCCTGATTAACCAAGTTCCGCTGAGAGTGTG 540
Db 2305 CTGAGATACACCCGGTGTCTGAGCCTGATTAACCAAGTTCCGCTGAGAGTGTG 2364
Qy 541 GGGCTGCCAGGCTGTGGAATGTATGAGGACTTGAACGAGCTGTGGGCAACCTTTGG 600
Db 2365 GGGCTGCCAGGCTGTGGAATGTATGAGGACTTGAACGAGCTGTGGGCAACCTTTGG 2424
Qy 601 ACTTGACCTGTAAACGCCGACGACATAGGTGTAAACCTGTGATGTGCTGTGTAA 660
Db 2425 ACTTGACCTGTAAACGCCGACGACATAGGTGTAAACCTGTGATGTGCTGTGTAA 2484
Qy 661 CGCCTTGTGTTGCTGAATGAGTTGATGTAAATTAAGGCTGAGATATGTTAACT 720
Db 2485 CGCCTTGTGTTGCTGAATGAGTTGATGTAAATTAAGGCTGAGATATGTTAACT 2544
Qy 721 TGCATGGCGTGTAAATGGGGCGGGGCTTAAAGGGTATATATGCGCGTGGGCTAATCT 780
Db 2545 TGCATGGCGTGTAAATGGGGCGGGGCTTAAAGGGTATATATGCGCGTGGGCTAATCT 2604
Qy 781 TGGTTACATCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCTA 840
Db 2605 TGGTTACATCTGACCTCATGAGGCTTGGAGTGTGTTGGAAGATTTTCTGCTGTGCTA 2664
Qy 841 ACTTGTGGAACAGAGCTCTTAACATCTCTTGTGTTGAGGTTTCTGTGGGCTCAT 900
Db 2665 ACTTGTGGAACAGAGCTCTTAACATCTCTTGTGTTGAGGTTTCTGTGGGCTCAT 2724
Qy 901 CCGAGGCAAGTTAGTGTGCGAATTAAGAGGATTAAGTGGGAATTTGAAGAGCTTT 960
Db 2725 CCGAGGCAAGTTAGTGTGCGAATTAAGAGGATTAAGTGGGAATTTGAAGAGCTTT 2784
Qy 961 TGAATCTGTGTGAGCTGTTGATCTTGTGAATCTGGGTACACAGCGCTTTTCCAG 1020
Db 2785 TGAATCTGTGTGAGCTGTTGATCTTGTGAATCTGGGTACACAGCGCTTTTCCAG 2844
Qy 1021 AGAAGTCAATCAAGACTTTGATTTTCCACACCGGGGCGGCTGTGCTGTGCTT 1080
Db 2845 AGAAGTCAATCAAGACTTTGATTTTCCACACCGGGGCGGCTGTGCTGTGCTT 2904

QY 1081 TTTTGAAGTTTATTAAGATTAATGAGCGAAGAAACCATCTTGACCGGGGGTAACTTGC 1140
DB 2905 TTTTGAAGTTTATTAAGATTAATGAGCGAAGAAACCATCTTGACCGGGGGTAACTTGC 2964
QY 1141 TGGATTTTCTGGCCAGTCATCTGTGAGAGCGGTTGTGAGACACAAGATGCGCTGCTAC 1200
DB 2965 TGGATTTTCTGGCCAGTCATCTGTGAGAGCGGTTGTGAGACACAAGATGCGCTGCTAC 3024
QY 1201 TGTGTCTTCCGTCGCGCCGCGGATTAACCGAGGAGAGCAGCAGCAGCAGAGG 1260
DB 3025 TGTGTCTTCCGTCGCGCGCGGATTAACCGAGGAGAGCAGCAGCAGCAGAGG 3084
QY 1261 AAGCCAGCGCGCGCGCGCAGAGCAGAGCCCATGGAACCCGAGCCGCTGACCTTC 1320
DB 3085 AAGCCAGCGCGCGCGCGCAGAGCAGAGCCCATGGAACCCGAGCCGCTGACCTTC 3144
QY 1321 GGGAAATGAATGTTGTACAGGTGGCTGAACCTGTATCCAGAACTGAGACGATTTGACAT 1380
DB 3145 GGGAAATGAATGTTGTACAGGTGGCTGAACCTGTATCCAGAACTGAGACGATTTGACAT 3204
QY 1391 TACAGAGATGCGCAGGCGCTTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGCTTAC 1440
DB 3205 TACAGAGATGCGCAGGCGCTTAAAGGGGTAAAGAGGAGCGGGGGCTTGTGAGCTTAC 3264
QY 1441 AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGTCTGAGTATTAAC 1500
DB 3265 AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGTCTGAGTATTAAC 3324
QY 1501 TTTTCAACAGATCAAGATTAATTTGGCTTAATGAGCTTGAATCGGCGAGAAATATTC 1560
DB 3325 TTTTCAACAGATCAAGATTAATTTGGCTTAATGAGCTTGAATCGGCGAGAAATATTC 3384
QY 1561 CATNAGAGAGCTGACCACTTACTGCTGACGAGGAGATGATTTTGAAGGCTATTAAG 1620
DB 3385 CATNAGAGAGCTGACCACTTACTGCTGACGAGGAGATGATTTTGAAGGCTATTAAG 3444
QY 1621 GGTATATTCAGAAAGGTGCACTTAAGCCAGATTTGCAAGTACAGCAAACTTGTAA 1680
DB 3445 GGTATATTCAGAAAGGTGCACTTAAGCCAGATTTGCAAGTACAGCAAACTTGTAA 3504
QY 1681 TATCAGAAATGTTGCTACATTTCTGGGAGCGGGCCGAGGTGAGATGATTAAGGAGGA 1740
DB 3505 TATCAGAAATGTTGCTACATTTCTGGGAGCGGGCCGAGGTGAGATGATTAAGGAGGA 3564
QY 1741 TAGGGTGCCCTTGAATGATGATTAATATATGTCGCGGGGGTCTTGGCATGAGAG 1800
DB 3565 TAGGGTGCCCTTGAATGATGATTAATATATGTCGCGGGGGTCTTGGCATGAGAG 3624
QY 1801 GGTGCTTATTAATGAATGATGATTAATGTCGCGCCCAATTTTGAAGGATCGTTTCTG 1860
DB 3625 GGTGCTTATTAATGAATGATGATTAATGTCGCGCCCAATTTTGAAGGATCGTTTCTG 3684
QY 1861 CAATACCAACCTTATCTTACACGAGTAAAGCTTCTATGAGTTTAACTTACCTGATGGA 1920
DB 3685 CAATACCAACCTTATCTTACACGAGTAAAGCTTCTATGAGTTTAACTTACCTGATGGA 3744
QY 1921 AGCCTGAGCCGATGATGAGGTTGCGGGCTGTCCTTTTACTGCTGAGAAAGGGGTGT 1980
DB 3745 AGCCTGAGCCGATGATGAGGTTGCGGGCTGTCCTTTTACTGCTGAGAAAGGGGTGT 3804
QY 1981 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAGGTGATCTTGGG 2040
DB 3805 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAGGTGATCTTGGG 3864
QY 2041 TATCTGCTGAGGGTAACTCAAGGGTGCAGCAATGAGCTTCCGATGCTGATGCTT 2100
DB 3865 TATCTGCTGAGGGTAACTCAAGGGTGCAGCAATGAGCTTCCGATGCTGATGCTT 3924
QY 2101 CATGCTAGTAAAGAGCTGCTGTGATTAAGCATTAACATGATGATGCAATCTGAGAGA 2160
DB 3925 CATGCTAGTAAAGAGCTGCTGTGATTAAGCATTAACATGATGATGCAATCTGAGAGA 3984

QY 2161 CAGGCGCTCTGAGATGCTGACCTGCTCGGACGGCACTGTCACTCTGTAAGAACATTTCA 2220
DB 3985 CAGGCGCTCTGAGATGCTGACCTGCTCGGACGGCACTGTCACTCTGTAAGAACATTTCA 4044
QY 2221 CGTAGCCAGCACTCTCGCAAGGCGCTGCGCAGGTGTTGAGCATTAACATGACCGGCTG 2280
DB 4045 CGTAGCCAGCACTCTCGCAAGGCGCTGCGCAGGTGTTGAGCATTAACATGACCGGCTG 4104
QY 2281 TTCTTGTGATTTGGGTAAACAGAGGGGGGTGTCTTCACTTACCAATGCAATTTGATCA 2340
DB 4105 TTCTTGTGATTTGGGTAAACAGAGGGGGGTGTCTTCACTTACCAATGCAATTTGATCA 4164
QY 2341 CACTAAGATTTTGTGTTGAGCCCGAGAGCATGTCCAAAGTGAACCTGAAACGGGGTATTGA 2400
DB 4165 CACTAAGATTTTGTGTTGAGCCCGAGAGCATGTCCAAAGTGAACCTGAAACGGGGTATTGA 4224
QY 2401 CATGACATGAAGATCTGGAAGGTGCTGAGGATGAGATGAGACCCGACAGGTGAGACC 2460
DB 4225 CATGACATGAAGATCTGGAAGGTGCTGAGGATGAGATGAGACCCGACAGGTGAGACC 4284
QY 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACAGCTGTGATGCTGATGATGACCGAGA 2520
DB 4285 CTGCGAGTGTGGCGGTAAACATATTAGGAACAGCTGTGATGCTGATGATGACCGAGA 4344
QY 2521 GCTGAGGCGCGCATCACTTGTGCTGCTGCTGACACCGGCTGAGTTGGCTTACGAGTGA 2580
DB 4345 GCTGAGGCGCGCATCACTTGTGCTGCTGCTGACACCGGCTGAGTTGGCTTACGAGTGA 4404
QY 2581 AGATPACAGATTGAG 2594
DB 4405 AGATPACAGATTGAG 4418

RESULT 8
US-09-482-682-12
; Sequence 12, Application US/09482682
; Publication No. US20030157688B1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALENEBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.001001
; CURRENT APPLICATION NUMBER: US/09/482.682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 11152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-12

Query Match 100.0%; Score 2594; DB 10; Length 11152;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATCTTACCTTCCAGAGAGCTGCTTTTCCACCCAGTGAAGAGATGAAGAGGT 60
DB 1825 ATGATCTTACCTTCCAGAGAGCTGCTTTTCCACCCAGTGAAGAGATGAAGAGGT 1884
QY 61 GAGAGATTTGTGTTAATTAATGATGAGACACCCGGGAGACAGTTTCAAGTCTTGTCAATTAT 120
DB 1885 GAGAGATTTGTGTTAATTAATGATGAGACACCCGGGAGACAGTTTCAAGTCTTGTCAATTAT 1944
QY 121 CACCGAGAGAAATACGGGGGAGACCCAGATATTATGTTGCTTGTATGATGAGACCTGT 180
DB 1945 CACCGAGAGAAATACGGGGGAGACCCAGATATTATGTTGCTTGTATGATGAGACCTGT 2004

QY 181 GGCATGTTTGTCTACAGTAAGTGAATAATTATGGGCAATGGGTGATAGATGGTGGTTTG 240
DB 2005 GGCATGTTTGTCTACAGTAAGTGAATAATTATGGGCAATGGGTGATAGATGGTGGTTTG 2064
QY 241 GTGTGTAAATTTTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATTTGA 300
DB 2065 GTGTGTAAATTTTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGAAATTTTGTATTTGA 2124
QY 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCGAGCCAGAACCCGAGCTTG 360
DB 2125 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCGAGCCAGAACCCGAGCTTG 2184
QY 361 CAAGACCTAACCCGCGCTCTAAATAGGCGCTGATCTGAGACGCGCGACATCACTG 420
DB 2185 CAAGACCTAACCCGCGCTCTAAATAGGCGCTGATCTGAGACGCGCGACATCACTG 2244
QY 421 TGTCTAGAGAAATGCATAATAGTATCGATAGCTGATCTCGGTCTCTTCAACACCTC 480
DB 2245 TGTCTAGAGAAATGCATAATAGTATCGATAGCTGATCTCGGTCTCTTCAACACCTC 2304
QY 481 CTGAGATACACCCGCTGCTCCGCTGTGCCCATTTAAACAGTTGCCGTGAGATTGGTG 540
DB 2305 CTGAGATACACCCGCTGCTCCGCTGTGCCCATTTAAACAGTTGCCGTGAGATTGGTG 2364
QY 541 GCGGTCCGACGCTGTGATATGATCGAGACTTGCTTAAGAGCTGGGCACTTTGG 600
DB 2365 GCGGTCCGACGCTGTGATATGATCGAGACTTGCTTAAGAGCTGGGCACTTTGG 2424
QY 601 ACTTGAAGCTTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTCGCTGTGTGTTAA 660
DB 2425 ACTTGAAGCTTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTCGCTGTGTGTTAA 2484
QY 661 CGCCTTTGTGTCTGAATGATGATGATTAATTAAGGGTGAATTAATGTTTAACT 720
DB 2485 CGCCTTTGTGTCTGAATGATGATGATTAATTAAGGGTGAATTAATGTTTAACT 2544
QY 721 TGCATGCGGTGTTAAATGGGCGGGGCTTAAAGGGTATATATGCGCGTGGCTAACT 780
DB 2545 TGCATGCGGTGTTAAATGGGCGGGGCTTAAAGGGTATATATGCGCGTGGCTAACT 2604
QY 781 TGTGTTACATCTGACCTCATGAGGCTTGGAGTGTGGAAATTTTCTGCTGTGCTGA 840
DB 2605 TGTGTTACATCTGACCTCATGAGGCTTGGAGTGTGGAAATTTTCTGCTGTGCTGA 2664
QY 841 ACTTGTCTGGAACAGAGCTCTTAACAGTACTCTTGTGTTTGAAGTTTCTGTGGGCTCAT 900
DB 2665 ACTTGTCTGGAACAGAGCTCTTAACAGTACTCTTGTGTTTGAAGTTTCTGTGGGCTCAT 2724
QY 901 CCCAGGCAAAAGTTAGTCTGAGAAATTAAGAGATTAAGAGGGAATTTGAAGGCTTT 960
DB 2725 CCCAGGCAAAAGTTAGTCTGAGAAATTAAGAGATTAAGAGGGAATTTGAAGGCTTT 2784
QY 961 TGAATCTGTGTGAGTGTGTTTGAATCTTGAATCTGGGTCAACGAGCGCTTTTCCAG 1020
DB 2785 TGAATCTGTGTGAGTGTGTTTGAATCTTGAATCTGGGTCAACGAGCGCTTTTCCAG 2844
QY 1021 AGAAGGTATCAAGACTTTGGAATTTTCCACACCGGGGCGGCTGCGGCTGTGTGCTT 1080
DB 2845 AGAAGGTATCAAGACTTTGGAATTTTCCACACCGGGGCGGCTGCGGCTGTGTGCTT 2904
QY 1081 TTTTGAAGTTTAAAGATTAATGAGAGCAAAACCATCTGAGCGGGGGGTACCTGC 1140
DB 2905 TTTTGAAGTTTAAAGATTAATGAGAGCAAAACCATCTGAGCGGGGGGTACCTGC 2964
QY 1141 TGAATTTTCTGGCCATGCTGTGAGAGCGGTTGTGAGACACAAGATGCGCTGTAC 1200
DB 2965 TGAATTTTCTGGCCATGCTGTGAGAGCGGTTGTGAGACACAAGATGCGCTGTAC 3024
QY 1201 TGTGTCTTCCGCTCGGCGCGGATTAATCGAGCGAGAGAGCAGACGACGAGAGG 1260
DB 3025 TGTGTCTTCCGCTCGGCGCGGATTAATCGAGCGAGAGAGCAGACGAGAGG 3084

QY 1261 AAGCCAGCGCGCGCGCAGAGCAGAGCCCATGGAACCCGAGCGCGCTGACCTTC 1320
DB 3085 AAGCCAGCGCGCGCGCAGAGCAGAGCCCATGGAACCCGAGCGCGCTGACCTTC 3144
QY 1321 GGAATGAATGTTGTACAGGTGTGCTGAACCTGTATCCAGAACTGAGACGATTTTGAACAT 1380
DB 3145 GGAATGAATGTTGTACAGGTGTGCTGAACCTGTATCCAGAACTGAGACGATTTTGAACAT 3204
QY 1381 TACAGAGATGGGAGGGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTAGGCTTAC 1440
DB 3305 TACAGAGATGGGAGGGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTAGGCTTAC 3264
QY 1441 AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACAGCCGCTGATATATAC 1500
DB 3265 AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACAGCCGCTGATATATAC 3324
QY 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGACCTTGTGTGCGCAGAAATATTC 1560
DB 3325 TTTTCAACAGATCAAGATTAATGCGCTAATGACCTTGTGTGCGCAGAAATATTC 3384
QY 1561 CATAGACAGCTGACCACTTAATGCTGCGACGCGAGGAGATTTTGAAGAGCTATTAG 1620
DB 3385 CATAGACAGCTGACCACTTAATGCTGCGACGCGAGGAGATTTTGAAGAGCTATTAG 3444
QY 1621 GGTATATGCAAAAGGTGGCACTTAGGCGAGATTGCAAGTACAGATCAAGCAACTTGTAA 1680
DB 3445 GGTATATGCAAAAGGTGGCACTTAGGCGAGATTGCAAGTACAGATCAAGCAACTTGTAA 3504
QY 1681 TATCAGAAATTTGTCTACATTTCTGAGAAACGGGGCGAGGTGAGATGATACGAGGA 1740
DB 3505 TATCAGAAATTTGTCTACATTTCTGAGAAACGGGGCGAGGTGAGATGATACGAGGA 3564
QY 1741 TAGGRTGCGCTTGAATGATGATGATTAATATGTCGCGGGGGTGTCTGGCAGTGAACG 1800
DB 3565 TAGGRTGCGCTTGAATGATGATGATTAATATGTCGCGGGGTGTCTGGCAGTGAACG 3624
QY 1801 GGTGTTATTAATGATTAAGATTAAGTTTACTGGCCCCCAATTTTACGCGTATCTGTC 1860
DB 3625 GGTGTTATTAATGATTAAGATTAAGTTTACTGGCCCCCAATTTTACGCGTATCTGTC 3684
QY 1861 CAATACCAACCTTAATCTTACACGCGTGAAGCTTATAGGGTTTAAATATCTGTGTGGA 1920
DB 3685 CAATACCAACCTTAATCTTACACGCGTGAAGCTTATAGGGTTTAAATATCTGTGTGGA 3744
QY 1921 AGCTGGAACGATGAAGGTTGCGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGT 1980
DB 3745 AGCTGGAACGATGAAGGTTGCGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGT 3804
QY 1981 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAGGTATACCTTGG 2040
DB 3805 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAGGTATACCTTGG 3864
QY 2041 TATCTGTCTGAGGGTAACTTCAAGGTTGCGCCCAATATGTTGCTTCCGCTGTGCTT 2100
DB 3865 TATCTGTCTGAGGGTAACTTCAAGGTTGCGCCCAATATGTTGCTTCCGCTGTGCTT 3924
QY 2101 CATGCTAGTGAAGCGGTGCTGATTAAGCAATTAAGTATGTTGCACTGAGAGA 2160
DB 3925 CATGCTAGTGAAGCGGTGCTGATTAAGCAATTAAGTATGTTGCACTGAGAGA 3984
QY 2161 CAGGGCTCTCAGATGCTGACCTGCTGAGCGGCACTGTCACTGTGAGAGACATTC 2220
DB 3985 CAGGGCTCTCAGATGCTGACCTGCTGAGCGGCACTGTCACTGTGAGAGACATTC 4044
QY 2221 CTGAGCAGCACTCTGCGAAGGCTTGGCCAGTGTGTTGAGCATTAATCTGACCGCTG 2280
DB 4045 CTGAGCAGCACTCTGCGAAGGCTTGGCCAGTGTGTTGAGCATTAATCTGACCGCGCTG 4104
QY 2281 TTTCTTGAATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTAACAAATGCAATTTGAGTCA 2340
DB 4105 TTTCTTGAATTTGGGTAAACAGAGAGGGGGTGTCTTCACTTAACAAATGCAATTTGAGTCA 4164
QY 2341 CACTAAGATATTTGCTTGAAGCCGAGACATGTCCAAAGTGAACCTGAAACGGGGTGTGGA 2400

Db 4165 CACTAAGATATTCCTTGAGCCCGAGACATGTCAGAGTGAACCTGAACCGGGGTTTGA 4224
Qy 2401 CATGACCATGAAGATCTGGAAGTGCTGAGGATGAGTGAAGACCCGACAGGTGAGACC 2460
Db 4225 CATGACCATGAAGATCTGGAAGTGCTGAGGATGAGTGAAGACCCGACAGGTGAGACC 4284
Qy 2461 CTGCGAGTGTCGGGTAAACATATTAGGAACCAAGCTGTGATGCTGAGATGTAACCGAGA 2520
Db 4285 CTGCGAGTGTCGGGTAAACATATTAGGAACCAAGCTGTGATGCTGAGATGTAACCGAGA 4344
Qy 2521 GCTGAGGCCCGATCACTGTGCTGCTGACCCGCGCTGAGTTTGCTAGCGATGA 2580
Db 4345 GCTGAGGCCCGATCACTGTGCTGCTGACCCGCGCTGAGTTTGCTAGCGATGA 4404
Qy 2581 AGATACAGATTGAG 2594
Db 4405 AGATACAGATTGAG 4418

RESULT 9
US-09-847-101B-15
; Sequence 15, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMERON, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; NUMBER OF SEQ. ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO. 15
; LENGTH: 14455
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-847-101B-15

Query Match 100.0%; Score 2594; DB 9; Length 14455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATCTTACCTGCGACGAGGCTGGCTTTCCACCCAGTGAACGAGATGAAGAGGT 60
Db 1825 ATGATCTTACCTGCGACGAGGCTGGCTTTCCACCCAGTGAACGAGATGAAGAGGT 1884
Qy 61 GAGAGTTTGTAGATTATGAGAGCAACCGGGGCGAGTTGCGAGTCTTGTCAATTAT 120
Db 1885 GAGAGTTTGTAGATTATGAGAGCAACCGGGGCGAGTTGCGAGTCTTGTCAATTAT 1944
Qy 121 CACCGAGGAATACGGGGGACCCAGATATTATGTTGCTTGTCTATATAGAACCTGT 180
Db 1945 CACCGAGGAATACGGGGGACCCAGATATTATGTTGCTTGTCTATATAGAACCTGT 2004
Qy 181 GGCATGTTTGTCTACATGAATGAATAATTATGGGCGATGGGTATAGATGTGGGTTTG 240
Db 2005 GGCATGTTTGTCTACATGAATGAATAATTATGGGCGATGGGTATAGATGTGGGTTTG 2064
Qy 241 GTGTGTAATTTTATTTTATTTTATTTTACAGTTTGTGTTTAAAGAAATTTTATTTGGA 300
Db 2065 GTGTGTAATTTTATTTTATTTTATTTTACAGTTTGTGTTTAAAGAAATTTTATTTGGA 2124
Qy 301 TTTTATTTAAAGGTCTGTGTCTGAACCTGAGCCCTGAGCCCGAGCCAGAACCGAGCCTG 360
Db 2125 TTTTATTTAAAGGTCTGTGTGTCTGAACCTGAGCCCTGAGCCCGAGAACCGAGCCTG 2184
Qy 361 CAAGACCTACCCGCGTCTTAAATGCGGCTGTCTATCTTGAAGACGCCGACATCACCTG 420

Db 2185 CAAGACCTACCCGCGTCTTAAATGCGGCTGTCTATCTTGAAGACGCCGACATCACCTG 2244
Qy 421 TGTCTAGAAATGCAATATGATAGTACGATATGCTGATCTCCGATCTCTTACACACCTC 480
Db 2245 TGTCTAGAAATGCAATATGATAGTACGATATGCTGATCTCCGATCTCTTACACACCTC 2304
Qy 481 CTGAGATACACCCGATGCTCCGCTGTGCTCCCATTTAAACAGTTGCGGTGAGATGTG 540
Db 2305 CTGAGATACACCCGATGCTCCGCTGTGCTCCCATTTAAACAGTTGCGGTGAGATGTG 2364
Qy 541 GGCCTGCGCAGGCTGTGAATATGAGAGACTTGTAAAGACCTGAGGACACCTTTGG 600
Db 2365 GGCCTGCGCAGGCTGTGAATATGAGAGACTTGTAAAGACCTGAGGACACCTTTGG 2424
Qy 601 ACTTGAAGCTGTAAACGCCCGACCATTAAGGTGTAAACCTGTGATGCTGTGTGTTAA 660
Db 2425 ACTTGAAGCTGTAAACGCCCGACCATTAAGGTGTAAACCTGTGATGCTGTGTGTTAA 2484
Qy 661 CGCCTTGTGTTGCTGAATGATGATGATTAATTAAGGTTGAGATTAATGTTTAACT 720
Db 2485 CGCCTTGTGTTGCTGAATGATGATGATTAATTAAGGTTGAGATTAATGTTTAACT 2544
Qy 721 TGCAATGCTGTGTTAAATGGGCGGGGCTTAAAGGTTAATAATGCGCGTGGCTAACT 780
Db 2545 TGCAATGCTGTGTTAAATGGGCGGGGCTTAAAGGTTAATAATGCGCGTGGCTAACT 2604
Qy 781 TGTTACATCTGACCTCATGAGAGCTTGGAGTGTGGAAGATTTTCTGTGCTGACSTA 840
Db 2605 TGTTACATCTGACCTCATGAGAGCTTGGAGTGTGGAAGATTTTCTGTGCTGACSTA 2664
Qy 841 ACTTGTGGAACAGAGCTTAAACAGTACCTTGTGTTTGGAGTTTCTGTGGGCTCAT 900
Db 2665 ACTTGTGGAACAGAGCTTAAACAGTACCTTGTGTTTGGAGTTTCTGTGGGCTCAT 2724
Qy 901 CCCGCGAAAGTTGATCTGCGAATTAAGAGATTAACATGGAATTTGAAGAGCTT 960
Db 2725 CCCGCGAAAGTTGATCTGCGAATTAAGAGATTAACATGGAATTTGAAGAGCTT 2784
Qy 961 TGAATCCTGTGAGAGCTGTTGATTTCTTGAATCTGAGTCAACAGGCTTTTCCAG 1020
Db 2785 TGAATCCTGTGAGAGCTGTTGATTTTCTTGAATCTGAGTCAACAGGCTTTTCCAG 2844
Qy 1021 AGAAGTCAATCAGACTTTGATTTTCCACACCGGGGCGGCTGCGGCTGTGCTT 1080
Db 2845 AGAAGTCAATCAGACTTTGATTTTCCACACCGGGGCGGCTGCGGCTGTGCTT 2904
Qy 1081 TTTTGAATTTTAAAGATTAATGAGCCGAAGAAACCATCTGAGCGGGGATACCTGC 1140
Db 2905 TTTTGAATTTTAAAGATTAATGAGCCGAAGAAACCATCTGAGCGGGGATACCTGC 2964
Qy 1141 TGAATTTTCCGATCATCTGTGAGAGAGGTTGTGAGACACAAGAAATGCTGTCTAC 1200
Db 2965 TGAATTTTCCGATCATCTGTGAGAGAGGTTGTGAGACACAAGAAATGCTGTCTAC 3024
Qy 1201 TGTGTCTTCCGTCGCTCCGCGATTAATACCGAGAGAGACAGACAGAGAGG 1260
Db 3025 TGTGTCTTCCGTCGCTCCGCGATTAATACCGAGAGAGACAGACAGAGAGG 3084
Qy 1261 AAGCAGCGCGCGCGGCGGACAGAGAGCCCATGGAACCCGAGAGCGGCTGTGACCTC 1320
Db 3085 AAGCAGCGCGCGCGGCGGACAGAGAGCCCATGGAACCCGAGAGCGGCTGTGACCTC 3144
Qy 1321 GGGAAATGATGTTGTATAGAGTGTGCTGAAGTATCCAGAACTGAGAGCAATTTTGA 1380
Db 3145 GGGAAATGATGTTGTATAGAGTGTGCTGAAGTATCCAGAACTGAGAGCAATTTTGA 3204
Qy 1381 TACAGAGATGGGCGGCTTAAAGGGGTTAAAGAGGAGCGGGGCTTGTGAGCTAC 1440
Db 3205 TACAGAGATGGGCGGCTTAAAGGGGTTAAAGAGGAGCGGGGCTTGTGAGCTAC 3264
Qy 1441 AGAGGAGCTAGGAATCTAGCTTTTACTTAAATGACAGACACCGTCTGAGTATTAAC 1500

```
Db 3265 AGAGAGGCTAGAACTAGCTTTAGCTTAATGACACGACCGCTCTGATGTATTAC 3324
Qy 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGAATCTGCGGCGCAAGTATTC 1560
Db 3325 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTTGAATCTGCGGCGCAAGTATTC 3384
Qy 1561 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATATTTTGAGAGGCTATTAG 1620
Db 3385 CATAGAGAGCTGACCACTTACTGCTGACAGGGGATATTTTGAGAGGCTATTAG 3444
Qy 1621 GGTATATGCAAAAGGTGCACTTGAAGCCAGATTGCAAGATCAAGATCAAGCAACTTGTAA 1680
Db 3445 GGTATATGCAAAAGGTGCACTTGAAGCCAGATTGCAAGATCAAGATCAAGCAACTTGTAA 3504
Qy 1681 TATCAGAAATTGTTGCTACATTTCTGCGGAGCGGGCCGAGGTGAGATAGATAGAGGAGA 1740
Db 3505 TATCAGAAATTGTTGCTACATTTCTGCGGAGCGGGCCGAGGTGAGATAGATAGAGGAGA 3564
Qy 1741 TAGGGTGGCTTTAGATGTAGCATGATTAATATATGTGCGCGGGGTGCTTGGCATGACGG 1800
Db 3565 TAGGGTGGCTTTAGATGTAGCATGATTAATATATGTGCGCGGGGTGCTTGGCATGACGG 3624
Qy 1801 GGTGTTATTAATGAATGAATGATTAAGCTTCTGCCCCCAATTTTACGGTACGGTTTCTGGC 1860
Db 3625 GGTGTTATTAATGAATGAATGATTAAGCTTCTGCCCCCAATTTTACGGTACGGTTTCTGGC 3684
Qy 1861 CAATACCAACCTTATCTCACAAGGTGTAAGCTTATGAGGTTTAAACAATACCTGTGAGA 1920
Db 3685 CAATACCAACCTTATCTCACAAGGTGTAAGCTTATGAGGTTTAAACAATACCTGTGAGA 3744
Qy 1921 AGCCTGGAACCGATGTAAAGGTTTCGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGT 1980
Db 3745 AGCCTGGAACCGATGTAAAGGTTTCGGGGCTGTGCTTTTACTGCTGCTGGAAGGGGGTGT 3804
Qy 1981 GTGTGCCCCCAAAAGCAGGGGCTTCAATTAAAGAAAGCTCTTGTGAAGGTGTACCTTGGG 2040
Db 3805 GTGTGCCCCCAAAAGCAGGGGCTTCAATTAAAGAAAGCTCTTGTGAAGGTGTACCTTGGG 3864
Qy 2041 TATCTGTCTAAGGGGTAACTCAAGGGTGGCCAAATGTGGCTCCGACTGGTGTGTT 2100
Db 3865 TATCTGTCTAAGGGGTAACTCAAGGGTGGCCAAATGTGGCTCCGACTGGTGTGTT 3924
Qy 2101 CATGCTAGTGAAGACGTGCTGTGATTTAGCATTAACATGTATGTGCAACTGCGAGA 2160
Db 3925 CATGCTAGTGAAGACGTGCTGTGATTTAGCATTAACATGTATGTGCAACTGCGAGA 3984
Qy 2161 CAGGGCTCTCTAGATGCTGACCTGCTCGGAGCGCACTGTCACTGCTGGAAGACATTCA 2220
Db 3985 CAGGGCTCTCTAGATGCTGACCTGCTCGGAGCGCACTGTCACTGCTGGAAGACATTCA 4044
Qy 2221 CGTAGCCAGCACTCTGCGAAGGCTGCGCAAGTGTGAGCATTAACATGACCCGCTG 2280
Db 4045 CGTAGCCAGCACTCTGCGAAGGCTGCGCAAGTGTGAGCATTAACATGACCCGCTG 4104
Qy 2281 TTCCTTGCAATTTGGGTAAACAGAGAGGGGGTGTTCCTACCTTAACCAATGCAATTTGAGTCA 2340
Db 4105 TTCCTTGCAATTTGGGTAAACAGAGAGGGGGTGTTCCTACCTTAACCAATTTGAGTCA 4164
Qy 2341 CACTTAAGTATTTGCTTGAAGCCCGAGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTTTGA 2400
Db 4165 CACTTAAGTATTTGCTTGAAGCCCGAGAGCATGTCCAAAGTGAACCTGAAACGGGGTGTTTGA 4224
Qy 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTAGATGAGACCCGACACAGGTGAGAGC 2460
Db 4225 CATGACCATGAAGATCTGGAAGGTGCTGAGGTAGATGAGACCCGACACAGGTGAGAGC 4284
Qy 2461 CTGCGAGTGTGGCGGTAAACAATTATAGAACCAAGCTGTGATGTGATGTGACCGAGA 2520
Db 4285 CTGCGAGTGTGGCGGTAAACAATTATAGAACCAAGCTGTGATGTGATGTGACCGAGA 4344
Qy 2521 GCTGAGGCCCGATCATCTTGTGTCTGCTGACACCGCGCTGAGTGTGGCTCTAGCGATGA 2580
Db 4345 GCTGAGGCCCGATCATCTTGTGTCTGCTGACACCGCGCTGAGTGTGGCTCTAGCGATGA 4404
```

```
Qy 2581 AGATACAGATTGAG 2594
Db 4405 AGATACAGATTGAG 4418

RESULT 10
US-09-482-682-15
; Sequence 15. Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALDENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 14455
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-15

Query Match 100.0%; Score 2594; DB 10; Length 14455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATCTTAACCTGCAACGAGGCTGCTTCCACCCAGTGAAGAGATGAAGAGGCT 60
Db 1825 ATGATCTTAACCTGCAACGAGGCTGCTTCCACCCAGTGAAGAGATGAAGAGGCT 1884
Qy 61 GAGAGTTTGTTAGTAAATTAATGTGAGACACCCCGGGGACGGTTGCAGTCTTGCATTAT 120
Db 1885 GAGAGTTTGTTAGTAAATTAATGTGAGACACCCCGGGGACGGTTGCAGTCTTGCATTAT 1944
Qy 121 CACCGAGAAATACGGGGGACCCAGATATTATGTTCGCTTGTCTATATAGAGACCTGT 180
Db 1945 CACCGAGAAATACGGGGGACCCAGATATTATGTTCGCTTGTCTATATAGAGACCTGT 2004
Qy 181 GGCATGTTTGTCTACATTAAGTGAATTAATGAGCACTGAGTGTGATGATGTGGGTTTG 240
Db 2005 GGCATGTTTGTCTACATTAAGTGAATTAATGAGCACTGAGTGTGATGATGTGGGTTTG 2064
Qy 241 GTGTGTTAATTTTATTTTAAATTTTACAGTTTGTGTTTAAAGAAATTTGTAATTGTA 300
Db 2065 GTGTGTTAATTTTATTTTAAATTTTAAAGTTTGTGTTTAAAGAAATTTGTAATTGTA 2124
Qy 301 TTTTAAAAAGTCTGTGCTGAACCTGAGCTGAGCCCGAAGCCGAGAGCTG 360
Db 2125 TTTTAAAAAGTCTGTGCTGAACCTGAGCTGAGCCCGAAGCCGAGAGCTG 2184
Qy 361 CAAGACCTAACCCGCGCTCTAAATGAGCGCTGCTATCTGAGACGCCGACATCACTG 420
Db 2185 CAAGACCTAACCCGCGCTCTAAATGAGCGCGCTGCTATCTGAGACGCCGACATCACTG 2244
Qy 421 TGTCTAAGAAATGAATAGTATGAGATGAGTGTGAGTGTGCTCGGCTCTTCTAACACACTC 480
Db 2245 TGTCTAAGAAATGAATAGTATGAGATGAGTGTGAGTGTGCTCGGCTCTTCTAACACACTC 2304
Qy 481 CTGAGATACACCCGAGTGTCCGCTGTGCCCCATTAAACAGTTGCGGTGAGATGTG 540
Db 2305 CTGAGATACACCCGAGTGTCCGCTGTGCCCCATTAAACAGTTGCGGTGAGATGTG 2364
Qy 541 GCGCTCGCAGGCTGTGGAATGTATCGAGGACTTGAACGAGCTGGGCAACTTTGG 600
```

Db 2365 GGCCTGCGACAGGCTGTGGAATGTATCGAGGACTTGTCTTAACGAGCCTGGGCAACCTTTGG 2424
Qy 601 ACTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAACCTGTGATTCGGTGTGGTTAA 660
Db 2425 ACTTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAACCTGTGATTCGGTGTGGTTAA 2484
Qy 661 GGCCTTGTGTGCTGAATGAGTGTGATGTAAAGTTTAAAGGTTGATTAAGTTTAACT 720
Db 2485 GGCCTTGTGTGCTGAATGAGTGTGATGTAAAGTTTAAAGGTTGATTAAGTTTAACT 2544
Qy 721 TGCATGCGGTGTAAATGAGGCGGCGCTTAAAGGTTATTAATGCGCGTGGCTAATCT 780
Db 2545 TGCATGCGGTGTAAATGAGGCGGCGCTTAAAGGTTATTAATGCGCGTGGCTAATCT 2604
Qy 781 TGGTATCATCTGACCTCATGAGGCTTGGAGTGTGTTGAGAGATTTTCTGCTGCGTA 840
Db 2605 TGGTATCATCTGACCTCATGAGGCTTGGAGTGTGTTGAGAGATTTTCTGCTGCGTA 2664
Qy 841 ACTGCTGGAACAGAGCTCTAACATGACCTCTTGGTTTGGAGTTTCTGCTGCGCTCAT 900
Db 2665 ACTGCTGGAACAGAGCTCTAACATGACCTCTTGGTTTGGAGTTTCTGCTGCGCTCAT 2724
Qy 901 CCGAGGCAAAAGTTAGTCTGCAAGATTTAAGAGGATTAACAAGTGGAAATTTGAAGACTT 960
Db 2725 CCGAGGCAAAAGTTAGTCTGCAAGATTTAAGAGGATTAACAAGTGGAAATTTGAAGACTT 2784
Qy 961 TGAATCTGTGTGAGCTGTGTTGATCTTTGAAATCTGGGTCAACAGGCGCTTTTCCAAG 1020
Db 2785 TGAATCTGTGTGAGCTGTGTTGATCTTTGAAATCTGGGTCAACAGGCGCTTTTCCAAG 2844
Qy 1021 AGAAGGTATCAAGACTTTGATTTTTCACACCGGGGCGCGCTGCTGTGTTGCTT 1080
Db 2845 AGAAGGTATCAAGACTTTGATTTTTCACACCGGGGCGCGCTGCTGTGTTGCTT 2904
Qy 1081 TTTTGAAGTTTATAAAGATTAATGAGCGAAGAAACCATCTGAGCGGAGGTTACTGTC 1140
Db 2905 TTTTGAAGTTTATAAAGATTAATGAGCGAAGAAACCATCTGAGCGGAGGTTACTGTC 2964
Qy 1141 TGGATTTTCTGGCCATGATCTGTGGAAGCGGTTGTGAGACACAAAGATGCGCTGTAC 1200
Db 2965 TGGATTTTCTGGCCATGATCTGTGGAAGCGGTTGTGAGACACAAAGATGCGCTGTAC 3024
Qy 1201 TGTGTCTTCCGCTCCGCGCGCGATTAATCCGACCGGAGAGACAGACAGACAGAGG 1260
Db 3025 TGTGTCTTCCGCTCCGCGCGCGATTAATCCGACCGGAGAGACAGACAGACAGAGG 3084
Qy 1261 AAGCAGGCGGCGGCGGAGAGAGAGCCCATGGAACCGGAGCGCGCTGTGACCCCTC 1320
Db 3085 AAGCAGGCGGCGGCGGAGAGAGAGCCCATGGAACCGGAGCGCGCTGTGACCCCTC 3144
Qy 1321 GGGAAATGATTTGTATCAGGTGCTGAACCTGTATCCAGAACTGAGACGATTTTGACAT 1380
Db 3145 GGGAAATGATTTGTATCAGGTGCTGAACCTGTATCCAGAACTGAGACGATTTTGACAT 3204
Qy 1381 TACAGAGATGAGGCGGCGCTTAAAGGGGTAAAGGAGGCGGCGGCTTGTGAGGCTAC 1440
Db 3205 TACAGAGATGAGGCGGCGCTTAAAGGGGTAAAGGAGGCGGCGGCTTGTGAGGCTAC 3264
Qy 1441 AGAGAGGCTAGGAATCTAGCTTTAGCTTAAATGACAGACACGCTCCAGAGTATTAAC 1500
Db 3265 AGAGAGGCTAGGAATCTAGCTTTAGCTTAAATGACAGACACGCTCCAGAGTATTAAC 3324
Qy 1501 TTTTCAACAGATCAAGATTAATTTGGCTTAATGAGCTTGAATCTGCTGGCGAGAAATATC 1560
Db 3325 TTTTCAACAGATCAAGATTAATTTGGCTTAATGAGCTTGAATCTGCTGGCGAGAAATATC 3384
Qy 1561 CATGAGAGAGCTGACCACTTACCTGCTGACAGCAGGAGATGATTTTGAAGAGGCTAATAG 1620
Db 3385 CATGAGAGAGCTGACCACTTACCTGCTGACAGCAGGAGATGATTTTGAAGAGGCTAATAG 3444
Qy 1621 GGTATATCAAAAGGTGCACTTAAAGCAGATTTGCAAGTACAAATCACTGTAA 1680
Db 3445 GGTATATCAAAAGGTGCACTTAAAGCAGATTTGCAAGTACAAATCACTGTAA 3504

Qy 1681 TATCAGGAATTTGTTGCTACATTTCTGGGACAGGGCCGAGGTGAGATGATACGAGGA 1740
Db 3505 TATCAGGAATTTGTTGCTACATTTCTGGGACAGGGCCGAGGTGAGATGATACGAGGA 3564
Qy 1741 TAGGGTGGCTTTGATGATGATGATTAATATGAGGCGGAGGCTTGGCATGAGG 1800
Db 3565 TAGGGTGGCTTTGATGATGATGATTAATATGAGGCGGAGGCTTGGCATGAGG 3624
Qy 1801 GGTGTTATTAATGATGATGATGATTAATGATGATGATGATGATGATGATGATGATGAT 1860
Db 3625 GGTGTTATTAATGATGATGATGATTAATGATGATGATGATGATGATGATGATGATGAT 3684
Qy 1861 CAATACCAACCTTATCTTACACGCTGTGATGATGATGATGATGATGATGATGATGATGAT 1920
Db 3685 CAATACCAACCTTATCTTACACGCTGTGATGATGATGATGATGATGATGATGATGATGAT 3744
Qy 1921 AGCCTGAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 3745 AGCCTGAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3804
Qy 1981 GTGTGCCCCAAAGCAGGCGCTTCAATTAAGAAATGCTCTTGTGAAGGTATCCTTGG 2040
Db 3805 GTGTGCCCCAAAGCAGGCGCTTCAATTAAGAAATGCTCTTGTGAAGGTATCCTTGG 3864
Qy 2041 TATCTGTCTGAGGTTAATCTCAAGGCTGCGCAATGTGCTTCCGACTGTGTTGCTT 2100
Db 3865 TATCTGTCTGAGGTTAATCTCAAGGCTGCGCAATGTGCTTCCGACTGTGTTGCTT 3924
Qy 2101 CATGCTATGAAAAGCGTGTGATTAAGCATTAACATGATGATGATGATGATGATGATGATGAT 2160
Db 3925 CATGCTATGAAAAGCGTGTGATTAAGCATTAACATGATGATGATGATGATGATGATGATGAT 3984
Qy 2161 CAGGCGCTCTGAGATGCTGACTGCTGCGACGCACTGTCACTGTGTAAGAACCATTTCA 2220
Db 3985 CAGGCGCTCTGAGATGCTGACTGCTGCGACGCACTGTCACTGTGTAAGAACCATTTCA 4044
Qy 2221 GGTAGCCAGCACTCTGCGAAGGCTGCGCAATGTGTTGAGCATTAATGATGATGATGATGATGAT 2280
Db 4045 GGTAGCCAGCACTCTGCGAAGGCTGCGCAATGTGTTGAGCATTAATGATGATGATGATGATGAT 4104
Qy 2281 TTCCTGATTTGGGTAAACAGAGGCGGCTGTCTTCACTTAACAAATGATGATGATGATGATGAT 2340
Db 4105 TTCCTGATTTGGGTAAACAGAGGCGGCTGTCTTCACTTAACAAATGATGATGATGATGATGAT 4164
Qy 2341 CACTAAGATATTGCTTGAAGCCGAGAGCATGTCCAAGGTGAACCTGAACGCGGCTTTGA 2400
Db 4165 CACTAAGATATTGCTTGAAGCCGAGAGCATGTCCAAGGTGAACCTGAACGCGGCTTTGA 4224
Qy 2401 CATGACATGAAAGATCTGGAAGGTGCTGAGGATGATGATGATGATGATGATGATGATGATGAT 2460
Db 4225 CATGACATGAAAGATCTGGAAGGTGCTGAGGATGATGATGATGATGATGATGATGATGATGAT 4284
Qy 2461 CTGGAAGTGTGCGGTAAACATTAAGAAACACGCTGTGATGCTGATGATGATGATGATGATGAT 2520
Db 4285 CTGGAAGTGTGCGGTAAACATTAAGAAACACGCTGTGATGCTGATGATGATGATGATGATGAT 4344
Qy 2521 GCTGAGGCCGATCATCTTGTGTGCTGCTGCAACCGGCTGAGTTTGGCTTACGAGATGA 2580
Db 4345 GCTGAGGCCGATCATCTTGTGTGCTGCTGCAACCGGCTGAGTTTGGCTTACGAGATGA 4404
Qy 2581 AGATACAGATTGAG 2594
Db 4405 AGATACAGATTGAG 4418

RESULT 11
US-10-766-307A-3
; Sequence 3, Application US/10766307A
; Publication No. US2004020263A1
; GENERAL INFORMATION:
; APPLICANT: Shanghai Sunway Biotech Co., LTD.
; TITLE OF INVENTION: Treatment for Metastatic Cancer

FILE REFERENCE: 121300.00003
CURRENT APPLICATION NUMBER: US/10/766.307A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 3
LENGTH: 32802
TYPE: DNA
ORGANISM: Adenovirus
US-10-766-307A-3

Query Match 100.0%; Score 2594; DB 21; Length 32802;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATCCATCTTACTGCGACAGAGCTGGCTTTCCACCCAGTACGACGAGATGGAAGGCT 60
917 ATCCATCTTACTGCGACAGAGCTGGCTTTCCACCCAGTACGACGAGATGGAAGGCT 976
61 GAGGAGTTTGTGTGATTAATGTGAGGACCCCGGGGACGGTTGCAAGGCTTGTCAATAT 120
977 GAGGAGTTTGTGTGATTAATGTGAGGACCCCGGGGACGGTTGCAAGGCTTGTCAATAT 1036
121 CACCGAGAAATACCGGGGACCCAGATATTAATGTGCGCTTGTGCTATATAGACCTGT 180
1037 CACCGAGAAATACCGGGGACCCAGATATTAATGTGCGCTTGTGCTATATAGACCTGT 1096
181 GGCATGTTTGTCTACAGTAAGTAAGAAATTAATGGGCAATGGGTAATAGTGGGTTTG 240
1097 GGCATGTTTGTCTACAGTAAGTAAGAAATTAATGGGCAATGGGTAATAGTGGGTTTG 1156
241 GTCGTGTAATTTTATTTTAAATTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGA 300
1157 GTGTGTATTTTATTTTATTTTAAATTTTACAGTTTGTGTTTAAAGAAATTTTGTATGTGA 1216
301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCGAGCCCGAGCCAGAACCGAGCCTG 360
1217 TTTTAAAAAGTCTGTGTCTGAACCTGAGCCGAGCCCGAGCCAGAACCGAGCCTG 1276
361 CAAGACTACCCCGCTCTTAAATAGGGGCTGCTATCTTGAGAGCCCGACATCACTG 420
1277 CAAGACTACCCCGCTCTTAAATAGGGGCTGCTATCTTGAGAGCCCGACATCACTG 1336
421 TGTCTAGAGAAATGCAATAGTATGATGAGATGAGTGTGATCGGCTCTTCAACACCTG 480
1337 TGTCTAGAGAAATGCAATAGTATGATGAGATGAGTGTGATCGGCTCTTCAACACCTG 1396
481 CTGAGATACACCCGGTGTGCTGCTGAGCCGCAATTAACCAAGTTGCGTGAAGTTGTG 540
1397 CTGAGATACACCCGGTGTGCTGCTGAGCCGCAATTAACCAAGTTGCGTGAAGTTGTG 1456
541 GCGCTGCGCAGGCTGTGAATGTATCGAGAGCTTGTCTTAAGAGCTGGGCAACTTTGG 600
1457 GCGCTGCGCAGGCTGTGAATGTATCGAGAGCTTGTCTTAAGAGCTGGGCAACTTTGG 1516
601 ACTTAGGCTGTAAAGCCCGCAGGCAATAGGTAAGCTGTGAAGTTGCGTGTGTTAA 660
1517 ACTTAGGCTGTAAAGCCCGCAGGCAATAGGTAAGCTGTGAAGTTGCGTGTGTTAA 1576
661 GCGCTTGTGTCTGAATGAGTTGATGTAAATTAATTAAGGGTGAATATGTTAACT 720
1577 GCGCTTGTGTCTGAATGAGTTGATGTAAATTAATTAAGGGTGAATATGTTAACT 1636
721 TGCATGGGCTGTAAATGGGGGCGGCTTAAAGGTAATTAATGGCGGCTGATATCT 780
1637 TGCATGGGCTGTAAATGGGGGCGGCTTAAAGGTAATTAATGGCGGCTGATATCT 1696
781 TGGTAACTCTGACCTCATGAGGCTTGGAGTGTGAGAAATTTCTGCTGTGCGTA 840
1697 TGGTAACTCTGACCTCATGAGGCTTGGAGTGTGAGAAATTTCTGCTGTGCGTA 1756
841 ACTTGTGAAACAGAGCTCTAACAGTACCTTGTGTTTGAAGGTTTCTGTGGGCTCAT 900

1757 ACTTGTGAAACAGAGCTCTAACAGTACCTTGTGTTTGAAGGTTTCTGTGGGCTCAT 1816
901 CCCAGGAAAGTTAGTCTGCAAGATTAAGAGATTCAAGTGGAAATTTGAAGGCTT 960
1817 CCCAGGAAAGTTAGTCTGCAAGATTAAGAGATTCAAGTGGAAATTTGAAGGCTT 1876
961 TGAATCTGTGTGAGCTGTTTGAATCTTGTGAATCTGGGTCAACAGGCGCTTTTCCAG 1020
1877 TGAATCTGTGTGAGCTGTTTGAATCTTGTGAATCTGGGTCAACAGGCGCTTTTCCAG 1936
1021 AGAAGTCTATCAGACTTTGGATTTTTCACACCGGGGCGGCTGCGGCTCTGTGCTT 1080
1937 AGAAGTCTATCAGACTTTGGATTTTTCACACCGGGGCGGCTGCGGCTCTGTGCTT 1996
1081 TTTTGAATTTATTAAGGATTAATGAGCGGAAGAACCCATCTGAGCGGGGGTAACTGCG 1240
1997 TTTTGAATTTATTAAGGATTAATGAGCGGAAGAACCCATCTGAGCGGGGGTAACTGCG 2056
1141 TGAATTTTCTGGCCATCATCTGTGAGAGCGGTTGTGAGACAGAAATCGCTGTAC 1200
2057 TGAATTTTCTGGCCATCATCTGTGAGAGCGGTTGTGAGACAGAAATCGCTGTAC 2216
1201 TGTGTCTTCCGTCGCCCGGCAATAATCCAGAGAGAGCAGCAGCAGCAGAGG 1260
2117 TGTGTCTTCCGTCGCCCGGCAATAATCCAGAGAGAGCAGCAGCAGCAGAGG 2176
1261 AAGCAGGCGCGGCGGAGAGAGCCCATGGAACCCGAGAGCGGCGCTGACCTC 1320
2177 AAGCAGGCGCGGCGGAGAGAGCCCATGGAACCCGAGAGCGGCGCTGACCTC 2236
1321 GGAATGAATGTTGTACAGGTGCTGAATGTATCCAGAACTGAGACGATTTTGACAT 1380
2237 GGAATGAATGTTGTACAGGTGCTGAATGTATCCAGAACTGAGAGCGATTTTGACAT 2296
1381 TACAGAGATGCGCAAGGCGCTAAAGGCGTAAAGGAGCGAGCGGCGCTGTGAGCTAC 1440
2297 TACAGAGATGCGCAAGGCGCTAAAGGCGTAAAGGAGCGAGCGGCGCTGTGAGCTAC 2356
1441 AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGCTCTGATGATTAAC 1500
2357 AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGCTCTGATGATTAAC 2416
1501 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTGATCTGTGCGCAGAAATATTC 1560
2417 TTTTCAACAGATCAAGATTAATGCGCTAATGAGCTGATCTGTGCGCAGAAATATTC 2476
1561 CATAGAGACTGACCACTTACTGTGCGCAGCCAGGGGATATTTTGAAGGCTATTAG 1620
2477 CATAGAGACTGACCACTTACTGTGCGCAGCCAGGGGATATTTTGAAGGCTATTAG 2536
1621 GGTATATGCAAAAGGTGGCACTTAGCCAGANTTGAAGTACAGAAATCACTTGTAA 1680
2537 GGTATATGCAAAAGGTGGCACTTAGCCAGANTTGAAGTACAGAAATCACTTGTAA 2596
1681 TATCAGGAATTTGTGCTACATTTCTGGGAACGSGGCGAGGTGAGATAGATACGAGGA 1740
2597 TATCAGGAATTTGTGCTACATTTCTGGGAACGSGGCGAGGTGAGATAGATACGAGGA 2656
1741 TAGGCTGCGCTTGAATGATGATGATTAATATGTGCGCGGGGCTGCTGGCATGACGG 1800
2657 TAGGCTGCGCTTGAATGATGATGATTAATATGTGCGCGGGGCTGCTGGCATGACGG 2716
1801 GGTGTTATTAATGATGATGATGATTAATGATGATTAATGATGATGATGATGATGATGAT 1860
2717 GGTGTTATTAATGATGATGATGATGATTAATGATGATTAATGATGATGATGATGATGATGAT 2776
1861 CAATACCAACTTATCTTACACGCTGTAGCTTATGAGTTTAAACAATACCTGTGTGA 1920
2777 CAATACCAACTTATCTTACACGCTGTAGCTTATGAGTTTAAACAATACCTGTGTGA 2836
1921 AGCCTGACCGATGTAAGGGTTCGGGCGTGTGCTTTTACTGCTGCTGGAAGGGGCTGT 1980
2837 AGCCTGACCGATGTAAGGGTTCGGGCGTGTGCTTTTACTGCTGCTGGAAGGGGCTGT 2896

QY 1981 GTGTGCCCCCAAGAGAGGCTTCAATTAAAGAAATGCTTTTGAAGGTGACTTGGG 2040
DB 2897 GTGTGCCCCCAAGAGAGGCTTCAATTAAAGAAATGCTTTTGAAGGTGACTTGGG 2956
QY 2041 TATCTGTCTGAGGGTAACTCCAGGGTGGCCCAATGTGGCTCGAGCTGTGGTCTT 2100
DB 2957 TATCTGTCTGAGGGTAACTCCAGGGTGGCCCAATGTGGCTCGAGCTGTGGTCTT 3016
QY 2101 CATGTCTAGTAAAGACGTGGCTGTGTATTAAGCATTAACATGTATGTGGCACTGGAGGA 2160
DB 3017 CATGTCTAGTAAAGACGTGGCTGTGTATTAAGCATTAACATGTATGTGGCACTGGAGGA 3076
QY 2161 CAGGGCTCTGAGAGTCTGACTGTCTGCGACGGCACTGTCACTCTGTGAAACATTTCA 2220
DB 3077 CAGGGCTCTGAGAGTCTGACTGTCTGCGACGGCACTGTCACTCTGTGAAACATTTCA 3136
QY 2221 CGTAGCCAGCCACTCTGCGAAGGCTGGCCAGTGTGAGCATTAACATGACTGACCCGCTG 2280
DB 3137 CGTAGCCAGCCACTCTGCGAAGGCTGGCCAGTGTGAGCATTAACATGACTGACCCGCTG 3196
QY 2281 TTCCTTGATTTGGGTAAACAGAGGGGGGTGTTCTTACCTTAACAATGATTTGATCA 2340
DB 3197 TTCCTTGATTTGGGTAAACAGAGGGGGGTGTTCTTACCTTAACAATGATTTGATCA 3256
QY 2341 CACTAAGATTTGCTTGAAGCCCGAGACATGTCGAAGTGAACCTGAAACGGGGTCTTGA 2400
DB 3257 CACTAAGATTTGCTTGAAGCCCGAGACATGTCGAAGTGAACCTGAAACGGGGTCTTGA 3316
QY 2401 CATGACCATGAAGATCTGAAAGGTGCTGAGGATGAGACCCGACAGGTGAGACC 2460
DB 3317 CATGACCATGAAGATCTGAAAGGTGCTGAGGATGAGACCCGACAGGTGAGACC 3376
QY 2461 CTGCGAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGTGAATGCCAGGA 2520
DB 3377 CTGCGAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGTGAATGCCAGGA 3436
QY 2521 GCTGAGGCCCATCACTGTGTGTGTGCTGACCCGCGCTGAGTTGGCTTGAAGCATGA 2580
DB 3437 GCTGAGGCCCATCACTGTGTGTGTGCTGACCCGCGCTGAGTTGGCTTGAAGCATGA 3496
QY 2581 AGATACAGATTGAG 2594
DB 3497 AGATACAGATTGAG 3510

RESULT 12
US-09-725-720-43
Sequence 43, Application US/09725720
Patent No. US20010049136A1
GENERAL INFORMATION:
APPLICANT: IMLER, Jean-Luc
APPLICANT: MEHTALI, Majid
APPLICANT: PAVIRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
STREET: 1737 King Street, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/725,720
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/379,452
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 029395-002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-725-720-43

Query Match 100.0%; Score 2594; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCATCTTACCTGCAAGAGGCTTTCACCCAGTGAAGACGAGATGAAGAGGCT 60
DB 917 ATGCATCTTACCTGCAAGAGGCTTTCACCCAGTGAAGACGAGATGAAGAGGCT 976
QY 61 GAGGAGTTTGTGTTAAGATTATGTGAGACACCCGGGACAGTGTGAGGCTTGTCAATTAT 120
DB 977 GAGGAGTTTGTGTTAAGATTATGTGAGACACCCGGGACAGTGTGAGGCTTGTCAATTAT 1036
QY 121 CACCGAGAGAAATACGGGGAGACCCAGATTTATGTGTTCCTTTGCTATATAGACCTGT 180
DB 1037 CACCGAGAGAAATACGGGGAGACCCAGATTTATGTGTTCCTTTGCTATATAGACCTGT 1096
QY 181 GGCATGTTTGTCTACAGTAAGTGAATTAATGAGGAGGAGTGAAGTGTGGCTTGG 240
DB 1097 GGCATGTTTGTCTACAGTAAGTGAATTAATGAGGAGGAGTGAAGTGTGGCTTGG 1156
QY 241 GTGTGTAATTTTATTTTATTTTATTTTACAGTTTGTGTGTTTAAAGATTTGTATTTGA 300
DB 1157 GTGTGTAATTTTATTTTATTTTATTTTACAGTTTGTGTGTTTAAAGATTTGTATTTGA 1216
QY 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTTGAAGCCCGAGCCAGACCGAGCTG 360
DB 1217 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTTGAAGCCCGAGCCAGACCGAGCTG 1276
QY 361 CAAGACCTACCGCGCGCTTAAATGAGGCGCTGCTATCTGAGACCGCCGACATCACCTG 420
DB 1277 CAAGACCTACCGCGCGCTTAAATGAGGCGCTGCTATCTGAGACCGCCGACATCACCTG 1336
QY 421 TGTCTAGAGATGCAATAGTATGATGAGTATGCTGATCTGCTCTTCTAACAACCTC 480
DB 1337 TGTCTAGAGATGCAATAGTATGATGAGTATGCTGATCTGCTCTTCTAACAACCTC 1396
QY 481 CTGAGATACACCGGTGTCTCCGCTGTGCCCCATTAAACAGTTGCCGTGAGATTGTG 540
DB 1397 CTGAGATACACCGGTGTCTCCGCTGTGCCCCATTAAACAGTTGCCGTGAGATTGTG 1456
QY 541 GGGGTGCGAGGCTGTGGAATGTATCGAGGACTTGAAGACCTGAGGAGGAGCACTTTGG 600
DB 1457 GGGGTGCGAGGCTGTGGAATGTATCGAGGACTTGAAGACCTGAGGAGGAGCACTTTGG 1516
QY 601 ACTGAGCTGTAAAGCCCGCAGCCATAGGTGTAAACCTGTGATGCGTGTGTGTTAA 660
DB 1517 ACTGAGCTGTAAAGCCCGCAGCCATAGGTGTAAACCTGTGATGCGTGTGTGTTAA 1576
QY 661 CGCCTTTGTTTCTGAATGAGTGTATGATTTAAATTAAGGGTGAAGATTAATGTTAACT 720
DB 1577 CGCCTTTGTTTCTGAATGAGTGTATGATTTAAATTAAGGGTGAAGATTAATGTTAACT 1636
QY 721 TGCATGCGGTGTAAAGGGGCGGGCTTAAAGGGTATATTAATGCGCGTGGGCTAATCT 780

Dh 1637 TGCATGGCGTGTAAATGCGGCGGGCTTAAAGGGTATATATAGCGCCGTGGCTAAATCT 1696
Qy 781 TGGTTACATCTGACCTCATGGAAGCTTGGAGGTGTTGGAAAGATTTTCTCTGTGGCTA 840
Db 1697 TGGTTACATCTGACCTCATGGAAGCTTGGAGGTGTTGGAAAGATTTTCTCTGTGGCTA 1756
Qy 841 ACTTGCTGGAACAGAGCTCTTAACAGTACCTCTTGATTTTGGAGTTTCTGTGGGGCTCAT 900
Db 1757 ACTTGCTGGAACAGAGCTCTTAACAGTACCTCTTGATTTTGGAGTTTCTGTGGGGCTCAT 1816
Qy 901 CCGAGCGAAAGTTAGTCTGCAAGATTTAAAGAGATTTCAAGTGGAAATTTGAAGAGCTTT 960
Db 1817 CCGAGCGAAAGTTAGTCTGCAAGATTTAAAGAGATTTCAAGTGGAAATTTGAAGAGCTTT 1876
Qy 961 TGAATCCTGTGGAGCTGTTTGAATTTCTTGAAATCTGGGTCAACAAGCCGCTTTTCCAG 1020
Db 1877 TGAATCCTGTGGAGCTGTTTGAATTTCTTGAAATCTGGGTCAACAAGCCGCTTTTCCAG 1936
Qy 1021 AGAAGTCAATCAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGTGCTT 1080
Db 1937 AGAAGTCAATCAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGTGCTT 1996
Qy 1081 TTTTGAAGTTTATTAAGATTAATGAGCCGAAGAAACCATCTGAACGGGGGTATCTGC 1140
Db 1997 TTTTGAAGTTTATTAAGATTAATGAGCCGAAGAAACCATCTGAACGGGGGTATCTGC 2056
Qy 1141 TGGATTTTCTGSCCATGATCTGTGAGAGAGGGGTTGTGAGACAAAGAAATGGCCCTGCAC 1200
Db 2057 TGGATTTTCTGSCCATGATCTGTGAGAGAGGGGTTGTGAGACAAAGAAATGGCCCTGCAC 2116
Qy 1201 TGTGTCTTCCGTCGCGCCGCGCGATTAATCCGACGAGAGAGACAGACAGACAGAGAGAG 1260
Db 2117 TGTGTCTTCCGTCGCGCCGCGCGATTAATCCGACGAGAGAGACAGACAGACAGAGAGAG 2176
Qy 1261 AAGCCAGCGCGCGCGCGAGAGACAGAGCCCATGTGAACCCGAGAGCCGCTGTGACCTTC 1320
Db 2177 AAGCCAGCGCGCGCGCGAGAGACAGAGCCCATGTGAACCCGAGAGCCGCTGTGACCTTC 2236
Qy 1321 GGGAAATGAATGTTTGAACAGTGGGCTGAACCTGATTCAGAACTGAGAGCGCATTTTGACAT 1380
Db 2237 GGGAAATGAATGTTTGAACAGTGGGCTGAACCTGATTCAGAACTGAGAGCGCATTTTGACAT 2296
Qy 1381 TACAGAGATGGGAGGCGGTAAAGGGGGTAAAGAGGAGCGGGGCTTGTGAGGCTAC 1440
Db 2297 TACAGAGATGGGAGGCGGTAAAGGGGGTAAAGAGGAGCGGGGCTTGTGAGGCTAC 2356
Qy 1441 AGAGAGGCTAGGAATCTAGCTTTAGCTTATATGACAGACACCGTCTGTAGTATTTAC 1500
Db 2357 AGAGAGGCTAGGAATCTAGCTTTAGCTTATATGACAGACACCGTCTGTAGTATTTAC 2416
Qy 1501 TTTTCAACAGATCAAGGATTAATGGGCTTAATGAGCTTGAATCTGCGGGCGAGAAATTTTC 1560
Db 2417 TTTTCAACAGATCAAGGATTAATGGGCTTAATGAGCTTGAATCTGCGGGCGAGAAATTTTC 2476
Qy 1561 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATATTTTGAAGAGCTATTAG 1620
Db 2477 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATATTTTGAAGAGGCTATTAG 2536
Qy 1621 GGTATATGCAAAAGGTGGCACTTAAAGCCAGATTGCAAGTACAGATCAGCAAACTTGTAAA 1680
Db 2537 GGTATATGCAAAAGGTGGCACTTAAAGCCAGATTGCAAGTACAGATCAGCAAACTTGTAAA 2596
Qy 1681 TATCAGGAATTTGTTGCTACATTTCTGGGAGAGGGGCGAGGTGAGATAGATAGAGAGGA 1740
Db 2597 TATCAGGAATTTGTTGCTACATTTCTGGGAGAGGGGCGAGGTGAGATAGATAGAGAGGA 2656
Qy 1741 TAGGCTGCGCTTTAGATGTAGCATGATTAATATGTGCGCGGGGCTTGTGCAATGAGAGG 1800
Db 2657 TAGGCTGCGCTTTAGATGTAGCATGATTAATATGTGCGCGGGGCTTGTGCAATGAGAGG 2716
Qy 1801 GGTGGTATTAATGAATGTAAAGTTTACTGGCCCAATTTTAAAGCGGTACGTTTCTGCGC 1860
Db 2717 GGTGGTATTAATGAATGTAAAGTTTACTGGCCCAATTTTAAAGCGGTACGTTTCTGCGC 2776

Qy 1861 CAATACCAACCTTATCTCTACACGGGTGATGCTTCTATGGGTTTAAACAATACCTGTGTGA 1920
Db 2777 CAATACCAACCTTATCTCTACACGGGTGATGCTTCTATGGGTTTAAACAATACCTGTGTGA 2836
Qy 1921 AGCCTGAGCGATGTAAAGGGTCTGGGGCTGTGCTTTTACTGTCTGTGAGAGGGGGTGT 1980
Db 2837 AGCCTGAGCGATGTAAAGGGTCTGGGGCTGTGCTTTTACTGTCTGTGAGAGGGGGTGT 2896
Qy 1981 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTACTTGGG 2040
Db 2897 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTTGAAGGTGTACTTGGG 2956
Qy 2041 TATCTGTGAGGGGTAACTCCAGGGTGGCGCAATGTGGCTCCGACTGTGGTGTCTT 2100
Db 2957 TATCTGTGAGGGGTAACTCCAGGGTGGCGCAATGTGGCTCCGACTGTGGTGTCTT 3016
Qy 2101 CATGCTAGTGAAGCGTGTGTGATTAAGCATTAACATGATGTGTGCAACTGCGAGGA 2160
Db 3017 CATGCTAGTGAAGCGTGTGTGATTAAGCATTAACATGATGTGTGCAACTGCGAGGA 3076
Qy 2161 CAGGGCTCTCAAGTGTGTGACCTGTGTGAGACGCACTGTCACTGTGAAAGACATTCA 2220
Db 3077 CAGGGCTCTCAAGTGTGTGACCTGTGTGAGACGCACTGTCACTGTGAAAGACATTCA 3136
Qy 2221 CGTAGCCAGCACTCTGCAAGGGCTGSCAGTGTGAGCATTAACATTAACCCGCTG 2280
Db 3137 CGTAGCCAGCACTCTGCAAGGGCTGSCAGTGTGAGCATTAACATTAACCCGCTG 3196
Qy 2281 TTCCTTGCATTTTGGGTAAACAGAGGGGGGTGTTCTTACTTAAACATGCAATTTGAGTCA 2340
Db 3197 TTCCTTGCATTTTGGGTAAACAGAGGGGGGTGTTCTTACTTAAACATGCAATTTGAGTCA 3256
Qy 2341 CACTTAAGTATTTGTTTGAAGCCCGAGACATGTCCAAAGTGAACCTGAACGGGGGTTTGA 2400
Db 3257 CACTTAAGTATTTGTTTGAAGCCCGAGACATGTCCAAAGTGAACCTGAACGGGGGTTTGA 3316
Qy 2401 CATGACCATGAAGATCTGGAAGGTGTGAGGTACATGATGAGACCCGACACAGGTGCAGACC 2460
Db 3317 CATGACCATGAAGATCTGGAAGGTGTGAGGTACATGATGAGACCCGACACAGGTGCAGACC 3376
Qy 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGTGATGTGATGTGACCGAGA 2520
Db 3377 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAAGCTGTGTGATGTGATGTGACCGAGA 3436
Qy 2521 GCTAGGCGCGATCACTTGTGTGTGCTGTGACCCCGGCTGAGTTTGGCTTACGAGTGA 2580
Db 3437 GCTAGGCGCGATCACTTGTGTGTGCTGTGACCCCGGCTGAGTTTGGCTTACGAGTGA 3496
Qy 2581 AGATACAGATTGAG 2594
Db 3497 AGATACAGATTGAG 3510

RESULT 13
US-09-782-378A-4
; Sequence 4, Application US/09782378A
; Patent No. US20020102731A1
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Nadie
; APPLICANT: Sandlenko, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONB-04970
; CURRENT APPLICATION NUMBER: US/09/782,378A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 35935

TYPE: DNA
ORGANISM: Human adenovirus type 5
US-09-782-378A-4

Query Match 100.0%; Score 2594; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCATCTTACCTGCGACGAGGCTGGCTTTCCACCGCATGACGACGAGATGAGAGGGT 60
Db ATGCATCTTACCTGCGACGAGGCTGGCTTTCCACCGCATGACGACGAGATGAGAGGGT 976

61 GAGGAGTTGATTAGATTATGTGAGGACCCCGGGGACGGTTGAGAGCTTTGTCATTAT 120
Db GAGGAGTTGATTAGATTATGTGAGGACCCCGGGGACGGTTGAGAGCTTTGTCATTAT 1036

977 GAGGAGTTGATTAGATTATGTGAGGACCCCGGGGACGGTTGAGAGCTTTGTCATTAT 1036
Db GAGGAGTTGATTAGATTATGTGAGGACCCCGGGGACGGTTGAGAGCTTTGTCATTAT 1096

121 CACCGAGAGAAATACGGGGGACCCAGATATTAATGTTGCTTTGCTATATAGACACTGT 180
Db CACCGAGAGAAATACGGGGGACCCAGATATTAATGTTGCTTTGCTATATAGACACTGT 1096

1097 GGCATGTTGCTCTACAGTAAATTAATGCGGAGTGGGTGATAGAGTGGGTTTG 1156
Db GGCATGTTGCTCTACAGTAAATTAATGCGGAGTGGGTGATAGAGTGGGTTTG 1156

241 GTGGGTAAATTTTTTTTAAATTTTACAGTTTGTGTTTAAAGATTTTGTATTTGA 300
Db GTGGGTAAATTTTTTTTAAATTTTACAGTTTGTGTTTAAAGATTTTGTATTTGA 1216

1157 GTGGGTAAATTTTTTTTAAATTTTACAGTTTGTGTTTAAAGATTTTGTATTTGA 1216
Db GTGGGTAAATTTTTTTTAAATTTTACAGTTTGTGTTTAAAGATTTTGTATTTGA 1216

301 TTTTAAAAAGTCTGTCTGAACTGAACTGAGCCGAGCCGAGCAGAACCGAGGCTTG 360
Db TTTTAAAAAGTCTGTCTGAACTGAACTGAGCCGAGCCGAGCAGAACCGAGGCTTG 1217

1217 TTTTAAAAAGTCTGTCTGAACTGAACTGAGCCGAGCCGAGCAGAACCGAGGCTTG 1276
Db TTTTAAAAAGTCTGTCTGAACTGAACTGAGCCGAGCCGAGCAGAACCGAGGCTTG 1276

361 CAAGACTACCCGCGCTCTAAATATGCGGCTGCTATCTGAGAGCGCCGACATCACTG 420
Db CAAGACTACCCGCGCTCTAAATATGCGGCTGCTATCTGAGAGCGCCGACATCACTG 1336

1277 CAAGACTACCCGCGCTCTAAATATGCGGCTGCTATCTGAGAGCGCCGACATCACTG 1336
Db CAAGACTACCCGCGCTCTAAATATGCGGCTGCTATCTGAGAGCGCCGACATCACTG 421

421 TGCTAGAGATGCAATAGTATCGGATACCTGATCTCGGCTCTCTAAACAACCTTC 480
Db TGCTAGAGATGCAATAGTATCGGATACCTGATCTCGGCTCTCTAAACAACCTTC 1337

1337 TGCTAGAGATGCAATAGTATCGGATACCTGATCTCGGCTCTCTAAACAACCTTC 1396
Db TGCTAGAGATGCAATAGTATCGGATACCTGATCTCGGCTCTCTAAACAACCTTC 481

481 CTGAGATACACCCGCGTGTCCGCTGTGCCCATTAACCAAGTTGCGTGAAGTTGCTG 540
Db CTGAGATACACCCGCGTGTCCGCTGTGCCCATTAACCAAGTTGCGTGAAGTTGCTG 1397

1397 CTGAGATACACCCGCGTGTCCGCTGTGCCCATTAACCAAGTTGCGTGAAGTTGCTG 1456
Db CTGAGATACACCCGCGTGTCCGCTGTGCCCATTAACCAAGTTGCGTGAAGTTGCTG 541

541 GGCCTCCGACGCTGTGAAATGTATCGAGACTTGCTTAACGAGCTGGGCAACTTTGG 600
Db GGCCTCCGACGCTGTGAAATGTATCGAGACTTGCTTAACGAGCTGGGCAACTTTGG 1457

1457 GGCCTCCGACGCTGTGAAATGTATCGAGACTTGCTTAACGAGCTGGGCAACTTTGG 1516
Db GGCCTCCGACGCTGTGAAATGTATCGAGACTTGCTTAACGAGCTGGGCAACTTTGG 601

601 ACTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATGCGTGTGTAA 660
Db ACTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATGCGTGTGTAA 1517

1517 ACTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATGCGTGTGTAA 1576
Db ACTGAGCTGTAAACGCCCCAGGCCATTAAGGTGTAAACCTGTGATGCGTGTGTAA 661

661 CGCCTTTGTTGCTGAATGAGTTGATGTAAATTAAGGAGTGAATTAAGTTAACT 720
Db CGCCTTTGTTGCTGAATGAGTTGATGTAAATTAAGGAGTGAATTAAGTTAACT 1577

1577 CGCCTTTGTTGCTGAATGAGTTGATGTAAATTAAGGAGTGAATTAAGTTAACT 1636
Db CGCCTTTGTTGCTGAATGAGTTGATGTAAATTAAGGAGTGAATTAAGTTAACT 721

721 TGCAATGCGTGTAAATGCGGCGCTTAAAGGATATTAATGCGGCGCTAACT 780
Db TGCAATGCGTGTAAATGCGGCGCTTAAAGGATATTAATGCGGCGCTAACT 1637

1637 TGCAATGCGTGTAAATGCGGCGCTTAAAGGATATTAATGCGGCGCTAACT 1696
Db TGCAATGCGTGTAAATGCGGCGCTTAAAGGATATTAATGCGGCGCTAACT 781

781 TGCTTAATCTGACCTCAATGAGGCTTGGAGGTTTGGAGATTTTCTGCTGTGCTA 840
Db TGCTTAATCTGACCTCAATGAGGCTTGGAGGTTTGGAGATTTTCTGCTGTGCTA 1697

1697 TGCTTAATCTGACCTCAATGAGGCTTGGAGGTTTGGAGATTTTCTGCTGTGCTA 1756
Db TGCTTAATCTGACCTCAATGAGGCTTGGAGGTTTGGAGATTTTCTGCTGTGCTA 841

841 ACTTGCTGAACAGAGCTCTAAACAGTACTCTTGTTTGAAGTTTCTGTGGGCTCAT 900
Db ACTTGCTGAACAGAGCTCTAAACAGTACTCTTGTTTGAAGTTTCTGTGGGCTCAT 1757

1757 ACTTGCTGAACAGAGCTCTAAACAGTACTCTTGTTTGAAGTTTCTGTGGGCTCAT 1816
Db ACTTGCTGAACAGAGCTCTAAACAGTACTCTTGTTTGAAGTTTCTGTGGGCTCAT 901

901 CCGAGGCAAGTATGCTGCAAGATTAAGAGATTAACAATGCGAATTTGAAGGCTTT 960
Db CCGAGGCAAGTATGCTGCAAGATTAAGAGATTAACAATGCGAATTTGAAGGCTTT 1817

1817 CCGAGGCAAGTATGCTGCAAGATTAAGAGATTAACAATGCGAATTTGAAGGCTTT 1876
Db CCGAGGCAAGTATGCTGCAAGATTAAGAGATTAACAATGCGAATTTGAAGGCTTT 961

961 TGAATCTGTGAGTGTGATTTGATTTTGAATCTGGTCAACAAGGCTTTTCCAG 1020
Db TGAATCTGTGAGTGTGATTTGATTTTGAATCTGGTCAACAAGGCTTTTCCAG 1020

1877 TGAATCTGTGAGTGTGATTTGATTTTGAATCTGGTCAACAAGGCTTTTCCAG 1936
Db TGAATCTGTGAGTGTGATTTGATTTTGAATCTGGTCAACAAGGCTTTTCCAG 1021

1021 AGAAGTCAATCAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 1080
Db AGAAGTCAATCAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 1937

1937 AGAAGTCAATCAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 1996
Db AGAAGTCAATCAAGCTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 1081

1081 TTTTGAATTTTAAAGATTAATGAGCGGAAGAACCCATCTGAGCGGGGGTAACTGCG 1140
Db TTTTGAATTTTAAAGATTAATGAGCGGAAGAACCCATCTGAGCGGGGGTAACTGCG 1997

1997 TTTTGAATTTTAAAGATTAATGAGCGGAAGAACCCATCTGAGCGGGGGTAACTGCG 1200

1141 TGGAATTTTCTGGGCAATGATCTGTGAGAGGCGTTGTGAGACAAAGATGCGCTGCTAC 1200
Db TGGAATTTTCTGGGCAATGATCTGTGAGAGGCGTTGTGAGACAAAGATGCGCTGCTAC 2057

2057 TGGAATTTTCTGGGCAATGATCTGTGAGAGGCGTTGTGAGACAAAGATGCGCTGCTAC 1201

1201 TGTTGCTTCCGTCGCGCCGCGGATTAATACCGAGCGAGAGCAGCAGCAGCAGAGG 1260
Db TGTTGCTTCCGTCGCGCCGCGGATTAATACCGAGCGAGAGCAGCAGCAGCAGAGG 2117

2117 TGTTGCTTCCGTCGCGCCGCGGATTAATACCGAGCGAGAGCAGCAGCAGCAGAGG 2176
Db TGTTGCTTCCGTCGCGCCGCGGATTAATACCGAGCGAGAGCAGCAGCAGCAGAGG 1281

1281 AAGCCAGGCGGCGGCGGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGACCTTC 1320
Db AAGCCAGGCGGCGGCGGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGACCTTC 2177

2177 AAGCCAGGCGGCGGCGGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGACCTTC 2236
Db AAGCCAGGCGGCGGCGGAGAGCAGAGCCCATGGAACCCGAGAGCCGCGCTGACCTTC 1321

1321 GGGATGGAATGTTGTAACAGTGGCTGAACTGTATCCAGAACTGAGAGCGCATTTTGAAT 1380
Db GGGATGGAATGTTGTAACAGTGGCTGAACTGTATCCAGAACTGAGAGCGCATTTTGAAT 2237

2237 GGGATGGAATGTTGTAACAGTGGCTGAACTGTATCCAGAACTGAGAGCGCATTTTGAAT 1381

1381 TACAGAGATGAGGAGGAGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 1440
Db TACAGAGATGAGGAGGAGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 2297

2297 TACAGAGATGAGGAGGAGGCTTAAAGGGGGTAAAGAGGAGCGGGGGCTTGTGAGGCTAC 1441

1441 AGAGAGGCTTNGAATCTAGCTTTTACCTTAATGACCAAGACACCGTCTGAGTATTAAC 1500
Db AGAGAGGCTTNGAATCTAGCTTTTACCTTAATGACCAAGACACCGTCTGAGTATTAAC 2357

2357 AGAGAGGCTTNGAATCTAGCTTTTACCTTAATGACCAAGACACCGTCTGAGTATTAAC 1501

1501 TTTTCAACAGATCAAGGATTAATGCGCTAAAGACTGTAATGCTGGGCGGAGATATTC 1560
Db TTTTCAACAGATCAAGGATTAATGCGCTAAAGACTGTAATGCTGGGCGGAGATATTC 2417

2417 TTTTCAACAGATCAAGGATTAATGCGCTAAAGACTGTAATGCTGGGCGGAGATATTC 1561

1561 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATGTTTGAAGAGCTATTAG 1620
Db CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATGTTTGAAGAGCTATTAG 2477

2477 CATAGAGAGCTGACCACTTACTGCTGACAGCCAGGGGATGTTTGAAGAGCTATTAG 1621

1621 GGTATATGCAAAAGGTGGCACTTAAAGCCAGATTGCAAGTACAAATCACTTTGAAA 1680
Db GGTATATGCAAAAGGTGGCACTTAAAGCCAGATTGCAAGTACAAATCACTTTGAAA 2537

2537 GGTATATGCAAAAGGTGGCACTTAAAGCCAGATTGCAAGTACAAATCACTTTGAAA 1681

1681 TATCAGAAATTTGTTGTAATTTCTGAGGAACGGGGCGGAGGTGAGATTAAGTACGAGAGA 1740
Db TATCAGAAATTTGTTGTAATTTCTGAGGAACGGGGCGGAGGTGAGATTAAGTACGAGAGA 2597

2597 TATCAGAAATTTGTTGTAATTTCTGAGGAACGGGGCGGAGGTGAGATTAAGTACGAGAGA 1741

1741 TAGGGTGGCTTTAGATGATGATTAATATATGTCGCGGGGTGCTTGGCATGAGACGG 1800
Db TAGGGTGGCTTTAGATGATGATTAATATATGTCGCGGGGTGCTTGGCATGAGACGG 2657

2657 TAGGGTGGCTTTAGATGATGATTAATATATGTCGCGGGGTGCTTGGCATGAGACGG 1801

1801 GGTGTTATTAATGATGATGATTTACTGCGCCCAATTTTACGGGTACGGTTTCTGCGC 1860
Db GGTGTTATTAATGATGATTTACTGCGCCCAATTTTACGGGTACGGTTTCTGCGC 2717

2717 GGTGTTATTAATGATGATTTACTGCGCCCAATTTTACGGGTACGGTTTCTGCGC 1861

1861 CAATACCAACCTTATCTTACACCGGTGAAGCTTATGAGGTTTAAACAATACCTGTGAGA 1920
Db CAATACCAACCTTATCTTACACCGGTGAAGCTTATGAGGTTTAAACAATACCTGTGAGA 2777

2777 CAATACCAACCTTATCTTACACCGGTGAAGCTTATGAGGTTTAAACAATACCTGTGAGA 1921

1921 AGCTGAGACGAGATTAAGGTTTCCGGGCTGTGCTTTTACTGCTGCTGAAGGGGGTGT 1980
Db AGCTGAGACGAGATTAAGGTTTCCGGGCTGTGCTTTTACTGCTGCTGAAGGGGGTGT 2837

2837 AGCTGAGACGAGATTAAGGTTTCCGGGCTGTGCTTTTACTGCTGCTGAAGGGGGTGT 1981

1981 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTAACCTTGGG 2040
Db GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTAACCTTGGG 2897

2897 GTGTGCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCTCTTTGAAAGGTGTAACCTTGGG 2041

2041 TATCTGTGAGAGGTTAATCTCAGGGTGGCCCAAAATGTCCTCCAGCTGTGTTGCTT 2100
Db TATCTGTGAGAGGTTAATCTCAGGGTGGCCCAAAATGTCCTCCAGCTGTGTTGCTT 2100

Db 2957 TATCCTGCTGAGGTAACCTCCAGAGGTGCGCCACCAATGTGGCTCCGACTGTGGTCTT 3016
Qy 2101 CATCTAGTGAAGGCTGGCTGTGATTAAGCATTAACATGTGTATGTGGCACTGCGAGGA 2160
Db 3017 CATCTAGTGAAGGCTGGCTGTGATTAAGCATTAACATGTGTATGTGGCACTGCGAGGA 3076
Qy 2161 CAGGAGCTCTCAGATGTGACCTGCTCGGACGGCAACTGTCACTGCTGCAAGACATTCA 2220
Db 3077 CAGGAGCTCTCAGATGTGACCTGCTCGGACGGCAACTGTCACTGCTGCAAGACATTCA 3136
Qy 2221 CGTAGCCAGCCTCTGCGCAAGGCTGCGCAGTGTGGAGCATTAACATTAAGTACCCGCTG 2280
Db 3137 CGTAGCCAGCCTCTGCGCAAGGCTGCGCAGTGTGGAGCATTAACATTAAGTACCCGCTG 3196
Qy 2281 TTCTTGATTTGGGTAAACAGAGAGGGGTGTCTTCACTTAACAAATGCAATTTGAGTCA 2340
Db 3197 TTCTTGATTTGGGTAAACAGAGAGGGGTGTCTTCACTTAACAAATGCAATTTGAGTCA 3256
Qy 2341 CACTAAGATATTGCTTGAGCCGAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGGA 2400
Db 3257 CACTAAGATATTGCTTGAGCCGAGAGCATGTCCAAAGGTGAACCTGAACGGGGTGTGGA 3316
Qy 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTAGCATGAGACCCGACCAAGTGCAGACC 2460
Db 3317 CATGACCATGAAGATCTGGAAGGTGCTGAGGTAGCATGAGACCCGACCAAGTGCAGACC 3376
Qy 2461 CTGGAAGTGTGCGGTAAACATTTAAGAACACAGCCTGTGATGTGTAATGTAACCGAGGA 2520
Db 3377 CTGGAAGTGTGCGGTAAACATTTAAGAACACAGCCTGTGATGTGTAATGTAACCGAGGA 3436
Qy 2521 GCTGAGGCCCATGCACTGTGTGCTGACCTGCAACCGCCTGATGTTGGCTCTAGCGATGA 2580
Db 3437 GCTGAGGCCCATGCACTGTGTGCTGACCTGCAACCGCCTGATGTTGGCTCTAGCGATGA 3496
Qy 2581 AGATACAGATTGAG 2594
Db 3497 AGATACAGATTGAG 3510

RESULT 14
US-09-782-378A-5
; Sequence 5, Application US/09782378A
; Patent No. US20020102731A1
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandelon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONY-04970
; CURRENT APPLICATION NUMBER: US/09/782,378A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: Human adenovirus type 5
; US-09-782-378A-5

Query Match 100.0%; Score 2594; DB 9; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCGATCTTACCTGCGCAGAGGCTGCTTTCACCAAGCATGACGAGAGATGAAGAGGT 60
Db 917 ATCGATCTTACCTGCGCAGAGGCTGCTTTCACCAAGCATGACGAGAGATGAAGAGGT 976
Qy 61 GAGAGTTTGTGTTAGATTATGTGAGACACCCCGGGACCGGTTGCAAGTCTTGTCAATTAT 120
Db 977 GAGAGTTTGTGTTAGATTATGTGAGACACCCCGGGACCGGTTGCAAGTCTTGTCAATTAT 1036

Qy 121 CACCGAGGAATACGGGGGAGCCGAGATATTATGTTGCTGCTTGTCTATATGAGACCTGT 180
Db 1037 CACCGAGGAATACGGGGGAGCCGAGATATTATGTTGCTGCTTGTCTATATGAGACCTGT 1096
Qy 181 GGCATGTTTGTCTACAGTAAATGTAATTAAGGCACTGAGTGTGATAGAGTGTGGTGTG 240
Db 1097 GGCATGTTTGTCTACAGTAAATGTAATTAAGGCACTGAGTGTGATAGAGTGTGGTGTG 1156
Qy 241 GTGTGTAATTTTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGAAATTTGTATGTGA 300
Db 1157 GTGTGTAATTTTTTTTTTAAATTTTACAGTTTGTGTGTTTAAAGAAATTTGTATGTGA 1216
Qy 301 TTTTAAAAAGGCTGTGTCTGAACCTGAGCTGAGCCCGAGCCAGAACCGGAGCCTG 360
Db 1217 TTTTAAAAAGGCTGTGTCTGAACCTGAGCTGAGCCCGAGCCAGAACCGGAGCCTG 1276
Qy 361 CAAGACCTACCCGCGTCTTAAATGAGCGCTGCTATCTTGAGACGCCCGACATCACTG 420
Db 1277 CAAGACCTACCCGCGTCTTAAATGAGCGCTGCTATCTTGAGACGCCCGACATCACTG 1336
Qy 421 TGTCTAAGAAATGCAATAGTAATGTAACGATAGCTGTGACTCGGTCCTTTCTTAACACACTC 480
Db 1337 TGTCTAAGAAATGCAATAGTAATGTAACGATAGCTGTGACTCGGTCCTTTCTTAACACACTC 1396
Qy 481 CTGAGATACACCCGCGTGTCCCGCTGTGCCCATTTAAACAGTGTGCGGTGAGAGTGTG 540
Db 1397 CTGAGATACACCCGCGTGTCCCGCTGTGCCCATTTAAACAGTGTGCGGTGAGAGTGTG 1456
Qy 541 GGCCTGCGCAGGCTGTGGAATGTATGAGGACTTGTAAAGCACTGTGGCAACTTTTG 600
Db 1457 GGCCTGCGCAGGCTGTGGAATGTATGAGGACTTGTAAAGCACTGTGGCAACTTTTG 1516
Qy 601 ACTTGAAGCTGTAAACGCCGCCATTAAGGTGTAACCTGTATGTGTGTGTGTTAA 660
Db 1517 ACTTGAAGCTGTAAACGCCGCCATTAAGGTGTAACCTGTGTATGTGTGTGTTAA 1576
Qy 661 CGCCTTGTGTTGCTGAATGAGTTGATGTAAATTAAGGAGTGAAGTAATGTTAACT 720
Db 1577 CGCCTTGTGTTGCTGAATGAGTTGATGTAAATTAAGGAGTGAAGTAATGTTAACT 1636
Qy 721 TGCATGCGGTGTTAAATGAGGCGGGGCTTAAAGGTAATTAATGCGCGGTGCTAACT 780
Db 1537 TGCATGCGGTGTTAAATGAGGCGGGGCTTAAAGGTAATTAATGCGCGGTGCTAACT 1696
Qy 781 TGGTTAATCTGACCTATGAGAGGCTTGGAGTGTGTTGAAAGATTTTCTGTGCTGCTA 840
Db 1697 TGGTTAATCTGACCTATGAGAGGCTTGGAGTGTGTTGAAAGATTTTCTGTGCTGCTA 1756
Qy 841 ACTTGTGGAACAGAGCTCTTAACAGTACTCTTGTGTTGAGGTTTCTGTGAGGCTCAT 900
Db 1757 ACTTGTGGAACAGAGCTCTTAACAGTACTCTTGTGTTGAGGTTTCTGTGAGGCTCAT 1816
Qy 901 CCGAGGCAAGTTAAGTCTGCAAGATTAAAGAGATTAAAGTGAAGTGAAGGCTTT 960
Db 1817 CCGAGGCAAGTTAAGTCTGCAAGATTAAAGAGATTAAAGTGAAGTGAAGGCTTT 1876
Qy 961 TGAATCTGTGTGAGCTGTTTGAATCTTGAATCTGAGTCAACAGGCGCTTTTCCAG 1020
Db 1877 TGAATCTGTGTGAGCTGTTTGAATCTTGAATCTGAGTCAACAGGCGCTTTTCCAG 1936
Qy 1021 AGAAGTCATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGCTGTGCTT 1080
Db 1937 AGAAGTCATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGCTGTGCTT 1996
Qy 1081 TTTTGAAGTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTATCCTGC 1140
Db 1997 TTTTGAAGTTTAAAGATTAATGAGCGAAGAAACCATCTGAGCGGGGGTATCCTGC 2056
Qy 1141 TGAATTTTCTGCGCATGATCTGTGAGAGGCTTGTGAGACACAAGAAATGCTGTCTAC 1200
Db 2057 TGAATTTTCTGCGCATGATCTGTGAGAGGCTTGTGAGACACAAGAAATGCTGTCTAC 2116

QY	1201	GGTGTCTTCGGTCCGCCCGGGAATTAATACGAGCGAGAGACGAGACGACGAGAG	1260
Db	2117	TGTTGTCTTCGGTCCGCCCGGGAATTAATACGAGCGAGAGACGAGACGAGAGG	2176
QY	1261	AAGCCAGCGCGCGCGGACGAGACGAGACCCCATGAAACCCGAGAGCCGGCTGACCTC	1320
Db	2177	AAGCCAGCGCGCGCGGACGAGACGAGACCCCATGAAACCCGAGAGCCGGCTGACCTC	2236
QY	1331	GGGAATGAATGTTGACAGGTGGCTGAACCTGTATCCAGAACTGAGCGCATTTTGACAA	1380
Db	2237	GGGAATGAATGTTGACAGGTGGCTGAACCTGTATCCAGAACTGAGCGCATTTTGACAA	2296
QY	1381	TACAGAGATGGGCGAGGGGCTTAAGGGGGTTAAAGGGAGCGGGGGCTTTGAGGCTAC	1440
Db	2287	TACAGAGATGGGCGAGGGGCTTAAGGGGGTTAAAGGGAGCGGGGGCTTTGAGGCTAC	2356
QY	1441	AGAGAGGCTAGGAATCTAGCTTTAGCTTAATGACACAGACCGCTCTGAGTGTATAC	1500
Db	2357	AGAGAGGCTAGGAATCTAGCTTTAGCTTAATGACACAGACCGCTCTGAGTGTATAC	2416
QY	1501	TTTTCAACAGATCAAGATTAATTGGCTTAATGAGCTTGATCTGGCGCAGAAATATC	1560
Db	2417	TTTTCAACAGATCAAGATTAATTGGCTTAATGAGCTTGATCTGGCGCAGAAATATC	2476
QY	1551	CATAGAGAGCTGACCACTTACTGGCTGCACACGAGGGATGATTTGAGAGGCTATAG	1620
Db	2477	CATAGAGAGCTGACCACTTACTGGCTGCACACGAGGGATGATTTGAGAGGCTATAG	2536
QY	1621	GGTATATCAAGAAGTGCACCTTAAGGCCAGATTTGCAAGTACAAAGATCAGCAACTTGTAA	1680
Db	2537	GGTATATCAAGAAGTGCACCTTAAGGCCAGATTTGCAAGTACAAAGATCAGCAACTTGTAA	2596
QY	1681	TATCAGGAATGTTGCTACATTTCTGGGAACGGGGCCGAGGTGAGATAGATACGAGGA	1740
Db	2597	TATCAGGAATGTTGCTACATTTCTGGGAACGGGGCCGAGGTGAGATAGATACGAGGA	2656
QY	1741	TAGGTTGGCTTTAGATGTACATGATTAATATGTGGCCGGGGGTGCTTGGCATGACGCG	1800
Db	2657	TAGGTTGGCTTTAGATGTACATGATTAATATGTGGCCGGGGGTGCTTGGCATGACGCG	2716
QY	1801	GGTGGTTATTAAGATGTAAAGTTTACTGGGCCCAATTTTAGCGGTACGGTTTCCTGGC	1860
Db	2717	GGTGGTTATTAAGATGTAAAGTTTACTGGGCCCAATTTTAGCGGTACGGTTTCCTGGC	2776
QY	1861	CAATACCAACCTTATCTTACAACGGTGAAGCTTCTATGGGTTTAAACAATACCTGTGGA	1920
Db	2777	CAATACCAACCTTATCTTACAACGGTGAAGCTTCTATGGGTTTAAACAATACCTGTGGA	2836
QY	1921	AGCTTGACCGATGTAAAGGTTTCGGGGCTGTGCTTTTACTGCTGCGAAGGGGGTGT	1980
Db	2837	AGCTTGACCGATGTAAAGGTTTCGGGGCTGTGCTTTTACTGCTGCGAAGGGGGTGT	2896
QY	1981	GTTGTGCCCCAAAAGCGGGCTTAAATTAAGAAATGCTCTTTTAAAGGTACTCTGGG	2040
Db	2897	GTTGTGCCCCAAAAGCGGGCTTAAATTAAGAAATGCTCTTTTAAAGGTACTCTGGG	2956
QY	2041	TATCTGTCTGAGGGTAACTCAGGGTGCGCACAAATGTGGCTCCGACTGTGTGTTCTT	2100
Db	2957	TATCTGTCTGAGGGTAACTCAGGGTGCGCACAAATGTGGCTCCGACTGTGTGTTCTT	3016
QY	2101	CATGTAGTGAATAAGCTGGCTGTGATTAAGCATPAACATGTATGTGGCAACTGCGAGA	2160
Db	3017	CATGTAGTGAATAAGCTGGCTGTGATTAAGCATPAACATGTATGTGGCAACTGCGAGA	3076
QY	2161	CAGGGGCTCTAGATGCTGACCTGTCTGGAACGGAACCTGTCTGGAAGACATTTCA	2220
Db	3077	CAGGGGCTCTAGATGCTGACCTGTCTGGAACGGAACCTGTCTGGAAGACATTTCA	3136
QY	2221	CGTAGCCAGCACTCTCGCAAGGCTGGCCAGTGTTTGAGATTAACATACGACCGCTG	2280
Db	3137	CGTAGCCAGCACTCTCGCAAGGCTGGCCAGTGTTTGAGATTAACATACGACCGCTG	3196
QY	2281	TTCTTTCGATTTGGGTAAACAGAGGGGGGTGTCTTACCTTACCAATGCAATTTGAATCA	2340

```

Db      3197  TTCTGTCATTGGGTAAACAGAGAGGGGGTGTCTTCACTTACCAAGTCAATTGGAGTCA 325656
QY      2341  CACTAAGATATTGGCTGTGAGCCCGAGAGCATGTCCAAAGGTGAACCGGGTGTTTGA 24000
Db      3257  CACTAAGATATTGGCTGTGAGCCCGAGAGCATGTCCAAAGGTGAACCGGGTGTTTGA 3316
QY      2401  CATGACCATGAAGATCTTGGAAGGTGCTGAGGTACGATGAGACCCGACCAAGTGCAGAC 24600
Db      3317  CATGACCATGAAGATCTTGGAAGGTGCTGAGGTACGATGAGACCCGACCAAGTGCAGAC 33767
QY      2461  CTGGAGGTGGCGGGTAAACATATTAGGAACCAACCTGTGATGCTGATGAGACCGAGGA 25200
Db      3377  CTGGAGGTGGCGGGTAAACATATTAGGAACCAACCTGTGATGCTGATGAGACCGAGGA 34368
QY      2521  GCTGAGGCCCATGACATGCTGCTGCTGCTGACCCGCGCTGAGTTGGCTTACGATGA 25800
Db      3437  GCTGAGGCCCATGACATGCTGCTGCTGCTGACCCGCGCTGAGTTGGCTTACGATGA 34968
QY      2581  AGATACAGATTGAG 2594
Db      3497  AGATACAGATTGAG 3510

RESULT 15
US-09-739-007-43
; Sequence 43, Application US/09739007
; Publication No. US20030170885A1
; GENERAL INFORMATION:
; APPLICANT: IMER, Jean-Luc
;              MEHLALI, Majid
;              PAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
;                   COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSSEE: BURNS, DOANE, SWECKER & MATHEIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,007
; FILING DATE: 19-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/379,452
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35935 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-739-007-43

Query Match      100.0%; Score 2594; DB 10; Length 35935;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 ATGATCTTACTGCGACGAGGCTGGCTTTCCACCAGTGAACAAGAGAGGCT 60
Db 917 ATCAATCTTACTGCGACGAGGCTGGCTTTCCACCAGTGAACAAGAGAGGCT 976
OY 61 GAGAGTTTGTAGTATGATGATGAGACCCCGGGACGGTTGACAGTCTTGTCAATAT 120
Db 977 GAGAGTTTGTAGTATGATGATGAGACCCCGGGACGGTTGACAGTCTTGTCAATAT 1036
OY 121 CACCGAGGAATACGGGGGACCCAGATATTAATGTGTGCTTTGCTATATAGACCTGT 180
Db 1037 CACCGAGGAATACGGGGGACCCAGATATTAATGTGTGCTTTGCTATATAGACCTGT 1096
OY 181 GGCATGTTGTCTACATGATGAGAAATTAATGGGAGAGGGGATAGAGTGGGTTTG 240
Db 1097 GGCATGTTGTCTACATGATGAGAAATTAATGGGAGAGGGGATAGAGTGGGTTTG 1156
OY 241 GTGTGTAAATTTTTTTTAAATTTTACAGTTTGTGTTAAAGAAATTTGTATGTGA 300
Db 1157 GTGTGTAAATTTTTTTTAAATTTTACAGTTTGTGTTTAAAGAAATTTGTATGTGA 1216
OY 301 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCGAGCCAGAACCGAGCTTG 360
Db 1217 TTTTAAAAAGTCTGTGTCTGAACCTGAGCTGAGCCGAGCCAGAACCGAGCTTG 1276
OY 361 CAAGACCTACCCGCGCTCTAAATGAGGCGCTGCTATCTGAGAGCCCGACATCACTG 420
Db 1277 CAAGACCTACCCGCGCTCTAAATGAGGCGCTGCTATCTGAGAGCCCGACATCACTG 1336
OY 421 TGTCTAGAGAAATGCAATAGTATGATGATGATGATGATGATGATGATGATGATG 480
Db 1337 TGTCTAGAGAAATGCAATAGTATGATGATGATGATGATGATGATGATGATGATG 1396
OY 481 CTGAGATCAACCCGCGTGTCCCGCTGTGCGCCCAATTAACCAAGTGGAGAGTTGGT 540
Db 1397 CTGAGATCAACCCGCGTGTCCCGCTGTGCGCCCAATTAACCAAGTGGAGAGTTGGT 1456
OY 541 GGCCTGCGCAGGCGTGTGAATGTATCGAGGACTTGAAGAGCTTGAAGAGCTTGG 600
Db 1457 GGCCTGCGCAGGCGTGTGAATGTATCGAGGACTTGAAGAGCTTGAAGAGCTTGG 1516
OY 601 ACTTGAGCTGTAAACGCCCGACAGCCATTAAGGTGAACCTGTGATGGCTGTGTAA 660
Db 1517 ACTTGAGCTGTAAACGCCCGACAGCCATTAAGGTGAACCTGTGATGGCTGTGTAA 1576
OY 661 CGCCTTGTGTGCTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 1577 CGCCTTGTGTGCTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1636
OY 721 TGCATGGGCTGTAAATGGGCGGGGCTTAAAGGATATTAATGGCGGTGGGCTAACT 780
Db 1637 TGCATGGGCTGTAAATGGGCGGGGCTTAAAGGATATTAATGGCGGTGGGCTAACT 1696
OY 781 TGTATACATCTGAACCTCATGAGAGCTTGGAGTGTGTTGAAGATTTTCTGCTGTG 840
Db 1697 TGTATACATCTGAACCTCATGAGAGCTTGGAGTGTGTTGAAGATTTTCTGCTGTG 1756
OY 841 ACTTGCTGAACAGAGCTTGAACAGTACCTCTTGTGTTTGAAGTTTCTGTGGGCTCAT 900
Db 1757 ACTTGCTGAACAGAGCTTGAACAGTACCTCTTGTGTTTGAAGTTTCTGTGGGCTCAT 1816
OY 901 CCCAGGCAAAAGTTAATCTGCAAGATTAAGAGAGATTAAGAGGGAATTTGAAGGCTT 960
Db 1817 CCCAGGCAAAAGTTAATCTGCAAGATTAAGAGAGATTAAGAGGGAATTTGAAGGCTT 1876
OY 961 TGAATCTGTGTGAGCTGTGTTGATCTTTGAATCTGGGTCAACGAGCGCTTTTCCAG 1020
Db 1877 TGAATCTGTGTGAGCTGTGTTGATCTTTGAATCTGGGTCAACGAGCGCTTTTCCAG 1936
OY 1021 AGAAGCTATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 1080
Db 1937 AGAAGCTATCAAGACTTTGATTTTTCACACCGGGGCGGCTGCGGCTGTGCTT 1996

OY 1081 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCAATCTGAGCGGGGGTACTGTC 1140
Db 1997 TTTTGAATTTTAAAGATTAATGAGCGAAGAAACCAATCTGAGCGGGGGTAACTGTC 2056
OY 1141 TGAATTTTCTGGCCATCTGTGAGAGCGTTGTGAACACAAGATTCCTGCTTAC 1200
Db 2057 TGAATTTTCTGGCCATCTGTGAGAGCGTTGTGAACACAAGATTCCTGCTTAC 2116
OY 1201 TGTGTCTTCCTGTCCTGCGCCGCTTAATACGAGGAGGACACACAGAGAGAGG 1260
Db 2117 TGTGTCTTCCTGTCCTGCGCCGCTTAATACGAGGAGGACACACAGAGAGAGG 2176
OY 1261 AAGCAGCGCGCGCGCAGAGAGAGCCATGAAACCGAGAGCGGCTGTGACCTTC 1320
Db 2177 AAGCAGCGCGCGCGCAGAGAGAGCCATGAAACCGAGAGCGGCTGTGACCTTC 2236
OY 1321 GGAATGAATGTTGTACAGGTGCTGAACCTGTATCCAGAACTGAGACGCAATTTTGACAT 1380
Db 2237 GGAATGAATGTTGTACAGGTGCTGAACCTGTATCCAGAACTGAGACGCAATTTTGACAT 2296
OY 1381 TACAGAGATGAGGAGGAGGCTTAAGAGGGGTAAAGAGGAGGGGGGCTTGTGAGCTTAC 1440
Db 2297 TACAGAGATGAGGAGGAGGCTTAAGAGGGGTAAAGAGGAGGGGGCTTGTGAGCTTAC 2356
OY 1441 AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGCTCTGAGTATTAC 1500
Db 2257 AGAGAGGCTAGGAATCTAGCTTTTACCTTAATGACAGACACCGCTCTGAGTATTAC 2416
OY 1501 TTTTCAACAGATCAAGATTAATGCGCTAATGACCTTGTGCTGCGCAGAAATATTC 1560
Db 2417 TTTTCAACAGATCAAGATTAATGCGCTAATGACCTTGTGCTGCGCAGAAATATTC 2476
OY 1561 CATAGACAGCTGACCACTTAATGCTGCGCAGCGGAGGAGTATTTAGAGGGCTATTAG 1620
Db 2477 CATAGACAGCTGACCACTTAATGCTGCGCAGCGGAGGAGTATTTAGAGGGCTATTAG 2536
OY 1621 GGTATATGCAAAAGGTGCACTTAAGCCAGATTGCAATGACAGATCAAGAACTTGTAA 1680
Db 2537 GGTATATGCAAAAGGTGCACTTAAGCCAGATTGCAATGACAGATCAAGAACTTGTAA 2596
OY 1681 TATCAGAAATTTGTTCTACATTTCTGAGAACCGGGCGAGGTGAGATATACGAGGA 1740
Db 2597 TATCAGAAATTTGTTCTACATTTCTGAGAACCGGGCGAGGTGAGATATACGAGGA 2656
OY 1741 TAGGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Db 2657 TAGGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2716
OY 1801 GGTGTTATTAATGATGATGAAGTTTACCTGCCCCCAATTTTATGCGGTACGTTTCTG 1860
Db 2717 GGTGTTATTAATGATGATGAAGTTTACCTGCCCCCAATTTTATGCGGTACGTTTCTG 2776
OY 1861 CAATACCAACCTTAATCTTACAGGCTGTAAGCTTCTATGAGTTTAAACAATACCTGTGGA 1920
Db 2777 CAATACCAACCTTAATCTTACAGGCTGTAAGCTTCTATGAGTTTAAACAATACCTGTGGA 2836
OY 1921 AGCTTGACCGAATGAAGGTTTGGGGCTGCTTTTACATGCTGCTGGAAGGGGGTGT 1980
Db 2837 AGCTTGACCGAATGAAGGTTTGGGGCTGCTTTTACATGCTGCTGGAAGGGGGTGT 2896
OY 1981 GTGTGCCCCCAAAAGCAGAGGCTTCAATTAAGAAATGCTCTTTGAAGAGTACCTTGGG 2040
Db 2897 GTGTGCCCCCAAAAGCAGAGGCTTCAATTAAGAAATGCTCTTTGAAGAGTACCTTGGG 2956
OY 2041 TATCTGTCTGAGGGTAACTTCAGAGGTGCGCAATATGTGCTTCCGACTGTGTTGCTT 2100
Db 2957 TATCTGTCTGAGGGTAACTTCAGAGGTGCGCAATATGTGCTTCCGACTGTGTTGCTT 3016
OY 2101 CATGCTAGTGAAGACGCTGCTGATTTTAAGCAATTAATGTTATGTGCACTGCGAGGA 2160
Db 3017 CATGCTAGTGAAGACGCTGCTGATTTTAAGCAATTAATGTTATGTGCACTGCGAGGA 3076
OY 2161 CAGGCGCTCTCAGATGTGACTGCTGCGACGGAACCTGTCACTGCTGAAGACCATTTCA 2220

Db	3077	CAGGECCTCAGATGCTGACCTGCTCGGACGGCACTGTCACTGCTGAAACCATTC	3136
QY	2221	CGTACCCAGCCACTCTCGCAAGGCTGCGCACTGTTTGAGCATTAACATCTGACCCGCTG	2280
Db	3137	CGTAGCCAGCCACTCTCGCAAGGCTGCGCACTGTTTGAGCATTAACATCTGACCCGCTG	3196
QY	2281	TTCCCTTGATTTGGGTAACAGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCA	2340
Db	3197	TTCCCTTGATTTGGGTAACAGAGGGGGGTGTTCTTACCTTACCAATGCAATTTGAGTCA	3256
QY	2341	CACCTAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTGTA	2400
Db	3257	CACCTAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTGTA	3316
QY	2401	CATGACCATGAAGATCTGGAAGGTGCTGAGTACGATGAGACCCGACAGGTGCAGACC	2460
Db	3317	CATGACCATGAAGATCTGGAAGGTGCTGAGTACGATGAGACCCGACAGGTGCAGACC	3376
QY	2461	CTGCGAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGCTGATGTGACCGAGGA	2520
Db	3377	CTGCGAGTGTGGCGGTAAACATATTAGAACCAAGCTGTGATGCTGATGTGACCGAGGA	3436
QY	2521	GCTGAGGCCCGATCACTTGCTGCTGACCCGCGCTGAGTTGGCTCTAGCGATGA	2580
Db	3437	GCTGAGGCCCGATCACTTGCTGCTGACCCGCGCTGAGTTGGCTCTAGCGATGA	3496
QY	2581	AGATACAGATTGAG	2594
Db	3497	AGATACAGATTGAG	3510

Search completed: October 31, 2005, 01:51:06
 Job time : 2043 secs

This Page Blank (uspto)